

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 6.44149 Seconds
(without alignments)
104.507 Million cell updates/sec

Title: US-09-641-801-1

Perfect score: 7

Sequence: 1 MQPPPLP 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database: PIR_76:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	71.4	18	2	PC2280
2	4	57.1	17	2	S1299
3	4	57.1	13	2	A60856
4	4	57.1	14	2	S1129
5	4	57.1	15	2	B39109
6	4	57.1	16	2	B58503
7	4	57.1	20	2	T44453
8	4	57.1	20	2	PC2030
9	3	42.9	7	2	P70283
10	3	42.9	8	2	S10783
11	3	42.9	10	2	PC2171
12	3	42.9	10	2	C39745
13	3	42.9	10	2	A36454
14	3	42.9	11	2	YHRT
15	3	42.9	11	2	YHHU
16	3	42.9	11	2	YHBO
17	3	42.9	11	2	YHXA
18	3	42.9	11	2	YHJFHY
19	3	42.9	11	2	D45900
20	3	42.9	12	2	S70337
21	3	42.9	12	2	PN0663
22	3	42.9	12	2	B39690
23	3	42.9	13	2	D39690
24	3	42.9	13	2	S21152
25	3	42.9	13	2	A05174
26	3	42.9	13	2	S09716
27	3	42.9	13	2	I84603
28	3	42.9	13	2	G61458
29	3	42.9	13	2	A86126

30	42.9	14	2	S12304	protein kinase (EC
31	42.9	15	2	PQ0545	capsid protein VP1
32	42.9	15	2	PT0037	light harvesting c
33	42.9	15	2	PA0060	protein QF200037 -
34	42.9	15	2	B61457	alpha-glucosidase
35	42.9	15	2	A60221	apolipoprotein A-I
36	42.9	16	2	I57530	gene c-fms protein
37	42.9	16	2	S57517	T cell receptor be
38	42.9	16	2	JH0517	insulin-like growt
39	42.9	17	2	S57991	hydroxyproline-ric
40	42.9	17	2	S59481	hydroxyproline-ric
41	42.9	17	2	S10786	enamelin, 28K - bo
42	42.9	18	2	S04229	N4-(beta-N-acetyl
43	42.9	18	2	I52614	u-plasminogen acti
44	42.9	18	2	C56211	progesterone recep
45	42.9	18	2	A54195	Na+/K+-exchanging
46	42.9	19	2	S60633	H+-transporting tw
47	42.9	19	2	G56819	PS I complex subun
48	42.9	19	2	S59486	cell wall protein,
49	42.9	19	2	A37968	neural surface pro
50	42.9	19	2	PH1352	Ig heavy chain DJ
51	42.9	19	2	S50018	hyaluronidase - sh
52	42.9	19	2	S25715	hypothetical prote
53	42.9	20	2	S29817	cytochrome P450 2C
54	42.9	20	2	D42842	antifungal 2S stor
55	42.9	20	2	S65605	dimeric protein (B
56	42.9	20	2	S46479	retinoid-X-recepto
57	42.9	20	2	A42267	J-kappa recombinat
58	42.9	20	2	A31516	lectin, galactose/
59	28.6	4	2	A32039	tyrosine-melanocyt
60	28.6	5	1	HOR0HA	proctolin - Americ
61	28.6	5	2	JN0860	peptidyl-di-peptida
62	28.6	5	2	E42364	flagellar protein
63	28.6	5	2	B37388	acid proteinase li
64	28.6	5	2	A60411	proctolin - Atlant
65	28.6	6	2	I67345	MHC H2-K-k cell su
66	28.6	6	4	A35039	hypothetical colla
67	28.6	7	2	A61081	tyrptophyllin, bas
68	28.6	7	2	PC1316	large granule L3 c
69	28.6	7	2	B39040	calsequestrin, fas
70	28.6	7	2	I48105	dihydrofolate redu
71	28.6	7	2	I48086	DNA topoisomerase
72	28.6	7	2	S66442	glutathione S-tran
73	28.6	7	2	A39690	neural cell adhesi
74	28.6	7	2	A58718	carnocin UI49 - Ca
75	28.6	7	2	S45648	Na+-transporting A
76	28.6	8	2	E24749	neuropeptide B - b
77	28.6	8	2	S43971	tumor-associated a
78	28.6	8	2	B39745	endoglycosylcerami
79	28.6	8	2	S16324	hypothetical prote
80	28.6	8	2	S21288	lectin - potato (f
81	28.6	8	2	PT0030	inulinase (EC 3.2.
82	28.6	8	2	G33098	205K exoantigen -
83	28.6	8	2	E47393	neuropeptide calla
84	28.6	8	2	A14683	aspartate transami
85	28.6	8	2	PT0559	T-cell receptor be
86	28.6	8	2	I57018	gene Cfr protein
87	28.6	8	2	C39630	neural cell adhesi
88	28.6	8	2	A35180	neural proteinase
89	28.6	8	4	I54017	granulocyte-colony
90	28.6	9	2	A91466	oxytocin - hippopo
91	28.6	9	2	A92774	oxytocin - spotted
92	28.6	9	2	A93147	oxytocin - finback
93	28.6	9	2	A93408	oxytocin - Austral
94	28.6	9	2	B90667	oxytocin - rabbit
95	28.6	9	2	PW0002	chlorophyll a/b-bi
96	28.6	9	2	A61358	bradykinin-like pe
97	28.6	9	2	A61057	Thr-6 bradykinin -
98	28.6	9	2	A26744	bradykinin-like pe
99	28.6	9	2	A61363	bradykinin - commo
100	28.6	9	2	A60579	bradykinin-like pe

ALIGNMENTS

RESULT 1

PC2280
prolylendopeptidase-inhibiting peptide - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-May-1997
C:Accession: PC2280
R:Ohmori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.
Biochem. Biophys. Res. Commun. 202, 809-815, 1994
A:Title: Isolation of prolylendopeptidase-inhibiting peptides from bovine brain.
A:Reference number: PC2280; PMID:94324971; PMID:8048952
A:Accession: PC2280
A:Molecule type: protein
A:Residues: 1-18 <OHM>
A:Experimental source: brain
C:Superfamily: cytoskeletal keratin

Query Match 71.4%; Score 5; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
| | | | |
Db 2 PPPLP 6

RESULT 2

S71299
ICL2 protein - Paramecium tetraurelia (fragment)
C:Species: Paramecium tetraurelia
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
C:Accession: S71299
R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
Eur. J. Biochem. 238, 121-128, 1996
A:Title: Characterization of centrin genes in Paramecium.
A:Reference number: S71298; PMID:96248429; PMID:8665928
A:Accession: S71299
A:Molecule type: protein
A:Residues: 1-7 <MAD>
A:Experimental source: strain d4-2
C:Genetics:
A:Genetic code: SGCS

Query Match 57.1%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPP 5
| | | |
Db 2 QPPP 5

RESULT 3

A60856
inhibin alpha chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60856
R:Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wattenhall
J. Endocrinol. 113, 213-221, 1987
A:Title: Isolation of inhibin from ovine follicular fluid.
A:Reference number: A60856; PMID:87224684; PMID:3585232
A:Accession: A60856
A:Molecule type: protein
A:Residues: 1-13 <LEV>
C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.
C:Superfamily: inhibin
C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match 57.1%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PPPLP 7
| | | | |
Db 3 PPPLP 6

RESULT 4

S11129
phosphoprotein, bone - chicken (fragment)
C:Species: Gallus gallus (Chicken)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 25-Oct-1996
C:Accession: S11129
R:Mikuni-Takagaki, Y.; Glimcher, M.J.
Biochem. J. 288, 585-591, 1990
A:Title: Post-translational processing of chicken bone phosphoproteins. Identification
A:Reference number: S11127; PMID:90303246; PMID:2363696
A:Accession: S11129
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <MIK>
C:Keywords: phosphoprotein

Query Match 57.1%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 6
| | | | |
Db 5 PPPLP 8

RESULT 5

B39109
hypothetical 1.5K protein - hepatitis C virus
N:Alternate names: hypothetical protein 2
C:Species: hepatitis C virus
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C:Accession: B39109; JQ1585
R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Teko
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A:Reference number: A39109; PMID:91156678; PMID:1705704
A:Accession: B39109
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-15 <HAN>
A:Cross-references: GB:M58406
R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992
A:Title: Cloning and sequencing of the structural region and expression of putative
A:Reference number: JQ1584; PMID:92300349; PMID:1318944
A:Accession: JQ1585
A:Molecule type: genomic RNA
A:Residues: 1-15 <KUM>
A:Experimental source: strain U.K.

Query Match 57.1%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPPLP 7
| | | | |
Db 9 PPPLP 12

RESULT 6

E58503
superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)
N:Alternate names: 21.3K bladder and kidney stone protein
C:Species: unidentified bacterium
C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 05-Mar-1999
C:Accession: E58503

R;Binette, J.P.; Binette, M.B.
 Submitted to the Protein Sequence Database, October 1996
 A;Description: The proteins of kidney and gallbladder stones.
 A;Reference number: A58501
 A;Accession: E58503
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-16 <BN>
 A;Experimental source: human bladder and kidney stones
 C;Function:
 A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C;Keywords: metalloprotein; oxidoreductase

Query Match 57.1%; Score 4; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
 Db 6 PPLP 9

RESULT 7
 T44453
 acetyl-CoA synthetase [imported] - Pseudomonas aeruginosa (fragment)
 C;Species: Pseudomonas aeruginosa
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C;Accession: T44453
 R;Nishijyo, T.; Park, S.M.; Lu, C.D.; Itoh, Y.; Abdelal, A.T.
 J. Bacteriol. 180, 5559-5566, 1998
 A;Title: Molecular characterization and regulation of an operon encoding a system for the
 A;Reference number: 222777; MUID:99008987; PMID:9791103
 A;Accession: T44453
 A;Status: preliminary; translated from GE/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-20 <NIS>
 A;Cross-references: EMBL:AF012637; NID:92668593; PIDN:AAC71069.1; PID:92668594
 A;Experimental source: strain PAOI

Query Match 57.1%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
 Db 10 PPLP 13

RESULT 8
 PC2030
 tumor-derived adhesion factor - human (fragment)
 N;Alternate names: 30K protein
 C;Species: Homo sapiens (man)
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 21-Jan-2000
 C;Accession: PC2030
 R;Akao, K.; Okabe, Y.; Funahashi, K.; Yoshitake, Y.; Nishikawa, K.; Yasumitsu, H.; Ume
 Biochem. Biophys. Res. Commun. 198, 1046-1053, 1994
 A;Title: Cell adhesion activity of a 30-kDa major secreted protein from human bladder ca
 A;Reference number: PC2030; MUID:94161713; PMID:8117260
 A;Accession: PC2030
 A;Molecule type: protein
 A;Residues: 1-20 <AKA>
 A;Experimental source: cell line EJ-1
 C;Comment: This protein relates with the aberrant cell adhesion of cancer cells.

Query Match 57.1%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
 Db 15 PPLP 18

RESULT 9
 PT0283
 Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0283
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
 A;Reference number: PT0222; MUID:91108337; PMID:1899102
 A;Accession: PT0283
 A;Molecule type: DNA
 A;Residues: 1-7 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotrimer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
 Db 5 QPP 7

RESULT 10
 SI0783
 enamelin f - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
 C;Accession: SI0783
 R;Strawich, E.; Glincher, M.J.
 Eur. J. Biochem. 191, 47-56, 1990
 A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a
 A;Reference number: SI0780; MUID:90336641; PMID:2379503
 A;Accession: SI0783
 A;Molecule type: protein
 A;Residues: 1-8 <STR>
 C;Keywords: enamel; phosphoprotein

Query Match 42.9%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7
 Db 2 PLP 4

RESULT 11
 PC2171
 triacylglycerol lipase (BC 3.1.1.3) I A chain - Rhizopus niveus (strain IFO 4759) (fr
 C;Species: Rhizopus niveus
 C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
 C;Accession: PC2171
 R;Kohno, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.
 Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994
 A;Title: Purification, characterization, and crystallization of two types of lipase f
 A;Reference number: PC2171; MUID:94319059; PMID:7765029
 A;Accession: PC2171
 A;Molecule type: protein
 A;Residues: 1-10 <KOH>
 A;Experimental source: This enzyme catalyzes the hydrolysis of the ester bonds.
 C;Keywords: carboxylic ester hydrolase

Query Match 42.9%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 Db 6 PPL 8

RESULT 12

C39745
sphingomyelinase - Rhodococcus sp. (fragment)
C:Species: Rhodococcus sp.
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: C39745
R:Itto, M.; Ikegami, Y.; Yamagata, T.
J. Biol. Chem. 266, 7919-7926, 1991
A>Title: Activator proteins for glycosphingolipid hydrolysis by endoglycoceramidases. El
ble using these activator proteins.
A:Reference number: A39745; MUID:91210321; PMID:1850427
A:Accession: C39745
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <ITO>

Query Match 42.9%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
|||
DB 3 PLP 5

RESULT 13

A36454
trypsin-modulating oostatic factor - yellow fever mosquito
C:Species: Aedes aegypti (yellow fever mosquito)
C>Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-May-1996
C:Accession: A36454; A61630
R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
FASEB J. 4, 3015-3020, 1990
A>Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi
A:Reference number: A36454; MUID:90367888; PMID:2394318
A:Accession: A36454
A:Molecule type: protein
A:Residues: 1-10 <BOR>
R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
Insect Biochem. Mol. Biol. 23, 703-712, 1993
A>Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost
A:Reference number: A61630; MUID:93357794; PMID:8353526
A:Accession: A61630
A:Molecule type: protein
A:Residues: 1-10 <BO2>
A>Note: none of the amino acids is modified
C:Function:
A:Description: Inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ep
C:Keywords: hormone

Query Match 42.9%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
DB 5 PPP 7

RESULT 14

YHRT
morphogenetic neuropeptide - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A>Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coele
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: A01427
A:Molecule type: protein

A:Residues: 1-11 <BOD>
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A>Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A>Note: the synthetic peptide was identical with the natural peptide in chemical stru
C:Comment: This peptide was first isolated from nerve cells of hydra and was called h
een found in mammalian intestine and hypothalamus.
C:Superfamily: unassigned animal peptides
A:Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutan
P:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
|||
DB 1 QPP 3

RESULT 15

YHHU
morphogenetic neuropeptide - human
C:Species: Homo sapiens (man)
C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: B01427; A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A>Title: Conserved amino acid sequence of a neuropeptide, the head activator, from c
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: B01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A>Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A>Note: the synthetic peptide was identical with the natural peptide in chemical str
C:Comment: This peptide was first isolated from nerve cells of hydra and was called i
malian intestine and hypothalamus.
C:Superfamily: unassigned animal peptides
A:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neur
P:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #st

Query Match 42.9%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
|||
DB 1 QPP 3

RESULT 16

YHEO
morphogenetic neuropeptide - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: C01427; A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A>Title: Conserved amino acid sequence of a neuropeptide, the head activator, from c
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: C01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A>Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Molecule type: protein

A:Contents: annotation; synthesis
 A>Note: the synthetic peptide was identical with the natural peptide in chemical structure
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head malleian intestine and hypothalamus.

C:Superfamily: unassigned animal peptides
 C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide
 F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
 ||||
 Db 1 QPP 3

RESULT 17

YHXAE morphogenetic neuropeptide - sea anemone (Anthopleura elegantissima)

N:Alternate names: head activator
 C:Species: Anthopleura elegantissima
 C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C:Accession: A93900; A01427

R:Schaller, H.C.; Bodenmuller, H.
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
 A:Reference number: A93900

A:Accession: A93900
 A:Molecule type: protein
 A:Residues: 1-11 <SCH>

R:Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981

A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Contents: annotation; synthesis

A>Note: the synthetic peptide was identical with the natural peptide in chemical structure
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head malleian intestine and hypothalamus.

C:Superfamily: unassigned animal peptides
 C:Keywords: growth factor; hormone; neuropeptide; pyrrolidone carboxylic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
 ||||
 Db 1 QPP 3

RESULT 18

YHJFHV morphogenetic neuropeptide - Hydra attenuata

N:Alternate names: head activator
 C:Species: Hydra attenuata
 C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C:Accession: B93900; A01427

R:Schaller, H.C.; Bodenmuller, H.
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
 A:Reference number: A93900

A:Accession: B93900
 A:Molecule type: protein
 A:Residues: 1-11 <SCH>

R:Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981

A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Contents: annotation; synthesis

A>Note: the synthetic peptide was identical with the natural peptide in chemical structure
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head

n mammalian intestine and hypothalamus.
 C:Superfamily: unassigned animal peptides
 C:Keywords: growth factor; hormone; neuropeptide; pyrrolidone carboxylic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
 ||||
 Db 1 QPP 3

RESULT 19

D45900 complement C3b receptor type 2 - mouse (clone 12) (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: D45900
 R:Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.
 J. Immunol. 144, 3581-3591, 1990

A:Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2
 A:Reference number: A45900; MUID:90229754; PMID:2139460

A:Accession: D45900

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
 A:Molecule type: mRNA
 A:Residues: 1-11 <KUR>

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5
 ||||
 Db 9 QPP 11

RESULT 20

S70337 napin small chain S2 - Swedish turnip (fragment)

C:Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)
 C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
 C:Accession: S70337
 R:Neumann, G.M.; Condrion, R.; Thomas, I.; Polya, G.M.
 Biochim. Biophys. Acta 1295, 23-33, 1996

A:Title: Purification and sequencing of multiple forms of Brassica napus seed napin S
 A:Reference number: S70336; MUID:96283790; PMID:8679670

A:Accession: S70337
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <NEU>

Query Match 42.9%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPP 3
 ||||
 Db 3 QPP 5

RESULT 21

PN0663

dystrophin-associated glycoprotein A3a-II - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
 C:Accession: PN0663
 R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
 J. Biochem. 114, 634-639, 1993

A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retain
 A:Reference number: PN0662; MUID:94156881; PMID:8113213

A:Accession: PN0663

A:Molecule type: protein
A:Residues: 1-12 <YOS>
C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C:Keywords: glycoprotein; skeletal muscle

Query Match 42.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
|||
Db 3 PLP 5

RESULT 22

B39690
neural cell adhesion molecule, cardiac splice form +,-,- rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: B39690
R:Reyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
A:Reference number: A39690; MUID:91141516; PMID:1996115
A:Accession: B39690
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-12 <REY>
A:Cross-references: GB:M63970
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 42.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 6 PPP 8

RESULT 23

B39690
neural cell adhesion molecule, cardiac splice form +,-,- rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: B39690
R:Reyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
A:Reference number: A39690; MUID:91141516; PMID:1996115
A:Accession: B39690
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-13 <REY>
A:Cross-references: GB:M63970
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like domain
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 6 PPP 8

RESULT 24

S21152
tryptophyllin-related peptide - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S21152

R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, F.E.B.S. Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of *Phyllomedusa bicolor*
A:Reference number: S21152; MUID:92339502; PMID:1633846
A:Accession: S21152
A:Molecule type: protein
A:Residues: 1-13 <MIG>
A:Experimental source: skin
C:Superfamily: unassigned animal peptides

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 7 PPP 9

RESULT 25

A05174
tryptophyllin-13 - Rohde's leaf frog
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Aug-2000
C:Accession: A05174
R:Montecucchi, P.C.; Gozzini, L.; Erspamer, V.
Int. J. Pept. Protein Res. 27, 175-182, 1986
A:Reference number: A05174
A:Accession: A05174
A:Molecule type: protein
A:Residues: 1-13 <MON>
C:Superfamily: unassigned animal peptides
C:Keywords: pyroglutamic acid; skin
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 7 PPP 9

RESULT 26

S09716
2S albumin large chain (1 and 2) nrl - rape (fragments)
N:Alternate names: 2S albumin large chain nrl
C:Species: Brassica napus (rape)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Aug-1998
C:Accession: S09716; S09718; S09717
R:Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
F.E.B.S. Lett. 263, 209-212, 1990
A:Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins
A:Reference number: S09720; MUID:90242974; PMID:2185951
A:Accession: S09716
A:Molecule type: protein
A:Residues: 1-9;10-13 <MON>
A:Experimental source: seed
A:Note: 3-Ser was also found
A:Accession: S09718
A:Molecule type: protein
A:Residues: 1-9;10-13 <MO2>
A:Experimental source: seed
A:Accession: S09717
A:Molecule type: protein
A:Residues: 1-9;10-13 <MO3>
A:Experimental source: seed

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 ||||
 Db 8 PPP 10

RESULT 27

184603
 deoxynucleotidyltransferase - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
 C:Accession: I84603
 R:Koizumi O.; Kaneda, T.; Morishita, R.
 Biochem. Biophys. Res. Commun. 144, 185-190, 1987
 A:Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in man
 A:Reference number: I45884; MUID:87213162; PMID:3579900
 A:Accession: I84603
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-13 <BRO>
 A:Cross-references: GB:I26144; NID:g951194; PIDN:AAA74588.1; PID:g951195
 C:Genetics:
 A:Gene: GDB:DNTT
 A:Cross-references: GDB:119100; OMIM:187410
 A:Map position: 10q23-10q24

Query Match 42.9%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
 ||||
 Db 9 PLP 11

RESULT 28

G61458
 Ig lambda chain V-II region (AZI) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
 C:Accession: G61458; PLO159
 R:Broutet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
 J. Exp. Med. 170, 1551-1558, 1989
 A:Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-associated glycoprotein
 A:Reference number: A61458; MUID:90039128; PMID:2478651
 A:Accession: G61458
 A:Molecule type: protein
 A:Residues: 1-13 <BRO>
 C:Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycoprotein
 C:Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
 ||||
 Db 6 QPP 8

RESULT 29

A86126
 hypothetical protein Z5883 [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: A86126
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grotbeck, E.O.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: A86126
 A>Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-13 <STO>
 A:Cross-references: GB:AB005174; NID:g12519285; PIDN:AAG59469.1; GSPDB:GN00145; UMGP:
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Z5883

Query Match 42.9%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQP 3
 ||||
 Db 1 MQP 3

RESULT 30

S12904
 protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)
 C:Species: Pisaster ochraceus
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
 C:Accession: S12904
 R:Saenger, J.S.; Abersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.
 FEBS Lett. 273, 223-226, 1990
 A:Title: Identification of the sites in myelin basic protein that are phosphorylated
 A:Reference number: S12904; MUID:91032186; PMID:1699809
 A:Accession: S12904
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <SAN>
 C:Keywords: phosphotransferase

Query Match 42.9%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 ||||
 Db 8 PPP 10

RESULT 31

PQ0545
 capsid protein VP19C - human herpesvirus 1 (fragment)
 C:Species: human herpesvirus 1
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: PQ0545
 R:Davidson, M.D.; Rixon, F.J.; Davidson, A.J.
 J. Gen. Virol. 73, 2709-2713, 1992
 A:Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of her
 A:Reference number: PQ0544; MUID:93019027; PMID:1328483
 A:Accession: PQ0545
 A:Molecule type: protein
 A:Residues: 1-15 <DAV>
 A:Experimental source: strain 17
 C:Genetics:
 A:Gene: UL38
 C:Keywords: capsid protein

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
 ||||
 Db 5 PLP 7

RESULT 32

PT0037
 light harvesting complex chain III/b, photosystem I - rice (fragment)
 C:Species: Oryza sativa (rice)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
 C:Accession: PT0037; PS0205

R;Uchiyama, Y.; Tsugita, A.
 Submitted to JIPID, June 1991
 A;Reference number: PS0189
 A;Accession: PT0037
 A;Molecule type: protein
 A;Residues: 1-15 <UCH>

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 ||||
 Db 8 PPP 10

RESULT 33

PA0060
 protein QF200037 - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C;Accession: PA0060
 R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
 A;Reference number: PA0051
 A;Accession: PA0060
 A;Molecule type: protein
 A;Residues: 1-15 <CHO>

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7
 ||||
 Db 4 PLP 6

RESULT 34

B61457
 alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)

C;Species: Tetrahymena pyriformis
 C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999
 C;Accession: B61457
 R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
 J. Protozool. 36, 562-567, 1989
 A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification
 A;Reference number: A61457; MUID:90095988; PMID:2689637

A;Accession: B61457
 A;Molecule type: protein
 A;Residues: 1-15 <BAN>

C;Genetics:

A;Genetic code: SGCS

C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monom

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 ||||
 Db 7 PPL 9

RESULT 35

A60221
 apolipoprotein A-I - common carp (fragment)

C;Species: Cyprinus carpio (common carp)
 C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Dec-1993
 C;Accession: A60221
 R;Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.
 J. Neurochem. 55, 1237-1243, 1990

A;Title: Fish apolipoprotein-A-I has heparin binding activity: implication for nerve
 A;Reference number: A60221; MUID:90376100; PMID:2118944
 A;Accession: A60221
 A;Molecule type: protein
 A;Residues: 1-15 <HAR>
 A;Note: protein from plasma and from optic nerve yielded the same sequence
 C;Keywords: lipid binding; lipoprotein

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
 ||||
 Db 2 QPP 4

RESULT 36

I57530

gene c-fms protein - mouse (fragment)

C;Species: Mus sp. (mouse)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-May-1997
 C;Accession: I57530
 R;Yue, X.; Favot, P.; Dunn, T.L.; Cassidy, A.I.; Hume, D.A.
 Mol. Cell. Biol. 13, 3191-3201, 1993

A;Title: Expression of mRNA encoding the macrophage colony-stimulating factor recept
 A;Reference number: I57530; MUID:93268269; PMID:8497248

A;Accession: I57530

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-16 <RES>

A;Cross-references: GB:S62219; NID:g386001

C;Genetics:

A;Gene: c-fms

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homo:

Query Match 42.9%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 ||||
 Db 5 PPL 7

RESULT 37

S57517

T cell receptor beta chain V region - human (fragment)

C;Species: Homo sapiens (man)
 C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
 C;Accession: S57517

R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.

submitted to the EMBL Data Library, June 1995

A;Description: T cell receptor repertoire for a viral epitope in humans is diversifi

A;Reference number: S57494

A;Accession: S57517

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-16 <BUR>

A;Cross-references: EMBL:Z49924; NID:g887480; PIDN:CAA90170.1; PID:g887481

C;Keywords: T-cell receptor

Query Match 42.9%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 ||||
 Db 5 PPL 7

RESULT 38

JH0517

insulin-like growth factor-binding protein 4 - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Mar-1995
 C:Accession: JH0517
 R:Colleman, M.E.; Pan, Y.C.E.; Etherton, T.D.
 Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991
 A:Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth
 A:Reference number: JH0515; MUID:92109718; PMID:1722398
 A:Accession: JH0517
 A:Molecule type: protein
 A:Residues: 1-16 <COL>
 A:Experimental source: serum

Query Match 42.9%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 7 PPP 9

RESULT 39

S57991
 hydroxyproline-rich protein - Sesbania rostrata (fragment)

C:Species: Sesbania rostrata
 C>Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 11-Jan-2000

C:Accession: S57991
 R:Goormachtig, S.; Valerio-Lepiniec, M.; Szczyglowski, K.; van Montagu, M.; Holsters, M.
 submitted to the EMBL Data Library, March 1995
 A:Description: Use of differential display to identify novel Sesbania rostrata genes enb
 A:Reference number: S57991

A:Accession: S57991
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-17 <GOO>
 A:Cross-references: EMBL:248673; NID:g899484; PID:g899485
 C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 42.9%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 10 PPP 12

RESULT 40

S59481

hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)

C:Species: Phaseolus vulgaris (kidney bean)
 C>Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998

C:Accession: S59481
 R:Wojtaszek, P.; Tretlowan, J.; Bolwell, G.P.
 Plant Mol. Biol. 28, 1075-1087, 1995
 A:Title: Specificity in the immobilisation of cell wall proteins in response to differ
 A:Reference number: S59481; MUID:96011753; PMID:7548825

A:Accession: S59481
 A:Molecule type: protein
 A:Residues: 1-17 <WOJ>
 C:Keywords: glycoprotein; hydroxyproline
 F:6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 8 PPP 10

RESULT 41

S10786

enamelin, 26K - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)
 C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
 C:Accession: S10786

R:Strawich, E.; Glimcher, M.J.
 Eur. J. Biochem. 191, 47-56, 1990
 A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a
 A:Reference number: S10780; MUID:90336641; PMID:2379503

A:Accession: S10786
 A:Molecule type: protein
 A:Residues: 1-17 <STR>

C:Keywords: enamel; phosphoprotein

Query Match 42.9%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
 |||
 Db 3 QPP 5

RESULT 42

S04229

N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24K chain - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Accession: S04229
 C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993

R:Tollersrud, O.K.; Aronson Jr., N.N.
 Biochem. J. 260, 101-108, 1989

A:Title: Purification and characterization of rat liver glycosylasparaginase.
 A:Reference number: S04228; MUID:89374025; PMID:2775174

A:Accession: S04229
 A:Molecule type: protein
 A:Residues: 1-18 <TOL>
 C:Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase
 C:Keywords: hydrolase

Query Match 42.9%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7
 |||
 Db 3 PLP 5

RESULT 43

I52614

u-plasminogen activator receptor precursor - human (fragment)

C:Species: Homo sapiens (man)
 C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000

C:Accession: I52614
 R:Soravia, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.
 Blood 86, 624-635, 1995

A:Title: A conserved TATA-less proximal promoter drives basal transcription from the
 A:Reference number: I52614; MUID:95329719; PMID:7605992

A:Accession: I52614
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-18 <RES>

A:Cross-references: GB:S78532; NID:g999307; PIDN:AAD14289.1; PID:g4261989
 C:Genetics:
 A:Gene: UPAR

C:Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 42.9%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
|||
Db 4 PPL 6

RESULT 44

C56211
progesterone receptor-related protein p23 - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000
C:Accession: C56211

R:Johnson, J.L.; Beito, T.G.; Krco, C.J.; Toft, D.O.

Mol. Cell. Biol. 14, 1956-1963, 1994

A:Title: Characterization of a novel 23-kilodalton protein of inactive progesterone receptor

A:Reference number: A56211; MUID:94158868; PMID:8114727

A:Accession: C56211

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <JOH>

C:Superfamily: Caenorhabditis elegans hypothetical protein ZC395.10

C:Keywords: steroid hormone receptor

Query Match 42.9%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 MQP 3
|||
Db 1 MQP 3

RESULT 45

A54195
Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)

C:Species: Squalus acanthias (spiny dogfish)

C:Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Apr-2002

C:Accession: A54195

R:Esmann, M.; Karlisch, S.J.; Sottrup-Jensen, L.; Marsh, D.

Biochemistry 33, 8044-8050, 1994

A:Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase

A:Reference number: A54195; MUID:94297020; PMID:8025109

A:Accession: A54195

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <ESM>

A:Experimental source: rectal gland

A>Note: sequence extracted from NCBI backbone (NCBIP:149363)

C:Keywords: hydrolase

Query Match 42.9%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 8 PPP 10

RESULT 46

S60633
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - brine shrimp mitochondrion

C:Species: mitochondrion Artemia sp. (brine shrimp)

A:Variety: strain La Mata

C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 03-Jun-2002

C:Accession: S60633

R:Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.

J. Mol. Evol. 38, 156-168, 1994

A:Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and parthenogenetic populations

A:Reference number: S60624; MUID:94223692; PMID:8169960

A:Accession: S60633

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-19 <PER>

A:Cross-references: EMBL:X67263; NID:g11210; PIDN:CAA47685.1; PID:g11211
A:Experimental source: strain La Mata
A>Note: the source is designated as Artemia parthenogenetica
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C:Genetics:

A:Gene: ATP8

A:Genome: mitochondrion

A:Genetic code: SGC4

C:Superfamily: H+-transporting ATP synthase protein 8

C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;

Query Match 42.9%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPL 7

|||

Db 6 PPL 8

RESULT 47

G56819

PS I complex subunit 6 - cucumber (fragment)

C:Species: Cucumis sativus (cucumber)

C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996

C:Accession: G56819

R:Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.

Biochim. Biophys. Acta 1059, 141-146, 1991

A:Title: Characterization of genes that encode subunits of cucumber PS I complex by

A:Reference number: A56819; MUID:91355209; PMID:1883835

A:Accession: G56819

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <IWA>

A>Note: sequence extracted from NCBI backbone (NCBIP:58604)

Query Match 42.9%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5

|||

Db 6 PPP 8

RESULT 48

S59486

cell wall protein, 22K - kidney bean (fragment)

C:Species: Phaseolus vulgaris (kidney bean)

C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C:Accession: S59486

R:Wojtaszek, P.; Iretrowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A:Title: Specificity in the immobilisation of cell wall proteins in response to diff

A:Reference number: S59481; MUID:96011753; PMID:7548825

A:Accession: S59486

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <WOU>

Query Match 42.9%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4

|||

Db 3 QPP 5

RESULT 49

A37968

neural surface protein Bravo - chicken (fragment)

C:Species: Gallus gallus (chicken)

C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 15-Aug-1997

C;Accession: A37968; A36345
 R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.
 J. Cell Biol. 112, 1049, 1991
 A;Reference number: A37968; MUID:91154309; PMID:1999455
 A;Contents: extratum
 A;Accession: A37968
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-19
 R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.
 J. Cell Biol. 111, 3067-3096, 1990
 A;Title: Topologically restricted appearance in the developing chick retinotectal system
 A;Reference number: A36345; MUID:91100421; PMID:2269667
 A;Accession: A36345
 A;Molecule type: protein
 A;Residues: 1-7,9-19 <DE2>

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;

QY 2 QPP 4
 ||||
 DB 15 QPP 17

RESULT 50

PH1352
 Ig heavy chain DJ region (clone C100-115) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: PH1352
 R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A;Reference number: PH1302; MUID:93094761; PMID:1460419
 A;Accession: PH1352
 A;Molecule type: DNA
 A;Residues: 1-19 <WAS>
 A;Note: the authors translated the stop codon for residue 2 as X
 C;Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 ||||
 DB 7 PPP 9

RESULT 51

S50018
 hyaluronidase - sheep (fragment)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 07-May-1999
 C;Accession: S50018
 R;Gacasa, P.; Civill, N.D.; Harrison, R.A.P.
 Biochem. J. 303, 335-336, 1994
 A;Title: PH-20 and sperm hyaluronidase: a conceptual conundrum in mammalian fertilization
 A;Reference number: S50018; MUID:95031981; PMID:7945261
 A;Accession: S50018
 A;Molecule type: protein
 A;Residues: 1-19 <GAC>

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
 ||||
 DB 5 PPL 7

RESULT 52

S25715
 hypothetical protein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S25715; S21390
 R;Bowtell, D.; Fu, P.; Simon, M.; Senior, P.
 Proc. Natl. Acad. Sci. U.S.A. 89, 6511-6515, 1992
 A;Title: Identification of murine homologues of the Drosophila Son of sevenless gene:
 A;Reference number: S25714; MUID:92335328; PMID:1631150

A;Accession: S25715
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-19 <BOW>
 A;Cross-references: EMBL:Z11578; NID:G54132; PIDN:CAA77665.1; PID:G54133
 R;Bowtell, D.D.; Fu, P.; Simon, M.A.; Senior, P.V.
 submitted to the EMBL Data Library, January 1992
 A;Description: Identification of murine homologues of the Drosophila Son of sevenless
 A;Reference number: S21390
 A;Accession: S21390
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-19 <BO2>
 A;Cross-references: EMBL:Z11578; NID:G54132; PIDN:CAA77665.1; PID:G54133

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 ||||
 DB 2 PPP 4

RESULT 53

S29817
 Cytochrome P450 2C23 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Mar-1999
 C;Accession: S29817
 R;Marie, S.; Roussel, F.; Cresteil, T.
 Biochim. Biophys. Acta 1172, 124-130, 1993
 A;Title: Age- and tissue-dependent expression of CYP2C23 in the rat.
 A;Reference number: S29817; MUID:93176794; PMID:7679925
 A;Accession: S29817
 A;Molecule type: mRNA
 A;Residues: 1-20 <MAR>
 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C;Keywords: heme; transmembrane protein

Query Match 42.9%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
 ||||
 DB 4 PLP 6

RESULT 54

D42842
 antifungal 2S storage albumin large chain - radish (fragment)
 C;Species: Raphanus sativus (radish)
 C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
 C;Accession: D42842
 R;Terras, F.R.; Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderleyd
 J. Biol. Chem. 267, 15301-15309, 1992
 A;Title: Analysis of two novel classes of plant antifungal proteins from radish (Raph
 A;Reference number: A42842; MUID:92348373; PMID:1639777
 A;Accession: D42842
 A;Status: preliminary

A:Reference number: A42267; MUID:92156146; PMID:1740450
A:Accession: A42267
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-20 <KAW>
A:Cross-references: GB:M81866

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 13 PPP 15

RESULT 58

A31516
lestin, galactose/N-acetylgalactosamine-specific - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C:Accession: A31516
R:Li, M.; Kawasaki, T.; Yamashina, I.
Biochem. Biophys. Res. Commun. 155, 720-725, 1988
A>Title: Structural similarity between the macrophage lectin specific for galactose/
A:Reference number: A31516; MUID:88339956; PMID:3421964
A:Accession: A31516
A:Molecule type: protein
A:Residues: 1-20 <IIX>

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 16 PPP 18

RESULT 59

A32039
tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C:Accession: A32039
R:Horvath, A.; Kastin, A.J.
J. Biol. Chem. 264, 2175-2179, 1989
A>Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting fac
A:Reference number: A32039; MUID:89123285; PMID:2563371
A:Accession: A32039
A:Molecule type: protein
A:Residues: 1-4 <HOR>
A:Experimental source: brain
A:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end
F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
|||
Db 2 PL 3

RESULT 60

HOROHA
proctolin - American cockroach
C:Species: Periplaneta americana (American cockroach)
C>Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 23-Aug-1996
C:Accession: A01644
R:Starratt, A.N.; Brown, B.E.

A:Molecule type: protein
A:Residues: 1-20 <TER>
A:Experimental source: seed
A>Note: sequence extracted from NCBI backbone (NCBIP:109925)
C:Superfamily: wheat alpha-amylase inhibitor

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
|||
Db 8 PPL 10

RESULT 55

S65605
dimeric protein (BDP) - barley (fragment)
C:Species: Hordeum vulgare (barley)
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
C:Accession: S65605
R:Garcia-Casado, G.; Armentia, A.; Sanchez-Monge, R.; Lopez-Otin, C.; Sal
FEBS Lett. 364, 36-40, 1995
A>Title: A major baker's asthma allergen from rye flour is considerably more active than
A:Reference number: S65604; MUID:95269763; PMID:7750539
A:Accession: S65605
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <GAR>

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
|||
Db 18 PLP 20

RESULT 56

S46479
retinoid-X-receptor-gamma - chicken
C:Species: Gallus gallus (chicken)
C>Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 28-May-1999
C:Accession: S46479
R:Seleiro, E.A.P.; Darling, D.; Brickell, P.M.
Biochem. J. 301, 283-288, 1994
A>Title: The chicken retinoid-X-receptor-gamma gene gives rise to two distinct species c
A:Reference number: S46478; MUID:94311845; PMID:8037682
A:Accession: S46479
A:Molecule type: mRNA
A:Residues: 1-20 <SEL>
A:Cross-references: GB:S72435; MID:G619294; PIDN:AB31348.1; PID:G619295

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQP 3
|||
Db 1 MQP 3

RESULT 57

A42267
J-kappa recombination sequence-binding protein RBP-2N - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: A42267; S23798
R:Kawauchi, M.; Oka, C.; Shibayama, S.; Koromilas, A.E.; Matsunami, N.; Hanaguchi, Y.; H
J. Biol. Chem. 267, 4016-4022, 1992
A>Title: Geromic organization of mouse J-kappa recombination signal binding protein (RBF

Life Sci. 17, 1253-1256, 1975
 A;Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects
 A;Reference number: A93048; MUID:7607408; PMID:576
 A;Accession: A01644
 A;Molecule type: protein
 A;Residues: 1-5 <STA>
 A;Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmacological properties as the natural peptide.
 R;O'Shea, M.; Adams, M.E.
 Science 213, 567-569, 1981
 A;Title: Pentapeptide (proctolin) associated with an identified neuron.
 A;Reference number: A94260; MUID:81225865; PMID:6113690
 A;Accession: B37988
 A;Contents: annotation; biological source
 A;Comment: This peptide is found in the lateral white neurons, which occur (in the cockroach) innervate the striated hindgut muscles in insects and stimulate contraction of these muscles.
 C;Superfamily: proctolin
 C;Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 3 LP 4

RESULT 61

JN0860
 peptidyl-diesterase A inhibitory peptide C107 - striped bonito
 C;Species: Sarda orientalis (striped bonito)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 A;Accession: JN0860
 R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
 A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide from the striped bonito.
 A;Reference number: JN0859; MUID:94060036; PMID:7764272
 A;Accession: JN0860
 A;Molecule type: protein
 A;Residues: 1-5 <MAT>
 A;Experimental source: intestine
 C;Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin I-converting enzyme inhibitory activity.
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 2 LP 3

RESULT 62

E42364
 flagellar protein flir - Salmonella typhimurium (fragment)
 C;Species: Salmonella typhimurium
 C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
 A;Accession: E42364
 R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
 J. Bacteriol. 173, 3564-3572, 1991
 A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and secretion.
 A;Reference number: A42364; MUID:91258342; PMID:1646201
 A;Accession: E42364
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-5 <VOG>
 A;Cross-references: GB:M62408

Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 4 LP 5

RESULT 63

B37988
 acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
 C;Species: Physarum polycephalum
 C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
 A;Accession: B37988
 R;Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki, J. Biol. Chem. 265, 19898-19903, 1990
 A;Title: Purification and characterization of a novel intracellular acid proteinase from Physarum polycephalum.
 A;Reference number: A37988; MUID:91060608; PMID:2246266
 A;Accession: B37988
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-5 <MUR>

Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
 ||
 Db 3 PP 4

RESULT 64

A60411
 proctolin - Atlantic horseshoe crab
 C;Species: Limulus polyphemus (Atlantic horseshoe crab)
 C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 17-Mar-1999
 A;Accession: A60411
 R;Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, P. J. Biol. Chem. 265, 205-211, 1990
 A;Title: Identification of proctolin in the central nervous system of the horseshoe crab.
 A;Reference number: A60411; MUID:90287800; PMID:2356151
 A;Accession: A60411
 A;Molecule type: protein
 A;Residues: 1-5 <GRO>
 C;Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horseshoe crab.
 C;Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 3 LP 4

RESULT 65

I67345
 MHC H2-K-k cell surface glycoprotein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 A;Accession: I67345
 R;Archibald, A.L.; Thompson, N.A.; Kvist, S.
 EMBO J. 5, 957-965, 1986
 A;Title: A single nucleotide difference at the 3' end of an intron causes differential splicing of the H2-K-k gene.
 A;Reference number: I53243; MUID:86247587; PMID:3013627
 A;Accession: I67345
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-6 <RES>
 A;Cross-references: GB:M26859; NID:919439; PIDN:AAA39612.1; PID:9387458

Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 3 LP 4

Query Match 28.6%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 1 LP 2

RESULT 66

A35039
 Hypothetical collagen alpha 2(I) intron 2 protein 1 - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C:Accession: A35039
 R:Bennett, V.D.; Adams, S.L.
 J. Biol. Chem. 265, 2223-2230, 1990
 A:Title: Identification of a cartilage-specific promoter within intron 2 of the chick alpha 2(I) collagen gene
 A:Reference number: A35039; MUID:90130479; PMID:1688851
 A:Accession: A35039
 A:Molecule type: mRNA
 A:Residues: 1-6 <BEN>
 A:Cross-references: GB:M33382; NID:g211043
 A:Note: This ORF is not translated in GenBank entry CHKA21CG
 C:Comment: This sequence is the translation of a cartilage specific alternative transcript
 C:Keywords: alternative splicing; cartilage

Query Match 28.6%; Score 2; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 4 LP 5

RESULT 67

A61081
 Cryptophyllin, basic - Rohde's leaf frog
 C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
 C:Accession: A61081
 R:Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.
 Int. J. Pept. Protein Res. 33, 391-395, 1989
 A:Title: Isolation, structure determination and synthesis of a novel cryptophyllin-containing peptide
 A:Reference number: A61081
 A:Accession: A61081
 A:Molecule type: protein
 A:Residues: 1-7 <MON>
 C:Comment: The biological activity of this peptide was not determined.
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end; hydroxyproline; skin
 F:3/Modified site: 4-hydroxyproline (Pro) #status experimental
 F:7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
 ||
 Db 2 PP 3

RESULT 68

PC1316
 large granule L3 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)
 C:Species: Tachyplesus tridentatus
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C:Accession: PC1316
 R:Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa
 J. Biochem. 114, 307-316, 1993
 A:Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridentatus)

A:Reference number: PC1309; MUID:94110249; PMID:8282718
 A:Accession: PC1316
 A:Molecule type: protein
 A:Residues: 1-7 <SHI>
 C:Comment: This protein participates in immobilization of invading microbes.

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
 ||
 Db 3 QP 4

RESULT 69

B39040
 calsequestrin, fast skeletal muscle - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
 C:Accession: B39040
 R:Calal, S.E.; Jones, L.R.
 J. Biol. Chem. 266, 391-398, 1991
 A:Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by calmodulin
 A:Reference number: A39040; MUID:91093153; PMID:1985907
 A:Accession: B39040
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <CAL>
 C:Keywords: phosphoprotein; skeletal muscle

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 6 LP 7

RESULT 70

I48105
 dihydrofolate reductase - Chinese hamster (fragment)
 C:Species: Cricetus griseus (Chinese hamster)
 C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
 C:Accession: I48105
 R:Aizkhan, J.C.; Vaughn, J.P.; Christy, R.J.; Hamlin, J.L.
 Biochemistry 25, 6228-6236, 1986
 A:Title: Nucleotide sequence and nuclelease hypersensitivity of the Chinese hamster dihydrofolate reductase
 A:Reference number: I48105; MUID:87076541; PMID:3024702
 A:Accession: I48105
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-7 <RES>
 A:Cross-references: GB:M14771; NID:g191055; PIDN:AAA36975.1; PID:g191056

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
 ||
 Db 4 PL 5

RESULT 71

I48086
 DNA topoisomerase II alpha - Chinese hamster (fragment)
 C:Species: Cricetus griseus (Chinese hamster)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I48086
 R:Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.
 J. Biol. Chem. 270, 25850-25858, 1995

A:Title: Molecular cloning and characterization of the promoter for the Chinese hamster
 A:Reference number: I48086; MUID:96029684; PMID:7592770
 A:Accession: I48086
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-7 <RES>
 A:Cross-references: EMBL:U34196; NID:g1041231; PIDN:AAC52315.1; PID:g1041232

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LP 6
 ||
 Db 5 PL 6

RESULT 72

S66442
 Glutathione S-transferase P - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C:Accession: S66442
 R:Nishihira, J.; Sakai, M.; Nishi, S.; Hatanaka, Y.
 Eur. J. Biochem. 232, 106-110, 1995
 A:Title: Identification of the electrophilic substrate-binding site of glutathione S-transferase P from Rattus norvegicus
 A:Reference number: S66442; MUID:96048035; PMID:7556138
 A:Accession: S66442
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <NIS>

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 2 LP 3

RESULT 73

A39690
 Neural cell adhesion molecule, cardiac splice form -, -, - - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
 C:Accession: A39690
 R:Reyes, A.A.; Small, S.J.; Akesson, R.
 Mol. Cell. Biol. 11, 1654-1661, 1991
 A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA from Rattus norvegicus
 A:Reference number: A39690; MUID:91141516; PMID:1996115
 A:Accession: A39690
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-7 <REY>
 A:Cross-references: GB:M63970
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
 ||
 Db 1 QP 2

RESULT 74

A58718
 carnocin UI49 - Carnobacterium sp. (fragment)
 C:Species: Carnobacterium sp.
 C:Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
 C:Accession: A58718

R:Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.
 Appl. Environ. Microbiol. 58, 1417-1422, 1992
 A:Title: Purification and characterization of a new bacteriocin isolated from a Carnobacterium strain
 A:Reference number: A58718; MUID:92321768; PMID:1622206
 A:Accession: A58718
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <STO>
 C:Keywords: antibiotic; lanthionine

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
 ||
 Db 5 QP 6

RESULT 75

S45648
 Na+-transporting ATP synthase (EC 3.6.1.1-) alpha chain - Acetobacterium woodii (fragment)
 N:Alternate names: ATPase alpha chain
 C:Species: Acetobacterium woodii
 C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
 C:Accession: S45648
 R:Reidlinger, J.; Mueller, V.
 Eur. J. Biochem. 223, 275-283, 1994
 A:Title: Purification of ATP synthase from Acetobacterium woodii and identification of its subunits
 A:Reference number: S45648; MUID:94307271; PMID:8033902
 A:Accession: S45648
 A:Molecule type: protein
 A:Residues: 1-374-7 <REI>
 A:Experimental source: DSM 1030
 C:Keywords: hydrolase

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 3 LP 4

Search completed: November 25, 2003, 18:28:11
 Job time : 7.44149 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 3.3893 Seconds
(without alignments)
97.154 Million cell updates/sec

Title: US-09-641-801-1
Perfect score: 7
Sequence: 1 MQPPPLP 7

Scoring table: OLIGO
Gapop 60.0 , Capext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	42.9	10	1	TM0F_AEDAE
2	3	42.9	11	1	MORN_HUMAN
3	3	42.9	11	1	TIN4_HOPTI
4	3	42.9	12	1	TIN2_HOPTI
5	3	42.9	12	1	TIN3_HOPTI
6	3	42.9	13	1	TY13_PHYRO
7	3	42.9	14	1	ECDC_LYMDI
8	3	42.9	15	1	AF1L_MALPA
9	3	42.9	15	1	PRP_MYCBO
10	3	42.9	16	1	IBPI_PIG
11	3	42.9	17	1	APID_BOMPA
12	3	42.9	19	1	PSAE_CUCSA
13	2	28.6	5	1	PRCT_PERAM
14	2	28.6	6	1	TRPI_PSEPU
15	2	28.6	6	1	VP19_HSV1K
16	2	28.6	7	1	LANC_CARUI
17	2	28.6	7	1	MNPI_LEPDE
18	2	28.6	7	1	TPFY_PACDA
19	2	28.6	7	1	UF04_MOUSE
20	2	28.6	7	1	UN06_PINPS
21	2	28.6	8	1	ALL5_CALVO
22	2	28.6	8	1	ALL6_CYDPO
23	2	28.6	8	1	COW2_CONFU
24	2	28.6	8	1	NPB_BOVIN
25	2	28.6	8	1	PPK2_PERAM
26	2	28.6	9	1	AL10_CARMA
27	2	28.6	9	1	COXE_THUOB
28	2	28.6	9	1	FAR3_PENMO
29	2	28.6	9	1	FAR4_PENMO
30	2	28.6	9	1	FAR9_ASCSU
31	2	28.6	9	1	PRF1_SARBU
32	2	28.6	9	1	KNL3_BOMVA
33	2	28.6	9	1	LMT3_LOEMI
34	2	28.6	9	1	OXYA_SQUAC
35	2	28.6	9	1	OXYT_RABIT
36	2	28.6	9	1	RS10_SERMA
37	2	28.6	9	1	RT33_BOVIN
38	2	28.6	9	1	UFA3_HUMAN
39	2	28.6	9	1	YBFR_AZOVI
40	2	28.6	10	1	AH3_FRUSE
41	2	28.6	10	1	BPP2_BOTJA
42	2	28.6	10	1	BPP2_BOTJA
43	2	28.6	10	1	BPP8_BOTIN
44	2	28.6	10	1	BPP_VIPAS
45	2	28.6	10	1	BRK_ONCMY
46	2	28.6	10	1	CATB_SHEEP
47	2	28.6	10	1	FAR6_PANRE
48	2	28.6	10	1	GONI_ALLMI
49	2	28.6	10	1	GONI_ONCKE
50	2	28.6	10	1	GONI_SQUAC
51	2	28.6	10	1	NO40_TOBAC
52	2	28.6	10	1	NS1_MYCTU
53	2	28.6	10	1	PSBF_CAPAN
54	2	28.6	10	1	TEMK_RANTE
55	2	28.6	10	1	TKL2_LOEMI
56	2	28.6	10	1	UPA2_HUMAN
57	2	28.6	10	1	UPA5_HUMAN
58	2	28.6	10	1	URE3_MORMO
59	2	28.6	11	1	BPP3_BOTIN
60	2	28.6	11	1	BPP4_BOTIN
61	2	28.6	11	1	BPP8_AKSHA
62	2	28.6	11	1	BPP_AKHP
63	2	28.6	11	1	BRK_MEGFL
64	2	28.6	11	1	BFG_CLOPA
65	2	28.6	11	1	LADD_ONCMY
66	2	28.6	11	1	LPW_THETH
67	2	28.6	11	1	PQOC_PSEFL
68	2	28.6	11	1	TKN1_PSEGU
69	2	28.6	11	1	TKN1_UPERU
70	2	28.6	11	1	TKN2_PSEGU
71	2	28.6	11	1	TKN3_PSEGU
72	2	28.6	11	1	TKN4_PSEGU
73	2	28.6	11	1	TKN5_PSEGU
74	2	28.6	11	1	TKN5_PSEGU
75	2	28.6	12	1	FAR7_PENMO
76	2	28.6	12	1	FARI_CALVO
77	2	28.6	12	1	FIFI_RANBU
78	2	28.6	12	1	GRAR_SARBU
79	2	28.6	12	1	HS9A_RAT
80	2	28.6	12	1	NUDM_CANFA
81	2	28.6	12	1	PPK4_PERAM
82	2	28.6	12	1	RS19_TOBBP
83	2	28.6	12	1	TKN2_KASMA
84	2	28.6	12	1	TM2A_METMA
85	2	28.6	13	1	ACT7_SOYBN
86	2	28.6	13	1	AH4_FRUSE
87	2	28.6	13	1	BPP1_BOTJA
88	2	28.6	13	1	BRK_PARDI
89	2	28.6	13	1	CRBL_ICASP
90	2	28.6	13	1	CRBL_VESAN
91	2	28.6	13	1	CRBL_VESCR
92	2	28.6	13	1	CRBL_VESLE
93	2	28.6	13	1	CRBL_VESMA
94	2	28.6	13	1	CRBL_VESXA
95	2	28.6	13	1	CRBL_VESXA
96	2	28.6	13	1	CRBL_VESXA
97	2	28.6	13	1	CRBL_VESXA
98	2	28.6	13	1	CRBL_VESXA
99	2	28.6	13	1	CRBL_VESXA
100	2	28.6	13	1	CRBL_VESXA

RESULT 1

ALIGNMENTS

P42999 squalus aca
P32878 oryctolagus
O69336 serratia ma
P82926 bos taurus
P30089 homo sapien
P25825 azotobacter
P29261 prunus sero
P30422 bothrops in
P01022 bothrops ja
P30426 bothrops in
P31351 vibera aspi
Q9PRZ1 oncorhynch
P83205 ovnis aries
P82660 panagrellus
P37041 alligator m
P27429 squalus aca
P55962 nicotiana t
P81135 mycobacteri
Q03367 capsicum an
P56923 rana tempor
P16224 locusta mig
P30888 homo sapien
P30091 homo sapien
P17339 morganella
P30423 bothrops in
P30424 bothrops in
P01021 agkistrodon
P04562 agkistrodon
P12797 megascolia
P81350 clostridium
P81018 oncorhynch
P05624 thermus the
P55173 pseudomonas
P42866 pseudophryn
P08612 uperoleia r
P42987 pseudophryn
P42988 pseudophryn
P42989 pseudophryn
P42990 pseudophryn
P01323 eledone mos
P83322 penaeus mon
P41869 calliphora
P83349 sarcophaga
P40754 rana rugosa
P82995 rattus norv
P54713 canis famli
Q56251 periplaneta
P08614 kassina mac
P08614 kassina mac
P15937 glycine max
P29262 prunus sero
P01020 bothrops ja
P42717 parapolybia
P17233 icaaria sp.
P17233 vespa anali
P01518 vespa crabr
P17235 vespa lew
P17232 vespa manda
P17231 vespa troth
P17234 vespa xanth
P17234 vespa xanth
P82098 litoria rub
P54963 homo sapien
P14478 oryctolagus
P28525 hordeum vul

TMOF_AEDAE ID TMOF_AEDAE STANDARD; PRT; 10 AA.
AC P19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RX STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating
RT trypsin-like enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RX STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=8353526;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
RT modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CC CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE
CC DEVELOPMENT.
CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
CC EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT
CC 36 HRS AND STOPS AT 56 HRS.
DR PIR; A36454; A36454.
KW Hormone.
FT DOMAIN 3 10 POLY-PRO.
FT VARIANT 1 2 YD -> DY (IN TMOF(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 5 PPP 7

RESULT 2
MORN_HUMAN ID MORN_HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuroepitide (Head activator) (HA).
OS Homo sapiens (Human).
OS Rattus norvegicus (Rat).
OS Bos taurus (Bovine).
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
RP SEQUENCE.
RX SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuroepitide, the head activator,
RT from coelenterates to humans.";
RL Nature 293:579-580(1981).

[2]
RP SEQUENCE.
RC SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
RT hydra.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RP SYNTHESIS.
RX MEDLINE=82950803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuroepitide, the head activator from hydra.";
RL FEBS Lett. 131:317-321(1981).
RN [4]
RP FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
RT in the G2/mitosis transition.";
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
CC IN THE G2/MITOSIS TRANSITION.
CC -!- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
DR PIR; A01427; YHET.
DR PIR; A93900; YHAE.
DR PIR; B01427; YHHU.
DR PIR; B93900; YHJFHY.
DR PIR; C01427; YHBO.
DR GK; P01163; -.
DR Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
DB 1 QPP 3

RESULT 3
TIN4_HOFTI ID TIN4_HOFTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.

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FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 42.9%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
Db |||
7 PLP 9

RESULT 4
TIN2_HOPI
ID TIN2_HOPI STANDARD; PRT; 12 AA.
AC P82652;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-2.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B. SUBTILIS, E. COLI,
CC S. AUREUS, M. LUTERUS, P. PUTIDA AND S. CEREBISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 42.9%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
Db |||
7 PLP 9

RESULT 5
TIN3_HOPI
ID TIN3_HOPI STANDARD; PRT; 12 AA.
AC P82653;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-3.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana

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RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B. SUBTILIS, E. COLI,
CC S. AUREUS, M. LUTERUS, P. PUTIDA AND S. CEREBISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1411 MW; C0717D8EFD37605D CRC64;

Query Match 42.9%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
Db |||
7 PLP 9

RESULT 6
TIN3_PHYRO
ID TIN3_PHYRO STANDARD; PRT; 13 AA.
AC P04096;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-13.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RA Montecucchi P.C., Gozzini L., Erspamer V.;
RT "Primary structure determination of a tryptophan-containing
RT tridecapeptide from Phyllomedusa rohdei.";
RL Int. J. Pept. Protein Res. 27:175-182(1986).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; A05174; A05174.
KW Amphibian defense peptide; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
Db |||
7 PPP 9

RESULT 7
ECDC_LYMDI
ID ECDC_LYMDI STANDARD; PRT; 14 AA.
AC P80940;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Testis edysiotropin peptide C (TE).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97387807; PubMed=9243792;

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RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
RT gonadotropin isolated from brains of Lymantria dispar pupae.";
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -!- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
CC OF LARVAE AND PUPAE.
SQ SEQUENCE 14 AA; 1553 MW; 17F479531A685CBB CRC64;

Query Match 42.9%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 5 PLP 7
DB 9 PLP 11

RESULT 8
AFIL_MALPA STANDARD; PRT; 15 AA.
AC P83141;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Antifungal protein 1 large subunit (CW-1) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX NCBI_TaxID=145753;
RN [1]
RP SEQUENCE AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=20568734; PubMed=11119343;
RA Wang X., Bunkers G.J.;
RT "Potent heterologous antifungal proteins from cheeseweed (Malva
RL parviflora).";
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC NOT F.graminearum.
CC -!- SUBUNIT: Heterodimer of a large and a small subunit.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC concentration.
CC GO: GO:0003799; F:antifungal peptide activity; IDA.
DR Fungicide; Antibiotic.
KW NON_TER 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1783 MW; 2CB3079F53C070F9 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.6e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 4 PPL 6
DB 8 PPL 10

RESULT 9
PRP_MYCBO STANDARD; PRT; 15 AA.
AC P80149;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE Proline-rich protein (Fragment).
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE.
RC STRAIN=BCG / Paris 1173 P2;

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RX MEDLINE=93281750; PubMed=8506381;
RA Romain F., Audier J., Pescher P., Marchal G.A.;
RT "Isolation of a proline-rich mycobacterial protein eliciting delayed-
RT type hypersensitivity reactions only in guinea pigs immunized with
RT living mycobacteria.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5322-5326(1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: IMMUNODOMINANT FOR DELAYED-TYPE HYPERSENSITIVITY
CC REACTIONS IN GUINEA PIGS.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1612 MW; 22659F848B922773 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.6e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 3 PPP 5
DB 7 PPP 9

RESULT 10
IBP4_PIG STANDARD; PRT; 16 AA.
AC P24854;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE (IGF-binding protein 4) (Fragment).
GN IGFBP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92109718; PubMed=1722398;
RA Coleman W.E., Pan Y.-C.E., Ehterton T.D.;
RT "Identification and NH2-terminal amino acid sequence of three
RT insulin-like growth factor-binding proteins in porcine serum.";
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC -!- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFS
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFS ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFS WITH THEIR CELL SURFACE RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 IGFBP domain.
CC -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.
DR PIR; JH0517; JH0517.
DR InterPro; IPR000867; Insl_gro_fac_pr.
DR InterPro; IPR000716; Thyroglobulin_1.
DR PROSITE; PS00222; IGF BINDING; PARTIAL.
DR PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 3 PPP 5
DB 7 PPP 9

RESULT 11
APID_BOMPA STANDARD; PRT; 17 AA.
ID APID_BOMPA
AC P81464;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)

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DT 15-SBP-2003 (Rel. 42, Last annotation update)
DE Apidaecin.
OS Bombus pascuorum (Brown bumble bee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=65598;
RN [1]_TaxID=65598;
RP SEQUENCE.
RC TISSUE=Hemolymph; PubMed=9219367;
RX MEDLINE=97362903;
RA Rees J.A., Montatte M., Bulet P.;
RT "Novel antibacterial peptides isolated from a European bumblebee,
RT Bombus pascuorum (Hymenoptera, Apoidea).";
RL Insect Biochem. Mol. Biol. 27:413-422(1997).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
CC BACTERIA.
CC -!- INDUCTION: By bacterial infection.
CC InterPro: IPR004828; Apidaecin.
DR Pfam: PF00807; Apidaecin; 1.
KW Insect immunity; Antibiotic; Hemolymph.
SQ SEQUENCE 17 AA; 1963 NW; CDID0D02C8BC23D1 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.4e-02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 8 PPP 10

RESULT 12
PSAE_CUCSA STANDARD; PRT; 19 AA.
AC P42047;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Photosystem I reaction center subunit IV (PSI-E) (Photosystem I 19.5
DE kDa protein) (PS I subunit 6) (Fragment).
GN PSAE.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]_TaxID=3659;
RP SEQUENCE.
RC TISSUE=Cotyledon; PubMed=1883835;
RX MEDLINE=91355209;
RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;
RT "Characterization of genes that encode subunits of cucumber PS I
RT complex by N-terminal sequencing.";
RL Biochim. Biophys. Acta 1059:141-148(1991).
CC -!- FUNCTION: Stabilizes the interaction between psac and the PSI
CC core, assists the docking of the ferredoxin to PSI and interacts
CC with ferredoxin-NADP oxidoreductase (By similarity).
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -!- SIMILARITY: BELONGS TO THE PSAE FAMILY.
DR PIR; G56819; G56819.
KW Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.
FT NONTER 19
FT SEQUENCE 19 AA; 1810 NW; A93E8BDD089FB738 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 6 PPP 8

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RESULT 13
PRCT_PERAM STANDARD; PRT; 5 AA.
ID PRCT_PERAM
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach), and
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]_TaxID=6978, 6850, 6759;
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]_TaxID=76074708;
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]_TaxID=81225865;
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]_TaxID=90287800;
RP SEQUENCE.
RC SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
DB 3 LP 4

RESULT 14
TRPT_PSEFU STANDARD; PRT; 6 AA.
ID TRPT_PSEFU
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)

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DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TrpBA operon transcriptional activator (Fragment).
 GN TRP1.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PPG1 C1S;
 RX MEDLINE=89335826; PubMed=2503057;
 RA Eberly L., Crawford I.P.;
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
 putida.";
 RL Biochimie 71:521-531(1989).
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
 CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
 CC INDUCER (INDOLEGALACTOL PHOSPHATE), TRP1 BINDS UPSTREAM OF THE
 CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
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 CC EMBL; X13299; CAA31660.1; -;
 DR InterPro; IPR000847; HTH_LysR.
 DR PROSITE; PS00044; HTH_LYSR FAMILY; PARTIAL.
 KW Tryptophan biosynthesis; Transcription regulation; Activator;
 KW DNA-binding.
 FT NON-TER 6
 SQ SEQUENCE 6 AA; 693 MW; 77672AA1EDD6F000 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 LP 7
 Db ||
 5 LP 6
 RESULT 15
 VPI9_HSV1K STANDARD; PRT; 6 AA.
 ID VPI9_HSV1K
 AC P23210;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Capsid assembly and DNA maturation protein (Virion protein UL38)
 DE (Capsid protein VP19C) (Fragment).
 GN UL38.
 OS Herpes simplex virus (type 1 / strain KOS).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=10306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=91101287; PubMed=1846198;
 RX Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
 RA Silverstein S., Wagner E.K.;
 RT "Analysis of the herpes simplex virus type 1 promoter controlling the
 RT expression of UL38, a true late gene involved in capsid assembly.";
 RL J. Virol. 65:769-786(1991).
 CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
 CC EMBEDDED. BINDS DNA.
 CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
 CC

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 CC
 CC EMBL; M57646; AAA5830.1; -;
 DR EMBL; M57646; AAA5830.1; -;
 KW Capsid assembly; Coat protein; DNA-binding.
 FT NON-TER 6
 SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PL 6
 Db ||
 5 PL 6
 RESULT 16
 LANC_CARUI STANDARD; PRT; 7 AA.
 ID LANC_CARUI
 AC P36960;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lantibiotic carnocin UI49 (Fragment).
 OS Carnobacterium sp. (strain UI49).
 OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
 OC Carnobacterium.
 OX NCBI_TaxID=35782;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92321768; PubMed=1622206;
 RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
 RA Nes I.F.;
 RT "Purification and characterization of a new bacteriocin isolated from
 RT a Carnobacterium sp.";
 RL Appl. Environ. Microbiol. 58:1417-1422(1992).
 CC -!- FUNCTION: LANTHONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
 CC ACTIVE ON GRAM-POSITIVE BACTERIA.
 KW Antibiotic; Bacteriocin; Lantibiotic.
 FT NON-TER 7
 SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QP 3
 Db ||
 5 QP 6
 RESULT 17
 MNPI_LEPDE STANDARD; PRT; 7 AA.
 ID MNPI_LEPDE
 AC P42984;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Myotropic neuropeptide 1 (Led-MNP-I).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Insecta; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
 OC Chrysomelini; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.

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RC TISSUE=Head;
RA MEDLINE=95380343; PubMed=7651886;
RA Spittels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leuven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotrophic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata";
RL Peptides 16:365-374(1998).
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD_RES 7
FT SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
Db 5 PL 6

RESULT 18
TPFY_PACDA
ID TPFY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Trypophyllin-1 (pdt-1)
OS Pachymedusa dactylosa (Giant mexican leaf frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
CC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]_TaxID=75988;
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.P., Shaw C.;
RA "Pachymedusa dactylosa tryptophyllin-1 (pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA.";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra...; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD_RES 3
FT MOD_RES 3 HYDROXYLATION.
FT MOD_RES 7
FT SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
Db 2 PP 3

RESULT 19
UF04_MOUSE
ID UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)

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DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE.
RC TISSUE=Fibroblast;
RA MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON_TER 7
FT SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
Db 3 PP 4

RESULT 20
UN06_PINPS
ID UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]_TaxID=71647;
RP SEQUENCE.
RC TISSUE=Needle;
RA MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON_TER 1
FT NON_TER 7
FT SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
Db 5 LP 6

RESULT 21
ALL5_CALVO
ID ALL5_CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Calliostatin 5 (Met-calliostatin 1) ([Hyp3]Met-calliostatin).
OS Calliphora vomitoria (Blue blowfly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93211980; PubMed=8460157;
 RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
 RA Thorpe A.;
 RA "Calliostatins: neuropeptides from the blowfly Calliphora vomitoria
 RT with sequence homology to cockroach allatostatins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
 RN [2]
 RP CHARACTERIZATION, AND HYDROXYLATION.
 RC TISSUE=Head;
 RX MEDLINE=94342269; PubMed=8063725;
 RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
 RA "[Hyp3]Met-calliostatin. Identification and biological properties of
 RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
 RL J. Biol. Chem. 269:21059-21066(1994).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
 CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
 CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
 CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
 CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
 CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 DR PIR; E47393.
 KW Neuropeptide; Amidation; Hydroxylation.
 FT MOD_RES 3 3 HYDROXYLATION (20%).
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PP 4
 DB 2 PP 3
 RESULT 22
 ALL6_CYPDPO STANDARD; PRT; 8 AA.
 AC P82157;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 6.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RA "Lepidopteran peptides of the allatostatin superfamily.";
 RT Peptides 18:1301-1309(1997).
 RL -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 LP 7
 DB 2 PP 3
 RESULT 23
 COM2_CONPU STANDARD; PRT; 8 AA.
 AC P58785;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leu-contryphan-P.
 OS Conus purpurascens (Purple cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorboconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=41690;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC STRAIN=Clipperton Island; TISSUE=Venom;
 RX MEDLINE=99388939; PubMed=10461743;
 RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
 RA Olivera B.M.;
 RA "A novel D-leucine-containing Conus peptide: diverse conformational
 RT dynamics in the contryphan family.";
 RL J. Pept. Res. 54:93-99(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
 CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
 KW Toxin; Hydroxylation; D-amino acid.
 FT DISULFID 2 8
 FT MOD_RES 4 4 D-LEUCINE.
 SQ SEQUENCE 8 AA; 890 MW; 75A367672732C5B8 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 LP 7
 DB 5 LP 6
 RESULT 24
 NPB_BOVIN STANDARD; PRT; 8 AA.
 AC P15507;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropeptide B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=86067985; PubMed=3865193;
 RA Yang H.-Y.T., Pratta W., Majane E.A., Costa E.;
 RA "Isolation, sequencing, synthesis, and pharmacological
 RT characterization of two brain neuropeptides that modulate the action
 RT of morphine.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7757-7761(1995).
 CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
 DR PIR; B24749; B24749.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 QY 6 LP 7
 DB 2 PP 3

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3

Db 4 QP 5

RESULT 25

PPK2 PERAM

ID _PPK2 PERAM STANDARD; PRT; 8 AA.

AC P82692;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;

OC Blattidae; Periplaneta.

OX NCBI_TaxID=6978;

RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=Corpora cardiaca;

RX MEDLINE=97353923; PubMed=9210163;

RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;

RT "Isolation and structural elucidation of two pyrokinins from the

RT retrocerebral complex of the American cockroach.";

RL Peptides 18:473-478(1997).

RN [2]

RP TISSUE SPECIFICITY.

RX MEDLINE=20189894; PubMed=10723010;

RA Predel R., Eckert M.;

RT "Tagma-specific distribution of FXPRLamides in the nervous system of

RT the American cockroach";

RL J. Comp. Neurol. 419:352-363(2000).

CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

CC (MYOTROPIC ACTIVITY).

CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.

CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.

CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

DR InterPro: IPR001484; Pyrokinin.

DR PROSITE: PS00539; PYROKININ; FALSE NEG.

KW Neuropeptide; Amidation; Pyrokinin.

FT MOD RES 8

SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match

Best Local Similarity 28.6%; Score 2; DB 1; Length 8;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PP 4

Db 2 PP 3

RESULT 26

AL10 CARMA

ID _AL10 CARMA STANDARD; PRT; 9 AA.

AC P81813;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Carcinustatin 10.

OS Carcinus maenas (Common shore crab) (Green crab).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

OC Eubrachyura; Portunoides; Portunidae; Carcinus.

OX NCBI_TaxID=6759;

RN [1]

RP SEQUENCE.

RC TISSUE=Cerebral ganglion, and Thoracic ganglion;

RX MEDLINE=98121193; PubMed=9461295;

RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

RA Thorpe A.;

RT "Isolation and identification of multiple neuropeptides of the

RT allatostatin superfamily in the shore crab Carcinus maenas.";

RL Eur. J. Biochem. 250:727-734(1997).

CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.

CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

KW Neuropeptide; Amidation; Multigene family.

FT MOD RES 9

SQ SEQUENCE 9 AA; 963 MW; 372D79DCB4776C7 CRC64;

Query Match

Best Local Similarity 28.6%; Score 2; DB 1; Length 9;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3

Db 3 QP 4

RESULT 27

COXE THUOB

ID _COXE THUOB STANDARD; PRT; 9 AA.

AC P80975;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).

OS Thunnus obesus (Bigeye tuna).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;

OC Scombridae; Thunnus.

OX NCBI_TaxID=8241;

RN [1]

RP SEQUENCE.

RC TISSUE=Heart;

RX MEDLINE=97454291; PubMed=9310366;

RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.;

RA Kadenbach B.;

RT "The subunit structure of cytochrome-c oxidase from tuna heart and

RL Eur. J. Biochem. 248:99-103(1997).

CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE

CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN

CC MITOCHONDRIAL ELECTRON TRANSPORT.

CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome

CC c + 2 H(2)O.

CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.

CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.

DR PIR; S77984; S77984.

DR InterPro: IPR001349; COX6A.

DR PROSITE: PS01329; COX6A; PARTIAL.

KW Oxidoreductase; Inner membrane; Mitochondrion.

FT NON TER 1

FT NON TER 9

SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match

Best Local Similarity 28.6%; Score 2; DB 1; Length 9;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3

Db 3 QP 4

RESULT 28

FAR3 PENMO

ID _FAR3 PENMO STANDARD; PRT; 9 AA.

AC P83318;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE FMRamide-like neuropeptide FLP3 (AOPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=VALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 2 QP 3

RESULT 29
FAR4_PENMO
ID FAR4_PENMO STANDARD; PRT; 9 AA.
AC P8319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP4 (SQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=VALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 2 QP 3

RESULT 30
FAR9_ASCSU
ID FAR9_ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF9.
OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
DB 6 PL 7

RESULT 31
FRFL_SARBU
ID FRFL_SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMRFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRFamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 9 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 1 QP 2

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RESULT 32

KNL3_BOMVA
ID_KNL3_BOMVA STANDARD; PRT; 9 AA.
AC P83058; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjorson A.J., McLean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens."
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
arterial smooth muscle and constriction of intestinal smooth
muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PP 4

Db 2 PP 3

RESULT 33

LMT3_LOCMI
ID_LMT3_LOCMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytropin 3 (LOM-WT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamytropin III and
IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamytropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3

Db 3 QP 4

RESULT 34

OXYA_SQUAC
ID_OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspartocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Bur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00284; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB444404B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PL 6

Db 7 PL 8

RESULT 35

OXYT_RABIT
ID_OXYT_RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit).
OS Hippopotamus amphibius (Hippopotamus),
OS Balaenoptera physalus (Finback whale) (Common rorqual), and
OS Tachyglossus aculeatus (Australian echidna), and
OS Hydrolagus colliiei (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RP SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophysial hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).


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RN RP SEQUENCE.
RC SPECIES=H.amphibius;
RA MEDLINE=71232719; PubMed=5406007;
RX Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RL neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
[3]
RN RP SEQUENCE.
RC SPECIES=B.physalus;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin.";
RL Nature 201:191-192(1964).
[4]
RN RP SEQUENCE.
RC SPECIES=A.aculeatus;
RX MEDLINE=73223515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Neurohypophysial hormones and evolution of tetrapods.";
RL Nature New Biol. 244:124-126(1973).
[5]
RN RP SEQUENCE.
RC SPECIES=H.collicia; PubMed=5366118;
RX MEDLINE=70088110;
RA Pickering B.T., Heller H.;
RT "Oxytocin as a neurohypophysial hormone in the holocephalian
RT elasmobranch fish, Hydrolagus collei";
RL J. Endocrinol. 45:597-606(1969).
CC -!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
CC UTERUS AND OF THE MAMMARY GLAND.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A91466; A91466.
DR PIR; A92774; A92774.
DR PIR; A93147; A93147.
DR PIR; A93408; A93408.
DR PIR; B90667; B90667.
DR PDB; 1XY1; 15-OCT-90.
DR PDB; 1XY2; 15-OCT-90.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Hypothalamus; Amidation; 3D-structure.
FT DISULFID 1
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
DB 7 PL 8

RESULT 36
RS10_SERMA STANDARD; PRT; 9 AA.
AC O68936;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S10 (Fragment).
GN RPSJ.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
[1]_TaxID=615;
RN [1]_
RP SEQUENCE FROM N.A.
RA Noorani S.M., Lindahl L., Zengel J.M.;
RA Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Involved in the binding of tRNA to the ribosomes (By
CC similarity). BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.
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DR EMBL; AF058451; AAC14294.1; -
DR HAMAP; MF_00508; -; 1.
DR InterPro; IPR001848; Ribosomal_S10.
DR PROSITE; PS00361; RIBOSOMAL_S10; PARTIAL.
KW Ribosomal protein.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1214 MW; DE3944004416D456 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQ 2
DB 1 MQ 2

RESULT 37
RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRPS33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 5 QP 6

RESULT 38
UPA3_HUMAN STANDARD; PRT; 9 AA.
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)

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DT 01-APR-1993 (Rel. 25, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RA MEDLINE=93092937; PubMed=1459097;
RX Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
DR SWISS-2DPAGE; P30089; HUMAN.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1056 MW; 2672B1BAF769C737 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
Db 2 PL 3

RESULT 39
YBFR AZOVI
ID YBFR AZOVI STANDARD; PRT; 9 AA.
AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3' region (Fragment).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196129; PubMed=1549605;
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RA Stiefel E.I.;
RT "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
CC -----
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CC -----
DR EMBL; M83692; AAA22122.1; -
DR FTR; B41983; B41983.
KW Hypothetical protein.
FT NON_TER 9
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
Db 3 PP 4

RESULT 40
AH3_PRUSE
ID AH3_PRUSE STANDARD; PRT; 10 AA.
AC P29261;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
DE Isozyme II) (AH II) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
CC Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
Db 3 PP 4

RESULT 41
BPP2_BOTIN
ID BPP2_BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR FTR; B37196; B37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1
FT MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

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Query Match      28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PP 4
DB      9 PP 10

RESULT 42
BPP2 BOTJA
ID_BPP2_BOTJA STANDARD; PRT; 10 AA.
AC P01022;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme inhibitor V-6-II).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
CC -|- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; A01255; XAVI6B.
DR Hypotensive agent; Pyrrolidone carboxylic acid.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT SEQUENCE 10 AA; 1232 MW; 30C53546C741773 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PP 4
DB      9 PP 10

RESULT 43
BPP8 BOTIN
ID_BPP8_BOTIN STANDARD; PRT; 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RA "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).

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CC -|- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; H37196; H37196.
DR Hypotensive agent; Pyrrolidone carboxylic acid.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PP 4
DB      9 PP 10

RESULT 44
BPP VIPAS
ID_BPP_VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting enzyme inhibitor).
OS Vipera aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90382616; PubMed=2169439;
RA Komori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting enzyme from the venom of Vipera aspis aspis.";
RL Int. J. Biochem. 22:767-771(1990).
CC -|- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; A60377; XASNPC.
DR Hypotensive agent; Pyrrolidone carboxylic acid.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PP 4
DB      9 PP 10

RESULT 45
BRK ONCMY
ID_BRK_ONCMY STANDARD; PRT; 10 AA.
AC Q9PRZ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.

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RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
RL trout plasma.";
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR; S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PP 4
Db 3 PP 4

RESULT 46
CATB_SHEEP
ID CATB_SHEEP STANDARD; PRT; 10 AA.
AC P83205;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).
GN CT5B.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22394055; PubMed=12506352;
RA El Amir B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,
RA Mboko H.B., Beckers J.-F.M.P.;
RT "Isolation and partial characterization of three pregnancy-associated
RT glycoproteins from the ewe placenta.";
RL Mol. Reprod. Dev. 64:199-206(2003).
CC -!- FUNCTION: Thiol protease which is believed to participate in
CC intracellular degradation and turnover of proteins. Has also been
CC implicated in tumor invasion and metastasis.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity
CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in
CC small molecule substrates (thus differing from cathepsin L). In
CC addition to being an endopeptidase, shows peptidyl-dipeptidase
CC activity, liberating C-terminal dipeptides
CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked
CC by a disulfide bond (By similarity).
CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR InterPro; IPR000169; SHP00t_acsite.
DR PROSITE; PS00640; THIOI_PROTEASE_ASN; PARTIAL.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; PARTIAL.
KW Hydrolase; Thiol protease; Lysosome.
FT NON TER 10
SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LP 7
Db 1 LP 2

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RESULT 47
FAR6_PANRE
ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of RMRamide-related
RT peptides (FARPs) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 10
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3
Db 5 QP 6

RESULT 48
GONI_ALLMI
ID GONI_ALLMI STANDARD; PRT; 10 AA.
AC P37041; P20407;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 4, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)
DE (Luliberin I).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR PIR; A60066; RHAQ1.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD RES 1
SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 8 QP 9

RESULT 49
GON3_ONCKE
ID GON3_ONCKE STANDARD; PRT; 10 AA.
AC P20367; P81751;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III) (LH-RH III) (Luliberin III).
GN GNRH3.
OS Onchorynchus keta (Chum salmon), and
OS Clupea pallasi (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018, 30724;
RN [1]
RP SPECIES=O.keta;
RC SPECIES=83195140; PubMed=6341999;
RX Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
RA "Characterization of a teleost gonadotropin-releasing hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
RN [2]
RP SEQUENCE, AND FUNCTION.
RC SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
RX MEDLINE=20114351; PubMed=10650929;
RA Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
hormones, including a novel form, from an ancient teleost, herring."
RL Endocrinology 141:505-512(2000).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
the secretion of both luteinizing and follicle-stimulating
hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
DR PIR; A21114; A21114;
DR InterPro: IPR002012; GNRH.
DR Pfam: PF00446; GNRH; 1.
DR PROSITE: PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 10 10
FT AMIDATION.
SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
DB 8 LP 9

RESULT 50
GONL_SQUAC
ID GONL_SQUAC STANDARD; PRT; 10 AA.
AC P27429;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin (Gonadotropin-releasing hormone) (GNRH) (LH-RH) (Luliberin).
OS Squalea acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92335300; PubMed=1631133;
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
RA Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in
dogfish brain provides insight into GNRH evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
DR PIR; A46030; A46030.
DR InterPro: IPR002012; GNRH.
DR Pfam: PF00446; GNRH; 1.
DR PROSITE: PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 10 10
FT AMIDATION.
SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
DB 8 LP 9

RESULT 51
NO40_TOBAC
ID NO40_TOBAC STANDARD; PRT; 10 AA.
AC P55962;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early nodulin 40 homolog.
GN ENOD40.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Petit Havana SRL;
RX MEDLINE=96320417; PubMed=8662527;
RA van de Sande K., Pawlowski K., Czaja I., Wieneke U., Schell J.,
RA Schmidt J., Waiden R., Matvienko M., Weillink J., van Kammen A.,
RA Franssen H., Bisseling T.;
RT "Modification of phytohormone response by a peptide encoded by ENOD40
of legumes and a nonlegume.";
RL Science 273:370-373(1996).
CC -!- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
GROWTH REGULATOR THAT ALTERS PHYTHORMONE RESPONSES.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X98716; CAA67267.1; -.
KW Modulation.
SQ SEQUENCE 10 AA; 1173 MW; 2A3248E05DDB1AB3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQ 2
DB 1 MQ 2

RESULT 52
NSL MYCTU
ID NSL MYCTU STANDARD; PRT; 10 AA.
AC P81135;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30 kDa non-secretory protein 1 (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE
RC STRAIN=H37Rv;
RA Prasad H.K., Annappurna P.S.;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -!- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37Rv.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
DB 4 PL 5

RESULT 53
PSBF CAPAN
ID PSBF CAPAN STANDARD; PRT; 10 AA.
AC Q03367;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytochrome b559 beta subunit (PSII reaction center subunit VI)
DE (Fragment).
GN PSBF.
OS Capsicum annuum (Bell pepper).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridaceae; lamiids; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lamuyo; TISSUE=Fruit, and Leaf;
RX MEDLINE=9309270; PubMed=1463853;
RA Kuntz M., Camara B., Weil J.-H., Schantz R.;
RT "The psbL gene from bell pepper (Capsicum annuum): plastid RNA
RT editing also occurs in non-photosynthetic chromoplasts."
RL Plant Mol. Biol. 20:1185-1188(1992).
CC -!- FUNCTION: This b-type cytochrome is tightly associated with the
CC reaction center of photosystem II and possibly is part of the
CC water-oxidation complex.
CC -!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC -!- SIMILARITY: Belongs to the psbE / psbF family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC
CC -----
DR EMBL; X65570; CAA46539.1; -.
DR PIR; S28055; S28055.
DR HAMAP; MF 00643; -; 1.
DR InterPro; IPR006216; Cyt_b559.
DR PROSITE; PS00537; CYTOCHROME_B559; PARTIAL.
KW Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT NON_TER 1
FT TRANSMEM <1 5 BY SIMILARITY.
FT DOMAIN 6 10 LUMENAL (POTENTIAL).
SQ SEQUENCE 10 AA; 1180 MW; 817D0F59D6D69DC5 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQ 2
DB 5 MQ 6

RESULT 54
TEMK RANTE
ID TEMK RANTE STANDARD; PRT; 10 AA.
AC P56923;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin K.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
DB 2 LP 3

RESULT 55
TKL2 LOCOMI
ID TKL2 LOCOMI STANDARD; PRT; 10 AA.
AC P16224;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustachykinin II (TK-II).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=90184489; PubMed=2311766;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Locustatachykinin I and II, two novel insect neuropeptides with
 RT homology to peptides of the vertebrate tachykinin family.";
 RL FEBS Lett. 261:397-401(1990).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
 CC OVIDUCT AND FOREGUT.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD RES 10 10
 FT AVIDATION.
 SQ SEQUENCE 10 AA; 1066 MW; 5D52CD8B59C86587 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PL 6
 DB 2 PL 3
 RESULT 56
 ID UP2A2 HUMAN STANDARD; PRT; 10 AA.
 AC P30088;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.4, ITS MW IS: 49 KDa.
 CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
 CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
 CC PROTEIN.
 DR SWISS-2DPAGE; P30088; HUMAN.
 FT NON TER 1 1
 FT VARIANT 9 9 G -> Y.
 FT /FTID=VAR_000002.
 FT NON TER 10 10
 FT SEQUENCE 10 AA; 1079 MW; 51AC54AAB777587 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PP 4
 DB 5 PP 6
 RESULT 57
 ID UP2A5 HUMAN STANDARD; PRT; 10 AA.
 AC P30091;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.85, ITS MW IS: 40 KDa.
 CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
 CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
 CC PROTEIN.
 DR SWISS-2DPAGE; P30091; HUMAN.
 FT NON TER 1 1
 FT VARIANT 9 9 G -> Y.
 FT /FTID=VAR_000002.
 FT NON TER 10 10
 FT SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QP 3
 DB 3 QP 4
 RESULT 58
 ID URE3 MORMO STANDARD; PRT; 10 AA.
 AC P17339;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
 DE amidohydrolase) (Fragment).
 GN UREA.
 OS Morganella morganii (Proteus morganii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Morganella.
 OX NCBI_TaxID=582;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90264298; PubMed=2345135;
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.B.T.;
 RT "Morganella morganii urease: purification, characterization, and
 RT isolation of gene sequences.";
 RL J. Bacteriol. 172:3073-3080(1990).
 CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
 CC -!- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
 DR PIR; C35389; C35389.
 KW Hydrolase.
 FT NON TER 10 10
 FT SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQ 2
 DB 1 MQ 2

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RESULT 59
BPP3 BOTIN
ID_BPP3_BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -|- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; C37196; C37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
Db 4 PP 5

RESULT 60
BPP4 BOTIN
ID_BPP4_BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -|- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; D37196; D37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
Db 4 PP 5

RESULT 61
BPPB AGKHA
ID_BPPB_AGKHA STANDARD; PRT; 11 AA.
AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffi.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
CC -|- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; A01254; XASNBA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
Db 3 LP 4

RESULT 62
BPP AGKHP
ID_BPP_AGKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
RT from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -|- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.

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DR PIR: JC0002; XAVIBH.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
DB 4 PP 5

RESULT 63
BRK_MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megascollakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like peptide ([Thr6]bradykinin)].
OS Megascollia flavifrons (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Scolioidea;
OC Scoliidae; Megascollia.
CX NCBI_TaxID=7437;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=87293024; PubMed=3617088;
RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
RT "Two kinins isolated from an extract of the venom reservoirs of the solitary wasp Megascollia flavifrons.";
RL Toxicol 25:527-535 (1987).
RN [2]
RP SEQUENCE.
RC TISSUE=Venom;
RA Nakajima T., Piek T., Yasuhara T., Mantel P.;
RT "Two kinins isolated from the venom of Megascollia flavifrons.";
RL Toxicol 26:34-34 (1988).
CC -!- FUNCTION: Both proteins have bradykinin-like, although lower activities (e.g. smooth muscle contraction).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR; E26744; B26744.
KW Bradykinin; Vasodilator.
FT PEPTIDE 1 11 MEGASCOLIAKININ.
FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
DB 2 PP 3

RESULT 64
BFG_CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.

NCBI_TaxID=1501;
[1]
SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806 (1998).
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of the nascent protein chain from the A-site to the P-site of the ribosome.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACITOR GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON TER 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
DB 3 PL 4

RESULT 65
LADD_ONCMY STANDARD; PRT; 11 AA.
ID LADD_ONCMY
AC P81018;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Ladderlectin (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
CX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97293418; PubMed=9149391;
RA Jensen L.E., Thiel S., Petersen T.E., Jensenuis J.C.;
RT "A rainbow trout lectin with multimeric structure.";
RL Comp. Biochem. Physiol. 116B:385-390 (1997).
CC -!- FUNCTION: LECTIN THAT BINDS SEPHAROSE.
CC -!- COFACTOR: CALCIUM IS ESSENTIAL FOR SEPHAROSE BINDING.
CC -!- SUBUNIT: MULTIMERIC.
KW Lectin; Calcium.
FT NON TER 11
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
DB 9 PP 10

RESULT 66
LPW_THETH STANDARD; PRT; 11 AA.
ID LPW_THETH
AC P05624;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Tip operon leader peptide.
GN TREL.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN (1) SEQUENCE FROM N.A.
RP STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
RL HB8 trpE and trpG";
RL Biochim. Biophys. Acta 950:303-312(1988).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X07744; CAA30565.1; -.
DR Tryptophan biosynthesis; Leader peptide.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DCSA7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LP 7
Db 3 LP 4

RESULT 57
PQQC_PSEFL STANDARD; PRT; 11 AA.
ID PQQC_PSEFL
AC P55173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Coenzyme PQQ synthesis protein C (fragment).
GN PQQC.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN (1) SEQUENCE FROM N.A.
RP STRAIN=CHAO;
RX MEDLINE=96064397; PubMed=8526497;
RA Schnider U., Keel C., Defago G., Haas D.;
RT "R5-directed cloning of pqq genes from Pseudomonas fluorescens CHAO:
RT mutational inactivation of the genes results in overproduction of the
RT antibiotic pyoluteorin";
RL Appl. Environ. Microbiol. 61:3856-3864(1995).
CC -!- FUNCTION: REQUIRED FOR COENZYME PYRROLO-QUINOLINE-QUINONE (PQQ)
CC BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER BACTERIAL PQQC.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X87299; CAA60734.1; -.

DR PIR: S58244; S58244.
KW PQQ.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1182 MW; 89DF46B4C5B73771 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PL 6
Db 5 PL 6

RESULT 68
TKN1_PSEGU STANDARD; PRT; 11 AA.
ID TKN1_PSEGU
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-I (PG-KI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN (1) SEQUENCE.
RP TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: B60409; B60409.
DR InterPro: IPR003580; Protsachykinin.
DR InterPro: IPR002040; tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT MOD_RES 11 11
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3
Db 1 QP 2

RESULT 69
TKN1_UPERU STANDARD; PRT; 11 AA.
ID TKN1_UPERU
AC P08612;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperolein.
OS Uperoleia rugosa (wrinkled toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=75131227; PubMed=1120493;
 RA Anastasi A., Erspamer V., Edean R.;
 RT "Structure of uperolein, a physalaemin-like endcapeptide occurring
 in the skin of Uperoleia rugosa and Uperoleia marmorata.";
 RL Experientia 31:394-395(1975).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 DR Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
 KX MOD RES 1 1
 FT MOD RES 11 11
 SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.1e-03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
 ||
 Db 1 QP 2

RESULT 70

TKN2 PSEGU
 ID TKN2 PSEGU STANDARD; PRT; 11 AA.
 AC P42987;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-II (PG-KII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog Pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; C60409; C60409.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.

DR PROSITE: PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 1 1
 FT MOD RES 11 11
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
 ||
 Db 1 QP 2

RESULT 71

TKN3 PSEGU
 ID TKN3 PSEGU STANDARD; PRT; 11 AA.
 AC P42988;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-III (PG-KIII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog Pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; D60409; D60409.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 1 1
 FT MOD RES 11 11
 SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.1e-03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
 ||
 Db 1 QP 2

RESULT 72

TKN4 PSEGU
 ID TKN4 PSEGU STANDARD; PRT; 11 AA.
 AC P42989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Substance P-like peptide I (PG-SPI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; E60409; E60409.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
DR Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
DR Pyroglutamate carboxylic acid.
FT MOD_RES 1 11 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QP 3
Db ||
1 QP 2

RESULT 73
TKN5_PSEGU ID TKN5_PSEGU STANDARD; PRT; 11 AA.
AC P42390;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide II (Pg-SPII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; F60409; F60409.

DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
DR Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
DR Pyroglutamate carboxylic acid.
FT MOD_RES 1 11 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QP 3
Db ||
1 QP 2

RESULT 74
TKN_ELEMO ID TKN_ELEMO STANDARD; PRT; 11 AA.
AC P01293;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Eledoisin.
OS Eledone moschata (Musk octopus) (Ozaena moschata), and
OS Eledone cirrhosa (Curled octopus) (Ozaena cirrosa).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
OX NCBI_TaxID=6641, 102876;
RN [1]
RP SEQUENCE.
RA Anastasi A., Erspamer V.;
RT "The isolation and amino acid sequence of eledoisin, the active
RT endecapeptide of the posterior salivary glands of Eledone.";
RL Arch. Biochem. Biophys. 101:56-65(1963).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; A01561; EOOC.
DR PIR; B01561; EOOC.
DR PDB; 1MXQ; 18-FEB-03.
DR InterPro; IPR002040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; 1.
DR Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
DR 3D-structure.
FT MOD_RES 1 11 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QP 3
Db ||
1 QP 2

RESULT 75
FAR7_PENMO ID FAR7_PENMO STANDARD; PRT; 12 AA.
AC P83322;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DR PIR; F60409; F60409.

DE FMRamide-like neuropeptide FLP7 (GYRPPFNGSIF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1381.4; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1383 MW; 31209192EF49D777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
Db 5 PP 6

Search completed: November 25, 2003, 18:17:21
Job time : 5.3883 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 16.867 Seconds
(without alignments)
107.095 Million cell updates/sec

Title: US-09-641-801-1

Perfect score: 7

Sequence: 1 MQPPPLP 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6368

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: listing first 100 summaries

Database :

SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mbc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteria:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	4	57.1	18	12	Q84129		Q84129 influenza
2	4	57.1	19	4	Q9UC80		Q9UC80 homo sapien
3	4	57.1	20	2	O50180		O50180 pseudomonas
4	4	57.1	20	4	Q9UCA8		Q9UCA8 homo sapien
5	4	57.1	20	12	Q912B4		Q912B4 human eryth
6	3	42.9	9	2	P83157		P83157 anabaena sp
7	3	42.9	9	5	Q9TWV0		Q9TWV0 anthopleura
8	3	42.9	9	10	Q9S8J8		Q9S8J8 oryza sativ
9	3	42.9	9	10	P82429		P82429 nicotiana t
10	3	42.9	9	16	Q935G1		Q935G1 salmonella
11	3	42.9	10	8	Q8SHA8		Q8SHA8 rhampoleon
12	3	42.9	10	11	Q9QVF7		Q9QVF7 rattus sp.
13	3	42.9	10	11	Q8VHM9		Q8VHM9 mus musculu
14	3	42.9	10	12	Q9Q0W9		Q9Q0W9 polyomaviru
15	3	42.9	10	12	Q8JV70		Q8JV70 polyomaviru
16	3	42.9	10	12	Q9Q0W1		Q9Q0W1 polyomaviru

17	3	42.9	10	12	Q8JV68		Q8JV68 polyomaviru
18	3	42.9	10	12	Q9Q0V9		Q9Q0V9 polyomaviru
19	3	42.9	10	12	Q9Q0W7		Q9Q0W7 polyomaviru
20	3	42.9	10	12	Q8JV66		Q8JV66 polyomaviru
21	3	42.9	10	12	Q9Q0V7		Q9Q0V7 polyomaviru
22	3	42.9	10	12	Q8JV82		Q8JV82 polyomaviru
23	3	42.9	10	12	Q8JV76		Q8JV76 polyomaviru
24	3	42.9	10	12	P90391		P90391 tomato yell
25	3	42.9	10	12	Q8JV74		Q8JV74 polyomaviru
26	3	42.9	10	12	Q9Q0W5		Q9Q0W5 polyomaviru
27	3	42.9	10	12	Q9Q0X3		Q9Q0X3 polyomaviru
28	3	42.9	10	12	Q9Q0X5		Q9Q0X5 polyomaviru
29	3	42.9	10	12	Q9Q0W3		Q9Q0W3 polyomaviru
30	3	42.9	10	12	Q8JV80		Q8JV80 polyomaviru
31	3	42.9	10	12	Q9Q0X1		Q9Q0X1 polyomaviru
32	3	42.9	10	12	Q9Q0X9		Q9Q0X9 polyomaviru
33	3	42.9	10	12	Q8JV72		Q8JV72 polyomaviru
34	3	42.9	11	4	Q8IVG8		Q8IVG8 homo sapien
35	3	42.9	11	10	P82436		P82436 nicotiana t
36	3	42.9	11	13	Q8UTP1		Q8UTP1 xenopus lae
37	3	42.9	12	2	Q8KZ86		Q8KZ86 acinetobact
38	3	42.9	12	4	Q9BZ49		Q9BZ49 homo sapien
39	3	42.9	12	4	Q9NTQ2		Q9NTQ2 homo sapien
40	3	42.9	12	10	Q93X21		Q93X21 zea mays (m
41	3	42.9	12	10	P82328		P82328 pisum sativ
42	3	42.9	13	4	Q14182		Q14182 homo sapien
43	3	42.9	13	8	Q9T569		Q9T569 zea mays (m
44	3	42.9	13	11	Q88176		Q88176 mus musculu
45	3	42.9	13	12	Q67604		Q67604 squash leaf
46	3	42.9	13	16	Q8X4F5		Q8X4F5 escherichia
47	3	42.9	14	10	P82326		P82326 pisum sativ
48	3	42.9	15	6	Q9TR14		Q9TR14 bos taurus
49	3	42.9	15	10	Q9S8N8		Q9S8N8 hordeum vul
50	3	42.9	15	10	Q40562		Q40562 nicotiana t
51	3	42.9	15	10	Q40563		Q40563 nicotiana t
52	3	42.9	15	10	P82439		P82439 nicotiana t
53	3	42.9	16	4	Q9NNZ2		Q9NNZ2 homo sapien
54	3	42.9	16	5	Q9TNW7		Q9TNW7 toxoplasma
55	3	42.9	16	6	Q9BGG8		Q9BGG8 sorex arane
56	3	42.9	16	6	Q9TRQ7		Q9TRQ7 bos taurus
57	3	42.9	16	10	Q8RVF4		Q8RVF4 zea mays (m
58	3	42.9	16	12	Q83967		Q83967 influenzavi
59	3	42.9	16	12	Q83960		Q83960 influenzavi
60	3	42.9	16	12	Q84055		Q84055 influenzavi
61	3	42.9	17	4	Q96P96		Q96P96 homo sapien
62	3	42.9	17	4	Q14001		Q14001 homo sapien
63	3	42.9	17	6	Q9TR22		Q9TR22 bos taurus
64	3	42.9	17	6	Q9TR78		Q9TR78 didelphis m
65	3	42.9	17	6	Q9TRU8		Q9TRU8 bos taurus
66	3	42.9	17	10	Q49225		Q49225 glycine max
67	3	42.9	17	10	Q41400		Q41400 sesbania ro
68	3	42.9	17	13	Q9P839		Q9P839 carassius a
69	3	42.9	18	4	Q16244		Q16244 homo sapien
70	3	42.9	18	4	Q9UCT9		Q9UCT9 homo sapien
71	3	42.9	18	4	Q8NFB4		Q8NFB4 homo sapien
72	3	42.9	18	4	Q9H1I3		Q9H1I3 homo sapien
73	3	42.9	18	6	Q9TQR9		Q9TQR9 mammothus p
74	3	42.9	18	10	Q9S915		Q9S915 triticum tu
75	3	42.9	18	11	Q9JIE9		Q9JIE9 mus musculu
76	3	42.9	18	13	Q8QFT3		Q8QFT3 gallus gall
77	3	42.9	19	2	Q9R8V1		Q9R8V1 pseudomonas
78	3	42.9	19	4	Q9UCL3		Q9UCL3 homo sapien
79	3	42.9	19	4	Q9UCK6		Q9UCK6 homo sapien
80	3	42.9	19	8	Q31687		Q31687 artemia par
81	3	42.9	19	10	Q947T4		Q947T4 oryza sativ
82	3	42.9	19	10	P82941		P82941 hordeum vul
83	3	42.9	19	12	Q8UY03		Q8UY03 hepatitis c
84	3	42.9	19	12	Q8UXY5		Q8UXY5 hepatitis c
85	3	42.9	19	12	Q8UY00		Q8UY00 hepatitis c
86	3	42.9	19	12	Q8UXZ1		Q8UXZ1 hepatitis c
87	3	42.9	19	12	Q8UXZ7		Q8UXZ7 hepatitis c
88	3	42.9	19	12	Q8UXZ9		Q8UXZ9 hepatitis c
89	3	42.9	19	12	Q8UY02		Q8UY02 hepatitis c

90 Q69099 herpes simp
 91 Q8uxz4 hepatitis c
 92 Q8uy07 hepatitis c
 93 Q8uxz3 hepatitis c
 94 Q8uy04 hepatitis c
 95 Q8uxz6 hepatitis c
 96 Q9prt0 gallus gall
 97 Q91380 gallus gall
 98 Q9prn4 petromyzon
 99 Q9ps40 carassius a
 100 Q90rf8 human immun

ALIGNMENTS

RESULT 1
 Q84129 PRELIMINARY; PRT; 18 AA.
 AC Q84129;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Influenza A/Swine/Wisconsin/OM/2 (H1N1), non-structural protein (Seg
 8), COOH terminus of NS1 (Fragment).
 DE Influenzavirus A.
 OS Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses.
 OC NCBI_TaxID=197911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83303830; PubMed=6612993;
 RA Parvin J.D., Young J.P., Palese P.;
 RT "nonsense mutations affecting the lengths of the ns1 nonstructural
 RT proteins of influenza A virus isolates.";
 RL Virology 128:512-517(1983).
 DR ENBL; K00959; AAA43541.1; -;
 DR InterPro; IPR000256; Flu_NS1.
 DR Pfam; PF00600; Flu_NS1; 1.
 FT NON TER 1
 Q9UC80 PRELIMINARY; PRT; 19 AA.
 AC Q9UC80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE 21.5 kDa stone matrix protein (EC 1.15.1.1) (Superoxide dismutase
 DE [Mn/Fel] (Fragment)).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95215817; PubMed=7701298;
 RA Binette J.P., Binette M.B.;
 RT "Sequencing of proteins extracted from stones.";
 RL Scanning Microsc. 8:233-239(1994).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).

Query Match 57.1%; Score 4; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 Db 11 PPLP 14

RESULT 2
 Q9UC80 PRELIMINARY; PRT; 19 AA.
 AC Q9UC80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE 21.5 kDa stone matrix protein (EC 1.15.1.1) (Superoxide dismutase
 DE [Mn/Fel] (Fragment)).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95215817; PubMed=7701298;
 RA Binette J.P., Binette M.B.;
 RT "Sequencing of proteins extracted from stones.";
 RL Scanning Microsc. 8:233-239(1994).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).

Query Match 57.1%; Score 4; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 Db 11 PPLP 14

CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 19 AA; 2116 MW; A0D0DAB848EE7894 CRC64;

Query Match 57.1%; Score 4; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 Db 5 PPLP 8

RESULT 3

O50180 PRELIMINARY; PRT; 20 AA.
 AC O50180;
 DT 01-JAN-1999 (TrEMBLrel. 09, Created)
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Acetyl-CoA synthetase (Fragment).
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OC NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PA01;
 RX MEDLINE=99008987; PubMed=9791103;
 RA Nishijyo T., Park S.M., Lu C.D., Itoh Y., Abdelal A.T.;
 RT "Molecular characterization and regulation of an operon encoding a
 RT system for transport of arginine and ornithine and the ArgR regulatory
 RT protein in Pseudomonas aeruginosa.";
 RL J. Bacteriol. 180:5559-5566(1998).
 DR EMBL; AF012537; AAC71069.1; -;
 DR InterPro; IPR000873; AMP-bind.
 DR PROSITE; PS00455; AMP BINDING; PARTIAL.
 FT NON TER 1
 Q9UC80 PRELIMINARY; PRT; 20 AA.
 AC Q9UC80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Tumor-derived adhesion factor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94161713; PubMed=8117260;
 RA Akaogi K., Okabe Y., Funahashi K., Yoshitake Y., Nishikawa K.,
 RA Yasumitsu H., Umeda M., Miyazaki K.;
 RT "Cell adhesion activity of a 30-kDa major secreted protein from human
 RT bladder carcinoma cells.";
 RL Biochem. Biophys. Res. Commun. 198:1046-1053(1994).
 SQ SEQUENCE 20 AA; 1979 MW; EF6F9DC6DCA0AE8D CRC64;

Query Match 57.1%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 Db 10 PPLP 13

RESULT 4

O9UCA8 PRELIMINARY; PRT; 20 AA.
 AC Q9UCA8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Tumor-derived adhesion factor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94161713; PubMed=8117260;
 RA Akaogi K., Okabe Y., Funahashi K., Yoshitake Y., Nishikawa K.,
 RA Yasumitsu H., Umeda M., Miyazaki K.;
 RT "Cell adhesion activity of a 30-kDa major secreted protein from human
 RT bladder carcinoma cells.";
 RL Biochem. Biophys. Res. Commun. 198:1046-1053(1994).
 SQ SEQUENCE 20 AA; 1979 MW; EF6F9DC6DCA0AE8D CRC64;

Query Match 57.1%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 Db 10 PPLP 13

Query Match 57.1%; Score 4; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 ||||
 Db 15 PPLP 18

RESULT 5
 Q912B4 PRELIMINARY; PRT; 20 AA.
 AC Q912B4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 7.5-kDa nonstructural protein (Fragment).
 GN 7.5-KDA.
 OS Human erythrovirus V9.
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Erythrovirus.
 OX NCBI_TaxID=72197;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R234;
 RA Nguyen Q.T.;
 RT "Molecular cloning and sequencing of a novel human erythrovirus
 genome: new species beside B19 in the genus Erythrovirus.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ249875; CAC80689.1; -
 KW Nonstructural protein.
 FT NON_TER 1 20
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 1977 MW; F00971E8578CE490 CRC64;

Query Match 57.1%; Score 4; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 6
 ||||
 Db 4 PPPL 7

RESULT 6
 P83157 PRELIMINARY; PRT; 9 AA.
 AC P83157;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
 OS Anabaena sp. (strain L31).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TaxID=29412;
 [1]
 RP SEQUENCE.
 RA Apce S.K., Uhlemann E., Schmid R., Altendorf K.;
 RL Submitted (OCT-2001) to the SWISS-PROT data bank.
 CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
 CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 FAMILY.
 DR InterPro; IPR001189; SODismutase.
 DR PROSITE; PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Iron; Metal-binding.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1063 MW; C54267376B06C2C9 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
 ||||
 Db 6 PLP 8

RESULT 7
 Q9TWV0 PRELIMINARY; PRT; 9 AA.
 ID Q9TWV0;
 AC Q9TWV0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE ANTHO-RPAMIDE-NEUROPEPTIDE.
 DT Anthopleura elegantissima (Sea anemone).
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93126143; PubMed=1480510;
 RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
 RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPamide),
 an N-terminally protected, biologically active neuropeptide from sea
 anemones.";
 RL Peptides 13:851-857(1992).
 SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
 ||||
 Db 5 PLP 7

RESULT 8
 Q9S8J8 PRELIMINARY; PRT; 9 AA.
 ID Q9S8J8;
 AC Q9S8J8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE ORYZATENSIN-BIOACTIVE peptide.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 [1]
 RN SEQUENCE.
 RP MEDLINE=95102521; PubMed=7804141;
 RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
 RT "Isolation and characterization of oryzatensin: a novel bioactive
 peptide with ileum-contracting and immunomodulating activities derived
 from rice albumin.";
 RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
 DR Gramene; Q9S8J8; -
 SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 42.9%; Score 3; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
 ||||
 Db 6 PLP 8

RESULT 9


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P82429
ID P82429 PRELIMINARY; PRT; 9 AA.
AC
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 44 kDa cell wall protein (fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
KW NON_TER 9
FT SEQUENCE 9 AA; 986 MW; C22CQAD6C77776 CRC64;
SQ
Query Match 42.9%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
Db |||
2 QPP 4

RESULT 10
Q935G1 PRELIMINARY; PRT; 9 AA.
AC Q935G1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative membrane protein (fragment).
GN HCM1.01C.
OS Salmonella typhi.
OG Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=2153497; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Peltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL: AL513383; CAD09867.1; -.
KW Plasmid; Complete proteome.
FT NON_TER 9
FT SEQUENCE 9 AA; 904 MW; 5FCDC77776D86767 CRC64;
SQ
Query Match 42.9%; Score 3; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
Db |||
2 QPP 4

RESULT 11
Q8SHA8 PRELIMINARY; PRT; 10 AA.
ID Q8SHA8
AC Q8SHA8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytochrome c oxidase subunit I (fragment).
OS COI.
OS Rhampholeon spectrum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
OC Rhampholeon.
OX NCBI_TaxID=179929;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
RT Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF448772; AAL90598.1; -.
KW Mitochondrion.
KW NON_TER 10
FT SEQUENCE 10 AA; 1279 MW; 35BF8E27336409D7 CRC64;
SQ
Query Match 42.9%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOP 3
Db |||
1 MOP 3

RESULT 12
Q9QVF7 PRELIMINARY; PRT; 10 AA.
ID Q9QVF7
AC Q9QVF7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta 2-glycoprotein I, beta 2-GPI (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=921335065; PubMed=1777418;
RA Matsuura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,
RA Yasuda T., Koike T.;
RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by
RT cDNA cloning and inter-species differences of beta 2-GPI in
RT alternation of anticardiolipin binding.";
RL Int. Immunol. 3:1217-1221(1991).
FT NON_TER 1
FT NON_TER 10
FT SEQUENCE 10 AA; 1100 MW; 94E681B767376E1 CRC64;
SQ
Query Match 42.9%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
Db |||
5 PLP 7

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RESULT 13

Q8VHM9 PRELIMINARY; PRT; 10 AA.
 ID Q8VHM9
 AC Q8VHM9
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Interferon receptor 2a' (Fragment).
 GN IFNAR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
 RT "The genomic structure and expression patterns of the gene encoding
 RT the second chain of the murine interleukin 10 receptor, IL-10R2.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
 RT "The organization, transcriptional regulation and chromosomal
 RT localization of the locus encoding the gene for the murine type I
 RT interferon receptor, Ifnar2.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF440786; AAL40944.1; -.
 KW Receptor.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 10 AA; 1139 MW; 322A36A72449C737 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 Db 2 PPL 4

RESULT 14

Q9QOW9 PRELIMINARY; PRT; 10 AA.
 ID Q9QOW9
 AC Q9QOW9
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UME3;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119350; AAF24106.1; -.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 Db 7 PPP 9

RESULT 15

Q8JUV70 PRELIMINARY; PRT; 10 AA.
 ID Q8JUV70
 AC Q8JUV70
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USA 5;
 RX MEDLINE=21465052; PubMed=11591397;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL; AF304387; AAM97804.1; -.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 Db 7 PPP 9

RESULT 16

Q9QOW1 PRELIMINARY; PRT; 10 AA.
 ID Q9QOW1
 AC Q9QOW1
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CSFB;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119354; AAF24114.1; -.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 Db 7 PPP 9

RESULT 17

Q8JUV68 PRELIMINARY; PRT; 10 AA.
 ID Q8JUV68
 AC Q8JUV68;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

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DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA 6;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.; transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304388; AAM97806.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 7 PPP 9

RESULT 18
Q9QOV9 ID Q9QOV9 PRELIMINARY; PRT; 10 AA.
AC Q9QOV9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFE;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119355; AAF24116.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 7 PPP 9

RESULT 19
Q9QOW7 ID Q9QOW7 PRELIMINARY; PRT; 10 AA.
AC Q9QOW7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NANCY2;

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RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119351; AAF24108.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 7 PPP 9

RESULT 20
Q8UV66 ID Q8UV66 PRELIMINARY; PRT; 10 AA.
AC Q8UV66;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSF K;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304389; AAM97808.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 7 PPP 9

RESULT 21
Q9QOV7 ID Q9QOV7 PRELIMINARY; PRT; 10 AA.
AC Q9QOV7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFU;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119356; AAF24118.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

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Query Match          42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 7 PPP 9

RESULT 22
Q8JV82 ID Q8JV82 PRELIMINARY; PRT; 10 AA.
AC Q8JV82;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EI;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303944; AAM97792.1; -.
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match          42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 7 PPP 9

RESULT 23
Q8JV76 ID Q8JV76 PRELIMINARY; PRT; 10 AA.
AC Q8JV76;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA2;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303947; AAM97798.1; -.
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match          42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 7 PPP 9

RESULT 24
P90391 ID P90391 PRELIMINARY; PRT; 10 AA.
AC P90391;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE C2 protein (Fragment).
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TYLCV-Is;
RA Wernecke M.E., Roye M.E., McLaughlin W.A., Nakhla M.K., Maxwell D.P.;
RT "Identification of tomato yellow leaf curl geminivirus (TYLCV-Is) in
RT tomatoes and peppers in Jamaica.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84397; AAB47965.1; -.
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1058 MW; 25FF98B5A775A5A7 CRC64;

Query Match          42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQP 3
DB 1 MQP 3

RESULT 25
Q8JV74 ID Q8JV74 PRELIMINARY; PRT; 10 AA.
AC Q8JV74;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA3;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303948; AAM97800.1; -.
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match          42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 7 PPP 9

RESULT 26
Q9Q0W5 ID Q9Q0W5 PRELIMINARY; PRT; 10 AA.
AC Q9Q0W5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PRETORIA3;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage."
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119352; AAF24110.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 7 PPP 9

RESULT 27
 Q9Q0X3 PRELIMINARY; PRT; 10 AA.
 AC Q9Q0X3
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCN8;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage."
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119348; AAF24102.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 7 PPP 9

RESULT 28
 Q9Q0X5 PRELIMINARY; PRT; 10 AA.
 AC Q9Q0X5
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCN16;
 RX MEDLINE=20087544; PubMed=10618230;

RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage."
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119347; AAF24100.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 7 PPP 9

RESULT 29
 Q9Q0W3 PRELIMINARY; PRT; 10 AA.
 AC Q9Q0W3
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PRETORIA1;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage."
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119353; AAF24112.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 7 PPP 9

RESULT 30
 Q8JV80 PRELIMINARY; PRT; 10 AA.
 AC Q8JV80
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E2;
 RX MEDLINE=21465052; PubMed=11581397;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA."
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL; AF303945; AAN97794.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 DB 7 PPP 9

RESULT 31

Q9Q0X1 PRELIMINARY; PRT; 10 AA.
 AC Q9Q0X1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCN15;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119349; AAF24104.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03; - Indels 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 DB 7 PPP 9

RESULT 32

Q9Q0X9 PRELIMINARY; PRT; 10 AA.
 AC Q9Q0X9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCNU;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119345; AAF24096.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 DB 7 PPP 9

RESULT 33

Q8JV72 PRELIMINARY; PRT; 10 AA.
 AC Q8JV72;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USA 4;
 RX MEDLINE=21465052; PubMed=11581397;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL; AF304386; AAM97802.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 DB 7 PPP 9

RESULT 34

Q8IVG8 PRELIMINARY; PRT; 11 AA.
 AC Q8IVG8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Low density lipoprotein receptor related protein 1 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Schulz S., Schagdarsurengin U., Greiser P., Birkenmeier G.,
 RA Muller-Werdan U., Hagemann M., Riemann D., Werdan K., Glaser C.;
 RT "The LDL receptor-related protein (LRP1/A2MR) and coronary
 RT atherosclerosis - novel genomic variants and functional
 RT consequences.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y18524; CAD57169.1; -.
 KW Receptor; Lipoprotein.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1221 MW; 373D041E27273777 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
 DB 4 PPL 6

RESULT 35

P82436 PRELIMINARY; PRT; 11 AA.
 ID P82436
 AC P82436;

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DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 65 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1068 MW; 34FD25CCB325B867 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
Db 2 PPP 4

RESULT 36
Q8UUP1 PRELIMINARY; PRT; 11 AA.
ID Q8UUP1
AC Q8UUP1
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Beta-TrCP protein (Fragment).
GN BETA-TRCP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Carnevali F.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ballarino M.;
RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus
RT laevis.";
RL Thesis (2001), Department of Genetica e Biologia Molecolare,
RL University of Rome La Sapienza, Rome, Italy.
DR EMBL; AJ428930; CAD21927.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
Db 9 QPP 11

RESULT 37
Q8KZ86 PRELIMINARY; PRT; 12 AA.
ID Q8KZ86

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AC Q8KZ86;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Class I integron DNA integrase (Fragment).
GN INTI1.
OS Acinetobacter baumannii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=470;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=204A;
RA Dolzani L., Gombac F., Lagatolla C., Riccio M.L., Rossolini G.M.,
RA Tonin E., Monti-Bragadin C.;
RT "Carriage of class I and II integrons in Italian clinical isolates of
RT Acinetobacter baumannii.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ313334; CAC85941.1; -.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1296 MW; 90426B8F5E376DC1 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
Db 7 PLP 9

RESULT 38
Q9BZ49 PRELIMINARY; PRT; 12 AA.
ID Q9BZ49
AC Q9BZ49;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Glycophorin C (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,
RA Zimmerman P.A.;
RT "The association of the glycophorin C exon 3 deletion with
RT ovalocytosis and malaria susceptibility in the Wosera, Papua New
RT Guinea.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF342984; AAK01459.1; -.
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
Db 9 PPP 11

RESULT 39
Q9NTQ2 PRELIMINARY; PRT; 12 AA.
ID Q9NTQ2
AC Q9NTQ2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE DJ402L9.1 (Mu opiate receptor (MOR1)) (Fragment).

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GN DJ402L9.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RA Phillimore B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; ALI32774; CAB76846.1; -.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1296 MW; 68479422BDAB1DD8 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPL 7
Db 10 PPL 12

RESULT 40
Q93X21 PRELIMINARY; PRT; 12 AA.
ID Q93X21;
AC Q93X21;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Polyubiquitin homolog (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. INRA 258; TISSUE=Leaf;
RX MEDLINE=96236829; PubMed=8680303;
RA Didierjean L., Frendo P., Nasser W., Genot G., Marivet J., Burkard G.;
RT "Heavy-metal-responsive genes in maize: identification and comparison
of their expression upon various forms of abiotic stress.";
RL Planta 199;1-8(1996).
DR EMBL; S82313; AAB47175.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1277 MW; 250D2D2F6F340DD8 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
Db 2 PPP 4

RESULT 41
P82328 PRELIMINARY; PRT; 12 AA.
ID P82328;
AC P82328;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT110) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
[1]
RN SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;

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RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 21.3 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1264 MW; 96691C8C663B1B01 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
Db 9 PPL 11

RESULT 42
Q14182 PRELIMINARY; PRT; 13 AA.
ID Q14182;
AC Q14182;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Deoxynucleotidyltransferase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=87213162; PubMed=3579900;
RX Koizumi O., Kaneda T., Morishita R.;
RT "Analysis of human terminal deoxynucleotidyl transferase cDNA
expressible in mammalian cells.";
RL Biochem. Biophys. Res. Commun. 144:185-190(1987).
DR EMBL; M26144; AAA74588.1; -.
KW Transferase.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1442 MW; 25B7D365F34FC408 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPL 7
Db 9 PPL 11

RESULT 43
Q9T569 PRELIMINARY; PRT; 13 AA.
ID Q9T569;
AC Q9T569;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mitochondrial plasmid S-2 DNA, 5' end (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
[1]
RN SEQUENCE FROM N.A.

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RC TISSUE=Seed;
RA Traynor P.L., Levings C.S. III.;
RT "Transcription of the S-2 maize mitochondrial plasmid.";
RL Plant Mol. Biol. 7:255-263(1986).
DR EMBL; M16992; AAA70281.1; -.
KW Mitochondrion.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1626 MW; 7B5E03673918A1F4 CRC64;

Query Match 42.9%; Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQP 3
Db 1 MQP 3

RESULT 44
O88176 PRELIMINARY; PRT; 13 AA.
ID O88176
AC O88176;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM1 OR NCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb-c; TISSUE=Liver;
RX MEDLINE=98250618; PubMed=9582442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
of a muscle-specific exon in the mouse NCAM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncaml.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1496 MW; CC06098E54C72D732 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7
Db 3 PLP 5

RESULT 45
Q67604 PRELIMINARY; PRT; 13 AA.
ID Q67604
AC Q67604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Movement protein (Fragment).
GN BC1.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Los Mochis 1;
RA Loniello A.O., Ford R.E., Salinas R.A., Morales F.J., Maxwell D.P.;
RT "Diversity among geminiviruses associated with vegetables from Valle
del Fuerte, Sinaloa, Mexico.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL; L27273; AAA47820.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1376 MW; D471DE4D634E76C2 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
Db 7 QPP 9

RESULT 46
Q8X4F5 PRELIMINARY; PRT; 13 AA.
ID Q8X4F5
AC Q8X4F5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein z5883.
GN Z5883.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
DR EMBL; AE005659; AAG59469.1; -.
DR KX Hypothetical protein; Complete proteome.
SQ SEQUENCE 13 AA; 1520 MW; 414592273904D877 CRC64;

Query Match 42.9%; Score 3; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQP 3
Db 1 MQP 3

RESULT 47
P82326 PRELIMINARY; PRT; 14 AA.
ID P82326
AC P82326;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT107) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
targeting analysis of luminal and peripheral thylakoid proteins.";

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RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 18.3 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1580 MW; 314A6CB514E1B237 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
DB 6 PPL 8

RESULT 48
Q9TR14 ID Q9TR14 PRELIMINARY; PRT; 15 AA.
AC Q9TR14;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMELrel. 14, Last annotation update)
DE Troponin-T homolog/proteolysis CONDITIONING INDICATOR peptide
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_
RP SEQUENCE.
RX MEDLINE=96187384; PubMed=8611748;
RA Nakai Y., Shimizu M., Arai S.;
RT "Effects of freezing on the proteolysis of beef during storage at 4
RT degrees C.";
RL Biosci. Biotechnol. Biochem. 59:2255-2258(1995).
SQ SEQUENCE 15 AA; 1597 MW; C9A5B4A798A777 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 2 PPP 4

RESULT 49
Q9S8N8 ID Q9S8N8 PRELIMINARY; PRT; 15 AA.
AC Q9S8N8;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMELrel. 14, Last annotation update)
DE Protein E-22 (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]_
RP SEQUENCE.
RX MEDLINE=94170739; PubMed=8125056;
RA Flengsrud R.;
RT "Separation of acidic barley endosperm proteins by two-dimensional
RT electrophoresis.";
RL Electrophoresis 14:1060-1066(1993).
SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;

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Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
DB 4 QPP 6

RESULT 50
Q40562 ID Q40562 PRELIMINARY; PRT; 15 AA.
AC Q40562;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Small ras-related protein (Fragment).
GN RAN-A2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]_
RP SEQUENCE FROM N.A.
RX STRAIN=SR1;
RX MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein.";
RL Plant J. 6:555-565(1994).
DR EMBL; L16786; AAA73564.1; -.
KW GTP-binding.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1707 MW; 8AB89F924EA30CAF CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
DB 4 PLP 6

RESULT 51
Q40563 ID Q40563 PRELIMINARY; PRT; 15 AA.
AC Q40563;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Small ras-related protein (Fragment).
GN RAN-B2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]_
RP SEQUENCE FROM N.A.
RX STRAIN=SR1;
RX MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein.";
RL Plant J. 6:555-565(1994).
DR EMBL; L16788; AAA73565.1; -.
KW GTP-binding.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1604 MW; 9A57F48F1FFFFFAF CRC64;

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Query Match 42.9%; Score 3; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7
 |||
 Db 5 PLP 7

RESULT 52

ID P82439 PRELIMINARY; PRT; 15 AA.
 AC P82439;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE 200 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 FT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture";
 RL Planta 0:0-0(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall; Hydroxylation.
 FT MOD_RES 6 6 HYDROXYLATION.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1870 MW; 3E1E05A20A3C5681 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 6 PPP 8

RESULT 53

ID Q9NNZ2 PRELIMINARY; PRT; 16 AA.
 AC Q9NNZ2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Integrin alpha-2 subunit (Fragment).
 GN ITGA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98421383; PubMed=9746778;
 RA Krizlik M., Savage B., Nugent D.J., Santoso S., Ruggeri Z.M.,
 RA Kuniccki T.J.;
 RT "Nucleotide polymorphisms in the alpha2 gene define multiple alleles
 RT that are associated with differences in platelet alpha2 beta1
 RT density";
 RL Blood 92:2382-2388(1998).
 DR EMBL; AF062039; AAF77577.1; -.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1635 MW; F6A5FC64F83370A9 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7
 |||
 Db 10 PLP 12

RESULT 54

ID Q9TWN7 PRELIMINARY; PRT; 16 AA.
 AC Q9TWN7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Antigen P30-MAJOR surface immunodominant antigen (Fragment).
 OS Toxoplasma gondii.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
 OC Toxoplasma.
 OX NCBI_TaxID=5811;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94294203; PubMed=7517518;
 RA Bonhomme A., Thirion C., Boulanger F., Charton F., Bulet H.,
 RA Pinon J.M., Alix A.J.;
 RT "Toxoplasma gondii-structure variations of the antigen P30";
 RL Parasitology 108:281-287(1994).
 FT NON_TER 1 1
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1678 MW; FE4CFOA743A796CD CRC64;

Query Match 42.9%; Score 3; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 |||
 Db 3 PPL 5

RESULT 55

ID Q9BGG8 PRELIMINARY; PRT; 16 AA.
 AC Q9BGG8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Thyroid hormone receptor alpha (Fragment).
 GN THRA1.
 OS Sorex araneus (Eurasian common shrew) (European shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.
 OX NCBI_TaxID=42254;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Larkin D., Serov O., Zhdanova N.;
 RT "Mapping of five genes from human chromosome 17 to chromosome hn of
 RT the common shrew (Sorex araneus).";
 RL Acta Theriol. (Warsz) 45:143-146(2000).
 DR EMBL; AF314827; AAK13419.1; -.
 KW Receptor.
 FT NON_TER 1 1
 SQ SEQUENCE 16 AA; 1951 MW; 775186E3F5F52E2 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 |||
 Db 4 PPL 6

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RESULT 56
Q9TQZ7      PRELIMINARY;      PRT;      16 AA.
ID Q9TQZ7;
AC Q9TQZ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Factor H (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
CX NCB1_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96202005; PubMed=8615824;
RA Soames C.J., Day A.J., Sim R.B.;
RT "Prediction from sequence comparisons of residues of factor H involved
RT in the interaction with complement component C3b.";
RL Biochem. J. 315:523-531(1996).
SQ SEQUENCE 16 AA; 1871 MW; 7052751E485EC825 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 6 PPP 8

RESULT 57
Q8RVF4      PRELIMINARY;      PRT;      16 AA.
ID Q8RVF4;
AC Q8RVF4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Proline rich protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
CX NCB1_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. H98, and cv. CI23;
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
RA Morgante M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094252; AAM15708.1; -.
DR EMBL; AY094253; AAM15708.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 16 AA; 1720 MW; 02F6CD77295B5610 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
Db 12 PPL 14

RESULT 58
Q83967      PRELIMINARY;      PRT;      16 AA.
ID Q83967;
AC Q83967;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Influenza A/netherlands/84/68 (H2n2), non-structural protein (Seg 8),
DE cooh terminus of ns1 (Fragment).
OS Influenzavirus A.

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DE Influenza A/cameron/46 (H1n1), non-structural protein (Seg 8), cooh
DE terminus of ns1 (Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
CX Influenza A viruses.
CX NCB1_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural
RT proteins of influenza a virus isolates.";
RL Virology 128:512-517(1983).
DR EMBL; K00961; AAA43519.1; -.
DR InterPro; IPR000256; Flu_NSI.
DR Pfam; PF00600; Flu_NSI; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 16 AA; 1711 MW; 23F43C17AEFPB1E3 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
Db 11 PPL 13

RESULT 59
Q83960      PRELIMINARY;      PRT;      16 AA.
ID Q83960;
AC Q83960;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Influenza A/ann arbor/6/60 (H2n2), non-structural protein (Seg 8),
DE cooh terminus of ns1 (Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
CX NCB1_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural
RT proteins of influenza a virus isolates.";
RL Virology 128:512-517(1983).
DR EMBL; K00962; AAA43516.1; -.
DR InterPro; IPR000256; Flu_NSI.
DR Pfam; PF00600; Flu_NSI; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 16 AA; 1811 MW; 23F434B5AEFPAD93 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
Db 11 PPL 13

RESULT 60
Q84055      PRELIMINARY;      PRT;      16 AA.
ID Q84055;
AC Q84055;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Influenza A/netherlands/84/68 (H2n2), non-structural protein (Seg 8),
DE cooh terminus of ns1 (Fragment).
OS Influenzavirus A.

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*OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=197911;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=8303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural
RT proteins of influenza A virus isolates.";
RL Virology 128:512-517(1993).
DR EMBL; K00963; AAA43527.1; -.
DR InterPro; IPR000256; Flu_NS1.
DR Pfam; PF00600; Flu_NS1; 1.
FT NON TER
FT NON TER
SQ SEQUENCE 16 AA; 1810 MW; 23F43C17ABEFAD93 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
Db 11 PPL 13

RESULT 61
ID Q96P96 PRELIMINARY; PRT; 17 AA.
AC Q96P96;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NH22-like protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;
RT "Characterization of TPA-responsive genes in U937 cells using ordered
RT differential display PCR.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401217; AAL02173.1; -.
FT NON TER
FT NON TER
SQ SEQUENCE 17 AA; 1948 MW; AB699819BD70BCEF CRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPL 7
Db 14 PPL 16

RESULT 62
ID Q14001 PRELIMINARY; PRT; 17 AA.
AC Q14001;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cyclic nucleotide phosphodiesterase (Fragment).
GN CGIPDEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Loebbert R.W., Winterpacht A., Seipel B., Zabel B.U.;

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RT "Molecular cloning and chromosomal assignment of the human homologue
RT of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A)-A gene involved
RT in fat metabolism located at 11p15.1.";
RL Genomics 37:211-218(1996).
DR EMBL; X95522; CAA64776.1; -.
FT NON TER
FT NON TER
SQ SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
Db 15 QPP 17

RESULT 63
ID Q9TR22 PRELIMINARY; PRT; 17 AA.
AC Q9TR22;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE NONAMELOGENIN glycoprotein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96126798; PubMed=8564801;
RA Punzi J.S., DenBesten P.K.;
RT "Purification of nonamelogenin proteins from bovine secretory
RT enamel.";
RL Calcif. Tissue Int. 57:379-384(1995).
SQ SEQUENCE 17 AA; 2032 MW; 9D811CC8228B615D CRC64;

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Query Match 42.9%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 8 PPP 10

RESULT 64
ID Q9TR78 PRELIMINARY; PRT; 17 AA.
AC Q9TR78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-BOTHRIC complex 48,000 SUBUNIT (Fragment).
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE.
RX MEDLINE=95149299; PubMed=7846694;
RA Perales J., Moussatche H., Marangoni S., Oliveira B., Domont G.B.;
RT "Isolation and partial characterization of an anti-bothropic complex
RT from the serum of South American Didelphidae.";
RL Toxicol 32:1237-1249(1994).
SQ SEQUENCE 17 AA; 1947 MW; CB55FB40E73B2A2A CRC64;

Query Match 42.9%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 PPL 6
Db      8 PPL 10

RESULT 65
Q9TRU8
ID Q9TRU8 PRELIMINARY; PRT; 17 AA.
AC Q9TRU8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Leukemia inhibitory factor, LIF-INHIBITOR of aortic endothelial cell
   growth (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RX MEDLINE=92115728; PubMed=1370585;
RA Ferrara N., Winer J., Hensel W.J.;
RT "Pituitary follicular cells secrete an inhibitor of aortic endothelial
   cell growth: identification as leukemia inhibitory factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:698-702(1992).
FT NON_TER 1 17
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1763 MW; BE06BF41F3A2BF94 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PPL 7
Db      2 PPL 4

RESULT 66
O49225
ID O49225 PRELIMINARY; PRT; 17 AA.
AC O49225;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hydroxyproline-rich glycoprotein (fragment).
GN HRGP.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Essex; TISSUE=Root;
RX MEDLINE=94211912; PubMed=8159793;
RA Hong J.C., Cheong Y.H., Nagao R.T., Bahk J.D., Cho M.J., Key J.L.;
RT "Isolation and characterization of three soybean extensin cDNAs.";
RN Plant Physiol. 104:793-796(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Essex; TISSUE=Root;
RA Mahalingam R., Knap H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047052; AAC03558.1; -.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 2149 MW; 285E5874515A2222 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPL 6
Db      8 PPL 10

RESULT 67
Q41400
ID Q41400 PRELIMINARY; PRT; 17 AA.
AC Q41400;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Hydroxyproline-rich protein (Fragment).
OS Sesbania rostrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.
OX NCBI_TaxID=3895;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sesbania rostrata;
RX TISSUE=Bacterial infected stem located root primordia;
RX MEDLINE=96112737; PubMed=8664492;
RA Goernachtig S., Valerio-Lepiniec M., Szczylowski K., Van Montagu M.,
RA Holsters M., De Bruijn F.;
RT "Use of differential display to identify novel Sesbania rostrata genes
   enhanced by Azorhizobium caulinodans infection.";
RL Mol. Plant Microbes Interact. 8:816-824(1995).
DR EMBL; Z48673; CAA88592.1; -.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPP 5
Db      11 PPP 13

RESULT 68
Q9PS39
ID Q9PS39 PRELIMINARY; PRT; 17 AA.
AC Q9PS39;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE EXOGLYCOPROTEIN (Fragment).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE.
RX MEDLINE=93011782; PubMed=1397162;
RA Thormodsson F.R., Antonian E., Grafstein B.;
RT "Extracellular proteins of goldfish optic tectum labeled by
   intracellular injection of 3H-proline.";
RL Exp. Neurol. 117:260-268(1992).
SQ SEQUENCE 17 AA; 1946 MW; F227A01978AD0445 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPL 6
Db      8 PPL 10

RESULT 69

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Q16244
ID Q16244 PRELIMINARY; PRT; 18 AA.
AC Q16244;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE STS protein (Fragment).
GN STS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95038775; PubMed=7951263;
RA Yen P.H., Ferrero G.B., Chinault A.C., Mohandas T., Ballabio A.;
RT "Characterization of the deletion breakpoints in a patient with
RT steroid sulfatase deficiency.";
RL Hum. Mutat. 4:76-78(1994).
DR EMBL; S74383; AAD14153.1; -.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1958 MW; 3B3072711330CCFA CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPL 7
Db |||
2 PPL 4

RESULT 70
Q9UCT9
ID Q9UCT9 PRELIMINARY; PRT; 18 AA.
AC Q9UCT9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE PRG-PROLINE-rich glycoprotein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=91373355; PubMed=1894623;
RA Gillette-Castro B.L., Prakobphol A., Burlingame A.L., Leffler H.,
RA Fisher S.J.;
RT "Structure and bacterial receptor activity of a human salivary
RT proline-rich glycoprotein.";
RL J. Biol. Chem. 266:17358-17368(1991).
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1780 MW; 961F6FB0A83D2E40 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPL 5
Db |||
4 PPL 6

RESULT 71
Q8NFB4
ID Q8NFB4 PRELIMINARY; PRT; 18 AA.
AC Q8NFB4;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Mutant.enamelin (Fragment).

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kida M., Ariga T.;
RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused
RT by an enamel-in gene mutation at exon-intron boundary.";
RL J. Dent. Res. 0:0-0(2002).
DR EMBL; AF530444; AAM97323.1; -.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1893 MW; 492D2B2E3E8BE512 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPL 5
Db |||
3 PPL 5

RESULT 72
Q9H1I3
ID Q9H1I3 PRELIMINARY; PRT; 18 AA.
AC Q9H1I3;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Retinoic acid receptor gamma (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu H., Clifford J.L.;
RT "Genomic organization of the human retinoic acid receptor gamma
RT gene.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV013704; AAG41595.1; -.
KW Receptor.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1964 MW; A284A1EFB361A22 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
Db |||
16 PPL 18

RESULT 73
Q9TOR9
ID Q9TOR9 PRELIMINARY; PRT; 18 AA.
AC Q9TOR9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE VON WILLEBRAND factor (Fragment).
GN VWF.
OS Mammuthus primigenius (Siberian woolly mammoth).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Mammuthus.
OX NCBI_TaxID=37349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20022977; PubMed=10555277;

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RA Greenwood A.D., Capelli C., Possnert G., Paabo S.;
RT "Nuclear DNA sequences from late Pleistocene megafauna.";
RL Mol. Biol. Evol. 16:1466-1473(1999).
DR EMBL; AF154874; AAF12750.1; -.
DR EMBL; AF154873; AAF12749.1; -.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1914 MW; DFCB484B41F69236 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
Db 16 PPL 18

RESULT 74
Q9S915 PRELIMINARY; PRT; 18 AA.
AC Q9S915;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE TETRAMERIC alpha-amylase inhibitor 16 kDa subunit, CM16*
DE (Fragment).
OS Triticum turgidum (Poulard wheat) (Rivet wheat)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4571;
RN [1]_TaxID=4571;
RP SEQUENCE.
RX MEDLINE=92143804; PubMed=1736890;
RA Sanchez-Monge R., Gomez L., Barber D., Lopez-Otin C., Armentia A.,
RA Salcedo G.;
RT "Wheat and barley allergens associated with baker's asthma.
RT Glycosylated subunits of the alpha-amylase-inhibitor family have
RT enhanced IGE-binding capacity.";
RL Biochem. J. 281:401-405(1992).
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1988 MW; 681835D1F68C30F8 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPL 7
Db 16 PPL 18

RESULT 75
Q9JIE9 PRELIMINARY; PRT; 18 AA.
AC Q9JIE9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein arginine N-methyltransferase 1 (Fragment).
GN MGMT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=20307889; PubMed=10848611;
RA Pawlak M.R., Scherer C.A., Chen J., Roshon M.J., Ruley H.E.;
RT "Arginine N-methyltransferase 1 is required for early postimplantation
RT mouse development, but cells deficient in the enzyme are viable.";

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RL Mol. Cell. Biol. 20:4859-4869(2000).
DR EMBL; AF232718; AAF37294.1; -.
KW Methyltransferase; Transferase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1931 MW; 392E2C312C4A8372 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
Db 13 QPP 15

Search completed: November 25, 2003, 18:25:08
Job time : 19.917 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 22.6755 Seconds
(without alignments)
48.999 Million cell updates/sec

Title: US-09-641-801-1

Perfect score: 7

Sequence: 1 MQPPPLP 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched. 1107863 segs, 158726573 residues

Word size : 0
Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A_Geneseq_19Jun03:*

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- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	22	Colostrin derive
2	7	100.0	7	22	Colostrin peptid
3	7	100.0	7	22	Colostrin peptid
4	7	100.0	7	22	Ewe colostrin
5	7	100.0	7	23	Colostrin consti
6	7	100.0	7	23	Colostrin consti
7	7	100.0	7	23	Neural cell regula
8	7	100.0	8	22	Ewe colostrin pe
9	5	71.4	6	17	Prolyl endopeptida

83 SH3 antagonist pep
84 SH3 antagonist pep
85 Src antagonist pep
86 Src SH3 region bin
87 Amino acid sequenc
88 Amino acid sequenc
89 Amino acid sequenc
90 Human CAMP-specifi
91 Yeast 2C TCR CDR3a
92 Yeast 2C TCR CDR3a
93 Yeast 2C TCR CDR3a
94 Src homology3 (SH3
95 Src homology3 (SH3
96 Src homology3 (SH3
97 Src homology3 (SH3
98 Src homology3 (SH3
99 Src homology3 (SH3
100 Src homology3 (SH3

ALIGNMENTS

RESULT 1
AAB72246
ID AAB72246 standard; peptide; 7 AA.
XX
AC AAB72246;
XX
DT 14-MAY-2001 (first entry)
XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 1.
XX
KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
PN WO200111937-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22818.
XX
PR 17-AUG-1999; 99US-0149311.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REG-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX WPI; 2001-202804/20.
XX
PS Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -
XX
PS Claim 1; Page 34; 50pp; English.
XX
CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQPPPLP 7
Db 1 MQPPPLP 7
RESULT 2
AAB72500
ID AAB72500 standard; Peptide; 7 AA.
XX
AC AAB72500;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #1.
XX
KW Dermatological; oxidative stress regulator; colostrinin.
XX
OS Unidentified.
XX
PN WO200112650-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22665.
XX
PR 17-AUG-1999; 99US-0149310.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX WPI; 2001-218342/22.
XX
PT Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -
XX
PS Claim 6; Page 25; 48pp; English.
XX
CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQPPPLP 7
Db 1 MQPPPLP 7
RESULT 3
AAB72532
ID AAB72532 standard; Peptide; 7 AA.
XX
AC AAB72532;
XX
DT 09-MAY-2001 (first entry)
XX

DE Colostrinin peptide #1.
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX Unidentified.
 OS
 XX WO200112651-A2.
 PN
 XX 22-FEB-2001.
 PD
 XX 17-AUG-2000; 2000WO-US22774.
 PF
 XX 17-AUG-1999; 99US-0149633.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Boldogh I;
 PI
 XX WPI; 2001-226545/23.
 DR
 XX Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 XX
 XX Claim 6; Page 21; 35pp; English.
 PS
 XX The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 XX
 XX Sequence 7 AA;
 SQ

Query Match 100.0%; Score 7; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
 |||||
 Db 1 MQPPPLP 7

RESULT 4
 AAB59324
 ID AAB59324 standard; Peptide; 7 AA.
 XX
 AC AAB59324;
 XX
 XX 21-MAR-2001 (first entry)
 DT
 XX Ewe colostrinin peptide fragment B-9.
 DE
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 KW
 XX Ovis sp.
 OS
 XX WO200075173-A2.
 PN
 XX 14-DEC-2000.
 PD
 XX 02-JUN-2000; 2000WO-GB02128.
 PF
 XX 02-JUN-1999; 99GB-0012852.
 PR
 XX (REGE-) REGEN THERAPEUTICS PLC.
 PA
 XX Georgiades JA;
 PI
 XX WPI; 2001-071058/08.
 DR
 XX Peptides having an N-terminal amino acid sequence isolated from
 PT

PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 XX Claim 7; Page 27; 63pp; English.
 PS
 XX The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 XX Sequence 7 AA;
 SQ

Query Match 100.0%; Score 7; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
 |||||
 Db 1 MQPPPLP 7

RESULT 5
 AAE20228
 ID AAE20228 standard; peptide; 7 AA.
 XX
 AC AAE20228;
 XX
 XX 18-JUN-2002 (first entry)
 DT
 XX Colostrinin constituent peptide #1.
 DE
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnery.
 XX
 XX Unidentified.
 OS
 XX
 XX Key Location/Qualifiers
 FH Modified-site 7
 FT /note= "Optionally C-terminal amide"
 FT
 XX WO200213850-A1.
 PN
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22776.
 PF
 XX 17-AUG-2000; 2000WO-US22776.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Stanton GJ, Hughes TK, Boldogh I;
 PI WPI; 2002-269151/31.
 DR
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 XX
 XX Claim 6; Page 25; 51pp; English.
 PS
 XX The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/
 CC

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
 Db 1 MQPPPLP 7

RESULT 6
 AAMS1036
 ID AAMS1036 standard; Peptide; 7 AA.
 AC AAMS1036;

DT 30-MAY-2002 (first entry)
 DE Colostrinin constituent peptide.

XX Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FT Modified-site 7
 FT /note= "optional C-terminal amidation"

PN WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is preferred for use as an immunological regulator and as a
 CC blood cell regulator in claimed methods of the invention. It is
 CC classified as having a beta-casein homologue precursor. Methods
 CC are claimed for: inducing a cytokine in a cell by contact with an
 CC immunological regulator, where the cell is present in a cell
 CC culture, a tissue, an organ or an organism, and the cell is
 CC mammalian, including human; modulating an immune response in a cell
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a
 CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator
 CC is administered topically or as part of a dietary supplement, and
 CC where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation
 CC by contacting blood cells with a blood cell regulator, where the
 CC blood cells are present in a cell culture or an organism, are
 CC mammalian or human, and where the blood cells are increased in
 CC number or differentiated; and a method for modulating blood cell
 CC proliferation in a patent. A claimed cytokine-inducing composition
 CC comprises a pharmaceutical carrier and an active agent such as the
 CC present peptide. Cytokines induced by this peptide in human
 CC leucocyte cultures include interferon-gamma, tumour necrosis
 CC factor-alpha, interleukin-4, interleukin-6, interleukin-10 and
 CC interleukin-12. It was one of the best overall inducers in almost
 CC all cytokine and blood cell proliferation experiments conducted.

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
 Db 1 MQPPPLP 7

RESULT 7
 AAO14577
 ID AAO14577 standard; peptide; 7 AA.
 XX AAO14577;

DT 27-MAY-2002 (first entry)

DE Neural cell regulatory colostrinin peptide 1.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

OS Unidentified.

XX Key Location/Qualifiers

FT Modified-site 7
 FT /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich

PF 25-FEB-1994; 94WO-US01840.
 XX
 PR 26-FEB-1993; 93US-0023915.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 PI Cantley L, Kanteti P, Rudd CE;
 XX
 DR WPI; 1994-293868/36.
 XX
 XX Method for inhibiting or reducing signal transduction - utilizes
 PT peptide or corresp. nucleic acid which decreases association of
 PT PI 3- or 4- kinase with CD4/p56lck
 XX
 XX Example; Page 32; 46pp; English.
 XX
 CC In order for certain T cells to make an optimal response to antigen,
 CC it is necessary for the T cell surface antigen CD4 to couple to the
 CC protein-tyrosine kinase p56lck. (CD4-p56lck is known to associate
 CC with and functionally synergise with the TCR/CD3 complex.) CD4-p56lck
 CC complex in T cells associates with two lipid kinases: PI 3-kinase
 CC and PI 4-kinase, which suggests that these lipid kinases are also
 CC involved in intracellular signalling via the T cell receptor complex.
 CC The interaction of a lipid kinase, such as PI 3-kinase or PI 4-
 CC kinase, with CD4-p56lck, may be blocked by administering a peptide.
 CC This peptide may be a fragment of the cytoplasmic domain of CD4
 CC (eg AAR60987-R60991), a fragment of p56lck (eg AAR60992, AAR60993),
 CC a fragment of PI 3-kinase (eg AAR60994, AAR60995), or a fragment of
 CC PI 4-kinase. Other proline-rich peptides that bind to SH3 binding
 CC sequences can also be used, such as the fragment of
 CC 3BP1 protein that binds to the SH3 of the Abi kinase (AAR60997), or
 CC a sequence found in the SOS protein (AAR60999).
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 7 AA;
 Query Match 71.4%; Score 5; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0;
 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
 QY 3 PPPLP 7
 Db |||||
 1 PPPLP 5
 RESULT 11
 ID AAR91752
 XX AAR91752 standard; peptide; 7 AA.
 XX
 AC AAR91752;
 DT 14-AUG-1996 (first entry)
 XX
 DE Prolyl endopeptidase inhibitor peptide #7.
 XX
 KW Prolyl endopeptidase; PEP; inhibitory peptide; animal feed; therapy;
 KW prevention; dementia; human.
 XX
 OS Synthetic.
 XX
 PN JP08059697-A.
 XX
 PD 05-MAR-1996.
 XX
 PF 09-MAR-1995; 95JP-0079661.
 XX
 PR 15-JUN-1994; 94JP-0158031.
 XX
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (NIHA-) NIPPON HAM KK.
 XX
 DR WPI; 1996-184809/19.
 XX

PT Prolyl:endo;peptidase inhibitory peptide(s) - useful as additives
 PT for food and animal feed and to treat and prevent dementia
 XX
 PS Claim 1; Page 11; 11pp; Japanese.
 XX
 CC AAR91746-R91753 represent prolyl endopeptidase (PEP) inhibitory
 CC peptides. These peptides are useful as PEP inhibitors in functional foods
 CC and in animal feeds. They are used to prepare oral and parenteral
 CC pharmaceutical preparations for the treatment and prevention of dementia
 CC of animals, including humans. The advantage with using these peptides,
 CC is that they are safe and easily absorbed.
 XX
 SQ Sequence 7 AA;
 Query Match 71.4%; Score 5; DB 17; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db |||||
 2 PPPLP 6
 RESULT 12
 ID AAM46827
 XX AAM46827 standard; Peptide; 7 AA.
 AC AAM46827;
 XX
 DT 25-OCT-2001 (first entry)
 XX
 DE H11 binding site consensus conforming peptide (CCP) #3098.
 XX
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN CA2290722-A1.
 XX
 PD 08-JUN-2001.
 XX
 PF 08-DEC-1999; 99CA-2290722.
 XX
 PR 08-DEC-1999; 99CA-2290722.
 XX
 PA (NOVO-) NOVOPHARM BIOTECH INC.
 XX
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, MacDonald GC;
 XX
 DR WPI; 2001-425937/46.
 XX
 PT Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -
 XX
 PS Example 4; Page 112; 154pp; English.
 XX
 CC The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a

CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, oligodendroglioma, ependymoma, medulloblastoma, and primitive neural ectodermal tumour (PNET). (I) is useful as cancer immunogen including vaccines. (I) is useful for diagnostic and palliative use, for detecting or imaging cancer cells, and to monitor the course of amelioration of CC malignancy in an individual. AAM43707 to AAM47109 represent peptides which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 71.4%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 3 PPPLP 7

RESULT 13

AAM46851
ID AAM46851 standard; Peptide; 7 AA.

XX AC AAM46851;

XX 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #3122.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.

OS Synthetic.

XX CA2290722-A1.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress protein-peptide complexes associated with tumor, and isolated antigen-binding fragments of an antibody that binds specifically to the complex -

XX Example 4; Page 112; 154pp; English.
XX The present invention describes a composition (I) comprising stress protein-peptide complexes (SPPC) associated with tumours that is specifically immunogenically cross-reactive with cell surface-associated SPPCs specific to target cancer (TC). Also described is an isolated antigen-binding fragment of an antibody that binds specifically to SPPCs or a population of different SPPCs consisting of immunogenic cancer cell surface-associated SPPC of TC. (I) has cytostatic activity and can be used in vaccine production and as a tumour-specific immunogenic response inducer. (I) is useful for treating 71 types of cancers or tumours in a subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, oligodendroglioma, ependymoma, medulloblastoma, and primitive neural ectodermal tumour (PNET). (I) is useful as cancer immunogen including vaccines. (I) is useful for diagnostic and palliative use, for detecting

CC or imaging cancer cells, and to monitor the course of amelioration of CC malignancy in an individual. AAM43707 to AAM47109 represent peptides which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 71.4%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 3 PPPLP 7

RESULT 14

AAM46856
ID AAM46856 standard; Peptide; 7 AA.

XX AC AAM46856;

XX 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #3127.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.

OS Synthetic.

XX CA2290722-A1.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress protein-peptide complexes associated with tumor, and isolated antigen-binding fragments of an antibody that binds specifically to the complex -

XX Example 4; Page 112; 154pp; English.
XX The present invention describes a composition (I) comprising stress protein-peptide complexes (SPPC) associated with tumours that is specifically immunogenically cross-reactive with cell surface-associated SPPCs specific to target cancer (TC). Also described is an isolated antigen-binding fragment of an antibody that binds specifically to SPPCs or a population of different SPPCs consisting of immunogenic cancer cell surface-associated SPPC of TC. (I) has cytostatic activity and can be used in vaccine production and as a tumour-specific immunogenic response inducer. (I) is useful for treating 71 types of cancers or tumours in a subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, oligodendroglioma, ependymoma, medulloblastoma, and primitive neural ectodermal tumour (PNET). (I) is useful as cancer immunogen including vaccines. (I) is useful for diagnostic and palliative use, for detecting or imaging cancer cells, and to monitor the course of amelioration of CC malignancy in an individual. AAM43707 to AAM47109 represent peptides which are used in the exemplification of the present invention.


```

Db      3 PPPLP 7

RESULT 17
AAM46871
ID AAM46871 standard; Peptide; 7 AA.
XX
XX AAM46871;
AC
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #3147.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPpC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
XX Example 4; Page 112; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPpC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPpCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPpCs
CC or a population of different SPpCs consisting of immunogenic cancer cell
CC surface-associated SPpC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX
XX Sequence 7 AA;
SQ
Query Match 71.4%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 3 PPPLP 7
|||||
|||||

RESULT 19
AAM46973
ID AAM46973 standard; Peptide; 7 AA.
XX
XX AAM46973;
AC

Db      3 PPPLP 7

RESULT 18
AAM46871
ID AAM46871 standard; Peptide; 7 AA.
XX
XX AAM46871;
AC
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #3142.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPpC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
XX Example 4; Page 112; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPpC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPpCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPpCs
CC or a population of different SPpCs consisting of immunogenic cancer cell
CC surface-associated SPpC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX
XX Sequence 7 AA;
SQ
Query Match 71.4%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 3 PPPLP 7
|||||
|||||

RESULT 19
AAM46973
ID AAM46973 standard; Peptide; 7 AA.
XX
XX AAM46973;
AC

```

```

XX 25-OCT-2001 (first entry)
XX
XX
DE H11 binding site consensus conforming peptide (CCP) #3244.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
XX Example 4; Page 112; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
XX Sequence 7 AA;
XX
XX Query Match 71.4%; Score 5; DB 22; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 PPPLP 7
XX Db 3 PPPLP 7
XX
XX RESULT 20
XX AAM47027
XX ID AAM47027 standard; Peptide; 7 AA.
XX
XX AC AAM47027;
XX
XX DT 25-OCT-2001 (first entry)
XX
XX DE H11 binding site consensus conforming peptide (CCP) #3298.

```

```

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
XX Example 4; Page 112; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
XX Sequence 7 AA;
XX
XX Query Match 71.4%; Score 5; DB 22; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 PPPLP 7
XX Db 3 PPPLP 7
XX
XX RESULT 21
XX AAR71945
XX ID AAR71945 standard; Peptide; 8 AA.
XX
XX AC AAR71945;
XX
XX DT 25-MAR-2003 (updated)
XX DT 17-OCT-1995 (first entry)
XX
XX DE Human 3BP1 peptide.
XX
XX KW Grb3-3; cancer; apoptosis; AIDS; gene therapy; 3BP1; SH3 domain.

```

OS Synthetic.
 PN WO9507981-A1.
 XX
 XX 23-MAR-1995.
 PD
 XX 09-MAY-1994; 94WO-FR00542.
 XX
 XX 15-SEP-1993; 93FR-0010971.
 XX
 XX (RHON) RHONE POULENC RORER SA.
 XX
 XX Schweighoffer P, Tocco B;
 XX WPI; 1995-131349/17.
 DR
 XX New human Grb3-3 gene and vectors contg. it - useful in control
 PT of cell death etc. partic. for treating cancer and AIDS
 XX
 XX Example 2; Page 11; 31pp; French.
 PS
 CC The hSOS1 and 3BP1 peptides given in AAR71944-45 were used to
 CC demonstrate that the newly isolated human Grb3-3 protein was
 CC able to bind hSOS1, but not to the 3BP1 peptide, which
 CC corresponds to the SH3 domain of Abl and Src. A Grb3-3G162R
 CC mutant was unable to bind the hSOS1 peptide.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 8 AA;
 SQ

Query Match 71.4%; Score 5; DB 16; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 DB 1 PPPLP 5

RESULT 22
 AAR77371
 ID AAR77371 standard; Peptide; 10 AA.
 XX
 AC AAR77371;
 XX
 DT 17-JAN-1996 (first entry)
 XX
 DE SH3 binding domain 3BP-1.
 XX
 KW Carboxyamido-triazole resistance; CAI; CAIR-1; cancer;
 KW gene therapy; Src homology 3; SH3 binding domain; 3BP-1.
 XX
 XX Homo sapiens.
 OS
 XX WO9525125-A1.
 PN
 XX 21-SEP-1995.
 PD
 XX 14-MAR-1995; 95WO-US03610.
 PF
 XX 14-MAR-1994; 94US-0212190.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Kim YS, Kohn EC, Liotta LA;
 PI WPI; 1995-336944/43.
 DR
 XX DNA encoding CAI resistance proteins - used in gene therapy, and for
 PT detecting CAI resistance in biological samples
 XX
 PS Example 4; Page 40; 56pp; English.
 XX

CC CAIR-1 protein (AAR77365), responsible for CAI resistance in A2058
 CC human melanoma cells, contains a unique proline-rich sequence
 CC which fulfills the consensus definition for Src homology 3 (SH3)
 CC binding proteins (AAR77366). 4 Unique versions (AAR77367-70) are
 CC present that show homology to the known SH3 binding domains: 3BP-1,
 CC and the p85-alpha-1 and -2 subunits of phosphatidylinositol 3',
 CC kinase (AAR77371-73).
 XX
 XX Sequence 10 AA;
 SQ

Query Match 71.4%; Score 5; DB 16; Length 10;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 DB 5 PPPLP 9

RESULT 23
 AAW06853
 ID AAW06853 standard; peptide; 10 AA.
 XX
 AC AAW06853;
 XX
 DT 16-FEB-1997 (first entry)
 XX
 DE Peptide binding the Crk-SH3 domain, used to treat cancer.
 XX
 KW Peptide; binding; inhibition; binding domain; Crk-SH3; cancer;
 KW treatment; diagnosis; antibody; signal transduction; disease;
 KW disorder; intracellular signalling protein.
 XX
 OS Synthetic.
 XX
 XX WO9621011-A2.
 PN
 XX 11-JUL-1996.
 PD
 XX 28-DEC-1995; 95WO-US16979.
 PF
 XX 30-DEC-1994; 94US-0367070.
 PR
 XX (UYRQ) UNIV ROCKEFELLER.
 PA
 XX Cowburn D, Feller SM, Hanafusa H, Knudsen BS, Kuriyan J;
 PI Wu X, Zheng J;
 XX WPI; 1996-333986/33.
 DR
 XX New peptide(s) which bind the Crk-SH3 domain - used to develop
 PT prods. for the diagnosis and treatment of defects in intracellular
 PT signal transduction, partic. in cancer
 XX
 PS Claim 3; Page 92; 120pp; English.
 XX
 CC New peptides or proteins which comprise these peptides, bind
 CC to the Crk-SH3 domain and competitively inhibit the binding of
 CC intracellular signalling proteins. They can be used in the
 CC treatment of a disease or disorder associated with a defect in
 CC intracellular signal transduction, particularly cancer. They can
 CC also be used to diagnose such diseases and disorders. Antibodies
 CC raised against these proteins can be used for the same purposes. The
 CC peptides are derived from the Crk-SH3 binding domains of
 CC intracellular signalling proteins. Peptides related to the invention
 CC are described in AAW03149-63 and AAW06842-W06866.
 XX
 XX Sequence 10 AA;
 SQ

Query Match 71.4%; Score 5; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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XX OS Synthetic.
XX PN WC9737223-A1.
XX XX
XX PD 09-OCT-1997.
XX XX
XX PF 03-APR-1997; 97WO-US05547.
XX PR 03-APR-1996; 96US-0630916.
XX XX
XX PA (CYTO-) CYTOGEN CORP.
XX PN (UYNC-) UNIV NORTH CAROLINA.
XX PI Fowlkes DM, Kay BK, Pirozzi G;
XX DR WPI; 1997-503234/46.
XX XX
XX PT Identifying cell signalling and growth regulatory polypeptides by
XX PT reaction with multivalent recognition complex - polypeptides are
XX PT useful in targetted drug selection
XX XX
XX PS Disclosure; Fig 15B; 220pp; English.
XX XX
XX CC Peptides AAW38068-92 contain PPPPY-like motifs. The PPPY motif is
XX CC found in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides
XX CC containing this residue have been shown to bind the YAP WW domain, but
XX CC not the WW domain from dystrophin or to a panel of SH3 domains. Peptides
XX CC AAW38068-92 were biotinylated and complexed with alkaline streptavidin,
XX CC and used in a cross affinity mapping experiment. They were tested for
XX CC their ability to bind to the 3 WW domains of WWP4 (AAW36797), which were
XX CC expressed as glutathione-S-transferase expression proteins. The present
XX CC peptide, derived from formin, does not bind to the WW domains of the
XX CC novel protein. The WW domain is a small functional domain. Its name
XX CC is derived from the observation that two tryptophan residues, one in the
XX CC amino terminal portion of the WW domain and one in the carboxyl terminal
XX CC portion, are conserved. Most proteins containing WW domains have a
XX CC function involving cell signalling and growth regulation or the
XX CC organisation of the cytoskeleton. Polypeptides containing a WW domain
XX CC are identified by treating a multivalent recognition unit complex that
XX CC has selective binding affinity for a WW domain, with many polypeptides
XX CC and identifying those with selective affinity for the complex. Proteins
XX CC containing WW domains are used for targeted drug screening, i.e. to
XX CC identify potential modulators of specific WW domain interactions.
XX XX
XX SQ Sequence 10 AA;
XX XX
XX Query Match 71.4%; Score 5; DB 18; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 40;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 PPPLP 7
XX Db |||||
XX 5 PPPLP 9
XX
XX RESULT 27
XX AAB70933
XX ID AAB70933 standard; Protein; 10 AA.
XX AC
XX XX
XX AC AAB70933;
XX XX
XX DT 30-JUL-2001 (first entry)
XX XX
XX DE Polyoma virus VP1 variant PyVP1-WW150 proline-rich fragment.
XX XX
XX KW VP1; coat protein; WW domain; proline-rich; immobilization; biosensor;
XX KW bioreactor; protein packaging; PyVP1-WW150.
XX XX
XX OS Polyoma virus.
XX XX
XX PN WO200132684-A2.
XX PD
XX XX

PD 10-MAY-2001.
XX XX
XX PF 03-NOV-2000; 2000WO-BP10873.
XX XX
XX PR 03-NOV-1999; 99DE-1052956.
XX XX
XX PA (ACGT-) ACGT PROGENOMICS AG.
XX XX
XX PI Boehm G, Schmidt U, Parthier C, Guenther C;
XX XX
XX DR WPI; 2001-343471/36.
XX XX
XX PT Linking two or more molecules through adapter sequences, useful e.g.
XX PT for purifying recombinant proteins, by exploiting interaction between
XX PT WW domain and proline-rich sequence -
XX XX
XX PS Example 5; Page 26; 100pp; German.
XX XX
XX CC This invention describes a novel method (M1) for linking two or more
XX CC molecular substances (A) together via adapter sequences (AS). One (A) is
XX CC modified so that it contains, as AS, a WW domain or derived structure in
XX CC at least one region, and a second (A) is modified so that it contains,
XX CC as AS, a proline-rich sequence (PRS) able to bind to WW domain or its
XX CC derivative in at least one region and the modified components are
XX CC allowed to interact together through WW and PRS. The method is used to
XX CC provide permanent or temporary association between (A), e.g. temporary
XX CC immobilization, and matrix-assisted refolding, of recombinant proteins
XX CC from crude cell extracts or permanent immobilization in biosensors or
XX CC bioreactors, for directing packaging of proteins inside a virus-like
XX CC shell, or production of chimeric proteins (e.g. bispecific antibodies),
XX CC for medical, therapeutic, diagnostic or biotechnological use. Interaction
XX CC between WW and PRS is very strong (dissociation constant 20-100 nM) but
XX CC only temporary, and can be stabilized (e.g. against extremes of salt
XX CC concentration or temperature) by formation of disulfide bridges. Compared
XX CC with other systems with comparable properties, the WW/PRS system is
XX CC exceptionally small and compact and for many applications, e.g.
XX CC antibody-antigen interaction, is clearly superior to other ligand binding
XX CC domains. The system can only produce heterodimers. This sequence
XX CC represents a proline-rich fragment of the Polyoma virus coat protein VP1
XX CC variant PyVP1-WW150 construct which is used to illustrate the method of
XX CC the invention.
XX XX
XX SQ Sequence 10 AA;
XX XX
XX Query Match 71.4%; Score 5; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 40;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 PPPLP 7
XX Db |||||
XX 6 PPPLP 10
XX
XX RESULT 28
XX AAB86131
XX ID AAB86131 standard; Protein; 10 AA.
XX XX
XX AC AAB86131;
XX XX
XX DT 30-JUL-2001 (first entry)
XX XX
XX DE Proline-rich peptide.
XX XX
XX KW Transport system; gene therapy; infection; tumor LLO;
XX KW human immune deficiency virus; hemophilia; muscular dystrophy; capsid;
XX KW cystic fibrosis; virus-like particle; cell targeting; listeriolysin O.
XX XX
XX OS Unidentified.
XX XX
XX PN WO200132851-A2.
XX PD
XX PD 10-MAY-2001.
XX XX

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PF 03-NOV-2000; 2000WO-EP10876.
 XX
 PR 03-NOV-1999; 99DE-1052957.
 XX
 PA (ACGT-) ACGT PROGENOMICS AG.
 XX
 PI Boehm G, Rudolph R, Schmidt U, Esser D;
 XX
 DR WPI; 2001-316433/33.
 XX
 XX Transport system for compounds, useful e.g. in gene therapy, comprises
 PT mosaic-like assembly of different protein subunits able to encapsulate
 PT compounds -
 XX
 PS Example 11; Page 35; 106pp; German.
 XX
 CC This invention describes a novel transport system (A) for molecular
 CC substances (I) containing recombinantly prepared subunits (SU) based
 CC on amino acids (aa) comprising: (i) at least two modified SU with one
 CC difference; and/or (ii) one or more modified SU with at least two
 CC differences; and (iii) (optionally) unmodified SU. The various SU are
 CC combined in a mosaic fashion to form (A) in which (I) can be
 CC encapsulated. (A) Are used to deliver (I) specifically to cells,
 CC particularly DNA to eukaryotic cells for gene therapy, e.g. of infections
 CC by human immune deficiency virus, tumors and a wide range of inherited
 CC diseases such as hemophilia, muscular dystrophy or cystic fibrosis.
 CC Capsids or other virus-like particles can be assembled, simply and in
 CC modular fashion, in vitro, allowing control over stoichiometric
 CC composition. SU can be modified to impart a wide variety of selected
 CC properties, e.g. cell targeting, improved cellular uptake and reduced
 CC immunogenicity. (A) do not require extensive testing to ensure that they
 CC are safe (contrast replication-deficient viruses), also SU can be
 CC prepared in very pure form and are easily labeled fluorescently (for
 CC quality control or localization). This sequence represents a proline-rich
 CC peptide used in the construction of a *Listeria monocytogenes*
 CC listeriolysin LLO variant which is used to illustrate the method of the
 CC invention.
 XX
 SQ Sequence 10 AA;
 Query Match 71.4%; Score 5; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 6 PPPLP 10
 RESULT 29
 ID AAB86149 standard; Peptide; 10 AA.
 XX
 AC AAB86149;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Proline-rich peptide fragment.
 XX
 KW Packaging; protein shell; transport system; gene therapy; GFP-PPLP;
 KW icosahedral virus capsid; enhanced green fluorescent protein; eGFP;
 KW fusion construct; proline-rich.
 XX
 OS Unidentified.
 XX
 PN WO200132852-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-BF10878.
 XX
 PR 03-NOV-1999; 99DE-1052982.
 XX

PA (ACGT-) ACGT PROGENOMICS AG.
 XX
 PI Boehm G, Esser D, Schmidt U;
 XX
 DR WPI; 2001-316434/33.
 XX
 XX Packaging compounds in protein shells, useful e.g. in gene therapy, by
 PT binding a compound to immobilized shell fragment, then releasing it
 PT from the matrix and assembly into shells -
 XX
 PS Example 6; Page 26; 62pp; German.
 XX
 CC This invention describes a novel method for packaging molecular
 CC substances (I) in protein shells which comprises binding a shell
 CC fragment (II), via a first region, to a matrix (M), then treating bound
 CC (II) with (I) so that this binds through a second region of (II). The
 CC (I)-(II) product, or part of it, is separated from M and assembled, with
 CC other (II), to form the shells. The separation and assembly steps may be
 CC performed in either sequence. Packaging of (I) is used to prepare
 CC transport systems for genes or active agents, particularly in gene
 CC therapy. The process provides very efficient packaging of (I), including
 CC compounds that aggregate in solution or have other unfavorable
 CC properties. Even very long DNA can be packaged, when combined with a
 CC condensing agent, and the method is applicable to any sort of protein
 CC shell, not just icosahedral virus capsids. The integrated (II) can be
 CC screened for optimization of its packaging properties. e.g. maximum size
 CC of (I) that can be accommodated. This sequence represents a
 CC proline-rich peptide fragment used in the production of the fusion
 CC construct comprising the Aequorea victoria enhanced green fluorescent
 CC protein (eGFP) and a proline rich region which is used to illustrate the
 CC method of the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 71.4%; Score 5; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 6 PPPLP 10
 RESULT 30
 ID AAE16670 standard; peptide; 10 AA.
 XX
 AC AAE16670;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human YAP65 protein SH3 domain binding motif.
 XX
 KW Human; congestive heart failure; dilative cardiomyopathy; sudden death;
 KW hypertrophic cardiomyopathy; ischaemic cardiomyopathy; rhythm disorder;
 KW heart muscle disease; conduction disorder; coronary heart disease;
 KW systemic arterial hypertension; pulmonary hypertension; endocarditis;
 KW pulmonary heart disease; valvular heart disease; pericardial disease;
 KW congenital heart disease; gene therapy; syncope; transgenic animal;
 KW YAP65 protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200192567-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-EP06165.
 XX
 PR 30-MAY-2000; 2000US-207400P.
 XX
 PA (MEDI-) MEDIGENE AG.
 XX

PI Bunk D, Reuner B, Beck J, Henkel T;
XX WPI; 2002-122073/16.
DR
XX
XX Identifying a subject at risk for a heart disease e.g. congestive heart
PT failure, dilative cardiomyopathy, heart muscle disease, by quantifying
PT the polypeptide expressed by genes abnormally expressed in heart tissue
XX
XX Example 7; Page 71; 154pp; English.
PS
XX The patent discloses novel target genes abnormally expressed in heart
CC tissues and their corresponding proteins. The invention also relates to
CC methods for assessing the expression level of these genes. The method
CC is used for testing the predisposition of mammals and preferably humans
CC for a heart disease or for an acute state of such a disease. It is also
CC useful to treat diseases of the heart such as congestive heart failure,
CC dilative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardio-
CC myopathy, specific heart muscle disease, rhythm and conduction disorders,
CC syncope and sudden death, coronary heart disease, systemic arterial
CC hypertension, pulmonary hypertension, pulmonary heart disease, valvular
CC heart disease, congenital heart disease, pericardial disease and
CC endocarditis. Sequences of the invention are also used in gene therapy.
CC A transgenic non-human mammal comprising the sequences of the invention
CC are useful for the development for medicaments for the treatments of
CC heart diseases. The present sequence is the SH3 domain binding motif
CC of human YAP65 protein.
XX
SQ Sequence 10 AA;
Query Match 71.4%; Score 5; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QPPPL 6
DB 4 QPPPL 8
|||
|||
RESULT 31
AAB21126
ID AAB21126 standard; peptide; 11 AA.
XX
XX AAB21126;
AC AC
19-JAN-2001 (first entry)
DT XX
DE Src homology 3 domain binding peptide #3.
XX
XX Src homology domain 3; SH3; protein-protein interaction; cancer;
KW signal transduction inhibition; immune suppression-associated disease.
OS Synthetic.
XX WO200047607-A1.
PN 17-AUG-2000.
PD XX
PF 12-FEB-2000; 2000WO-KR00107.
XX
PR 12-FEB-1999; 99AU-0008643.
PR 02-JUN-1999; 99KR-0020282.
XX
PA (YOON/) YOON J H.
PA (HANY/) HAN Y T.
XX
XX Yoon JH, Han YT, Lee KY;
PI WPI; 2000-533010/48.
DR
XX Synthetic peptides useful for treating cancers and immunosuppressive
PT disorders by disrupting interactions of the SH (Src homology) 2 and SH3
PT motifs of Src family kinase proteins -
XX
XX
XX Claim 3; Page 71; 154pp; English.
PS
XX The present sequence is a synthetic peptide which has a high affinity for
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC involved in signal transduction pathways, and this peptide can be used to
CC inhibit these by disrupting protein-protein interactions, in the
CC treatment of cancer, particularly hepatocellular carcinoma, cervical
CC cancer, colon adenocarcinoma and fibrosarcoma, and immune
CC suppression-associated diseases.
XX
SQ Sequence 11 AA;
Query Match 71.4%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PPPLP 7
DB 4 PPPLP 8
|||
|||
RESULT 32
AAB21127
ID AAB21127 standard; peptide; 11 AA.
XX
XX AAB21127;
AC AC
19-JAN-2001 (first entry)
DT XX
DE Src homology 3 domain binding peptide #4.
XX
XX Src homology domain 3; SH3; protein-protein interaction; cancer;
KW signal transduction inhibition; immune suppression-associated disease.
OS Synthetic.
XX WO200047607-A1.
PN 17-AUG-2000.
PD XX
PF 12-FEB-2000; 2000WO-KR00107.
XX
PR 12-FEB-1999; 99AU-0008643.
PR 02-JUN-1999; 99KR-0020282.
XX
PA (YOON/) YOON J H.
PA (HANY/) HAN Y T.
XX
XX Yoon JH, Han YT, Lee KY;
PI WPI; 2000-533010/48.
DR
XX Synthetic peptides useful for treating cancers and immunosuppressive
PT disorders by disrupting interactions of the SH (Src homology) 2 and SH3
PT motifs of Src family kinase proteins -
XX
XX
XX Claim 3; Page 33; 40pp; English.
PS
XX The present sequence is a synthetic peptide which has a high affinity for
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC involved in signal transduction pathways, and this peptide can be used to
CC inhibit these by disrupting protein-protein interactions, in the
CC treatment of cancer, particularly hepatocellular carcinoma, cervical
CC cancer, colon adenocarcinoma and fibrosarcoma, and immune
CC suppression-associated diseases.
XX
SQ Sequence 11 AA;
Query Match 71.4%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      3 PPPLP 7
Db      4 PPPLP 8

RESULT 33
AAB21129
ID  AAB21129 standard; peptide; 11 AA.
XX  AC
XX  AAB21129;
XX  DT 19-JAN-2001 (first entry)
XX  DE Src homology 3 domain binding peptide #6.
XX  KW Src homology domain 3; SH3; protein-protein interaction; cancer;
XX  KW signal transduction inhibition; immune suppression-associated disease.
XX  OS Synthetic.
XX  PN WO200047607-A1.
XX  PD 17-AUG-2000.
XX  PF 12-FEB-2000; 2000WO-KR00107.
XX  PR 12-FEB-1999; 99AU-0008643.
XX  PR 02-JUN-1999; 99KR-0020282.
XX  PA (YOON/) YOON J H.
XX  PA (HANY/) HAN Y T.
XX  PI Yoon JH, Han YT, Lee KY;
XX  DR WPI; 2000-533010/48.
XX  PT Synthetic peptides useful for treating cancers and immunosuppressive
XX  PT disorders by disrupting interactions of the SH (Src homology) 2 and SH3
XX  PT motifs of Src family kinase proteins -
XX  PS Claim 3; Page 34; 40pp; English.
XX  CC The present sequence is a synthetic peptide which has a high affinity for
XX  CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
XX  CC involved in signal transduction pathways, and this peptide can be used to
XX  CC inhibit these, by disrupting protein-protein interactions, in the
XX  CC treatment of cancer, particularly hepatocellular carcinoma, cervical
XX  CC cancer, colon adenocarcinoma and fibrosarcoma, and immune
XX  CC suppression-associated diseases.
XX  SQ Sequence 11 AA;

Query Match 71.4%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PPPLP 7
Db      4 PPPLP 8

RESULT 34
AAB21132
ID  AAB21132 standard; peptide; 11 AA.
XX  AC
XX  AAB21132;
XX  DT 19-JAN-2001 (first entry)
XX  DE Src homology 3 domain binding peptide #9.
XX  DE Src homology domain 3; SH3; protein-protein interaction; cancer;
XX  KW signal transduction inhibition; immune suppression-associated disease.

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XX  OS Synthetic.
XX  PN WO200047607-A1.
XX  PD 17-AUG-2000.
XX  PF 12-FEB-2000; 2000WO-KR00107.
XX  PR 12-FEB-1999; 99AU-0008643.
XX  PR 02-JUN-1999; 99KR-0020282.
XX  PA (YOON/) YOON J H.
XX  PA (HANY/) HAN Y T.
XX  PI Yoon JH, Han YT, Lee KY;
XX  DR WPI; 2000-533010/48.
XX  PT Synthetic peptides useful for treating cancers and immunosuppressive
XX  PT disorders by disrupting interactions of the SH (Src homology) 2 and SH3
XX  PT motifs of Src family kinase proteins -
XX  PS Claim 3; Page 35; 40pp; English.
XX  CC The present sequence is a synthetic peptide which has a high affinity for
XX  CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
XX  CC involved in signal transduction pathways, and this peptide can be used to
XX  CC inhibit these, by disrupting protein-protein interactions, in the
XX  CC treatment of cancer, particularly hepatocellular carcinoma, cervical
XX  CC cancer, colon adenocarcinoma and fibrosarcoma, and immune
XX  CC suppression-associated diseases.
XX  SQ Sequence 11 AA;

Query Match 71.4%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PPPLP 7
Db      4 PPPLP 8

RESULT 35
AAB21165
ID  ABB99165 standard; peptide; 11 AA.
XX  AC ABB99165;
XX  DT 22-NOV-2002 (first entry)
XX  DE Formin-2 FH1 domain repeated proline motif.
XX  KW Formin-2; recurrent pregnancy loss; formin-2; Fmn-2; RPL;
XX  KW spontaneous abortion; miscarriage; FH1; proline motif.
XX  OS Unidentified.
XX  FH Key Location/Qualifiers
XX  FT Misc-difference 1 /label= Met, Val
XX  PN US2002098489-A1.
XX  PD 25-JUL-2002.
XX  PF 12-APR-2001; 2001US-0835232.
XX  PR 13-APR-2000; 2000US-196811P.
XX  PA {LEDE/} LEDE P.
XX  PA {LEAD/} LEADER B.

```


XX Leder P, Leader B;
 XX WPI; 2002-690474/74.
 XX
 XX Determining whether patient has increased risk for recurrent pregnancy
 PT loss by determining whether formin-2 (Fmn-2) gene of patient has
 PT mutation, or by measuring Fmn-2 biological activity or Fmn-2 expression
 PT in patient -
 XX
 XX Example 1; Page 7; 137pp; English.
 XX
 CC The invention relates to a novel method for determining whether a patient
 CC has an increased risk for recurrent pregnancy loss, involving determining
 CC whether the formin-2 (Fmn-2) gene of the patient has a mutation. The
 CC method of the invention is useful for determining whether a patient has a
 CC increased risk for recurrent pregnancy loss (RPL/recurrent spontaneous
 CC abortion/miscarriage). The sequence represents a proline motif which is
 CC repeated 11 times in tandem in the Fhl domain of formin-2.
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 71.4%; Score 5; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 6 PPPLP 10
 |||||
 RESULT 36
 ABB99166
 ID ABB99166 standard; peptide; 11 AA.
 AC ABB99166;
 XX
 XX 22-NOV-2002 (first entry)
 DT
 DE Formin-2 Fhl domain repeated proline motif #2.
 XX
 KW Formin-2; recurrent pregnancy loss; formin-2; Fmn-2; RPL;
 KW spontaneous abortion; miscarriage; Fhl; proline motif.
 XX
 OS Unidentified.
 XX
 PN US2002098489-A1.
 XX
 XX 25-JUL-2002.
 PD
 XX
 XX 12-APR-2001; 2001US-0835232.
 PF
 XX
 XX 13-APR-2000; 2000US-196811P.
 PR
 XX (LEDE/) LEDER P.
 PA (LEAD/) LEADER B.
 XX
 PI Leder P, Leader B;
 XX
 XX WPI; 2002-690474/74.
 DR
 XX Determining whether patient has increased risk for recurrent pregnancy
 PT loss by determining whether formin-2 (Fmn-2) gene of patient has
 PT mutation, or by measuring Fmn-2 biological activity or Fmn-2 expression
 PT in patient -
 XX
 XX Example 1; Page 7; 137pp; English.
 PS
 XX The invention relates to a novel method for determining whether a patient
 CC has an increased risk for recurrent pregnancy loss, involving determining
 CC whether the formin-2 (Fmn-2) gene of the patient has a mutation. The
 CC method of the invention is useful for determining whether a patient has a
 CC increased risk for recurrent pregnancy loss (RPL/recurrent spontaneous

CC abortion/miscarriage). The sequence represents a proline motif which is
 CC repeated in the Fhl domain of formin-2 in the brain clones of the
 CC invention.
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 71.4%; Score 5; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 7 PPPLP 11
 |||||
 RESULT 37
 AAW06845
 ID AAW06845 standard; peptide; 12 AA.
 XX
 AC AAW06845;
 XX
 XX 16-FEB-1997 (first entry)
 DT
 XX Peptide binding the Crk-SH3 domain, used to treat cancer.
 DE
 XX Peptide; binding; inhibition; binding domain; Crk-SH3; cancer;
 KW treatment; diagnosis; antibody; signal transduction; disease;
 KW disorder; intracellular signalling protein.
 XX
 OS Synthetic.
 XX
 PN WO9621011-A2.
 XX
 PD 11-JUL-1996.
 XX
 XX 28-DEC-1995; 95WO-US16979.
 PF
 XX 30-DEC-1994; 94US-0367070.
 PR
 XX (UVRQ) UNIV ROCKEFELLER.
 PA
 XX Cowburn D, Feller SM, Hanafusa H, Knudsen BS, Kuriyan J;
 PI Wu X, Zheng J;
 XX
 XX WPI; 1996-333986/33.
 DR
 XX New peptide(s) which bind the Crk-SH3 domain - used to develop
 PT prods. for the diagnosis and treatment of defects in intracellular
 PT signal transduction, partic. in cancer
 XX
 PS Claim 3; Page 92; 120pp; English.
 XX
 CC New peptides or proteins which comprise these peptides, bind
 CC to the Crk-SH3 domain and competitively inhibit the binding of
 CC intracellular signalling proteins. They can be used in the
 CC treatment of a disease or disorder associated with a defect in
 CC intracellular signal transduction, particularly cancer. They can
 CC also be used to diagnose such diseases and disorders. Antibodies
 CC raised against these proteins can be used for the same purposes. The
 CC peptides are derived from the Crk-SH3 binding domains of
 CC intracellular signalling proteins. Peptides related to the invention
 CC are described in AAW03149-63 and AAW06842-W06866.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 71.4%; Score 5; DB 17; Length 12;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 3 PPPLP 7
 |||||

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RESULT 38
AAW03154
ID AAW03154 standard; peptide; 12 AA.
XX
XX AAW03154;
AC
XX 16-FEB-1997 (first entry)
DT
XX
XX Potential Crk-SH3 binding sequence of protein mSos2/p1.
DE
XX
XX Peptide; binding; inhibition; binding domain; Crk-SH3; cancer;
KW treatment; diagnosis; antibody; signal transduction; disease;
KW disorder; intracellular signalling protein.
XX
XX Synthetic.
OS
XX
XX WO9621011-A2.
FN
XX
XX 11-JUL-1996.
PD
XX
XX 28-DEC-1995; 95WO-US16979.
PF
XX
XX 30-DEC-1994; 94US-0367070.
PR
XX
XX (UYRQ ) UNIV ROCKEFELLER.
PA
XX
XX Cowburn D, Feller SM, Hanafusa H, Knudsen BS, Kuriyan J;
PI Wu X, Zheng J;
PL
XX
XX WPI; 1996-333986/33.
DR
XX
XX New peptide(s) which bind the Crk-SH3 domain - used to develop
PT prods for the diagnosis and treatment of defects in intracellular
PT signal transduction, partic. in cancer
XX
XX Disclosure; Page 53; 120pp; English.
FS
XX
XX New peptides or proteins which comprise these peptides, bind
CC to the Crk-SH3 domain and competitively inhibit the binding of
CC intracellular signalling proteins. They can be used in the
CC treatment of a disease or disorder associated with a defect in
CC intracellular signal transduction, particularly cancer. They can
CC also be used to diagnose such diseases and disorders. Antibodies
CC raised against these proteins can be used for the same purposes. The
CC peptides are derived from the Crk-SH3 binding domains of
CC intracellular signalling proteins. Peptides related to the invention
CC are described in AAW03149-63 and AAW06842-W06866.
XX
XX
SQ Sequence 12 AA;
Query Match 71.4%; Score 5; DB 17; Length 12;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 PPPLP 7
Db 3 PPPLP 7
RESULT 39
AAW05101
ID AAW05101 standard; peptide; 12 AA.
XX
XX AAW05101;
AC
XX
XX 25-MAR-2003 (updated)
DT 17-DEC-1996 (first entry)
DT
XX
XX Proline-rich SH3 binding peptide pL35.
DE
XX
XX Src homology domain; SH3 domain; oncogene; consensus; lambda 35;
KW random display library.

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XX Synthetic.
OS
XX US5541109-A.
PN
XX 30-JUL-1996.
PD
XX
XX 19-APR-1994; 94US-0230047.
PF
XX
XX 19-APR-1994; 94US-0230047.
PR
XX
XX (RHON ) RHONE POULENC RORER PHARM INC.
PA
XX Ivashchenko YD, Ricca GA, Cheadle C, South VJ, Jaye MC, French SM;
PI Searfoss GH;
XX
XX WPI; 1996-361965/36.
DR
XX
XX New DNA encoding proteins that bind to Src-homology domain 3 - used
XX to inhibit signal transduction, e.g. in cases of T cell activation
PT
XX
XX Example 1; Column 16; 39pp; English.
FS
XX
XX A fusion protein of glutathione-S-transferase, protein kinase A and
CC Src SH3 domain was used to screen a mouse embryonal cDNA library in
CC lambda Exlox. Three positive clones were identified and were
CC designated L17, L14 and L35. The insert from clone L35 encodes a
CC protein which contains a proline-rich, putative SH3-binding
CC sequence. The present peptide sequence is derived from the putative
CC SH3-binding site (i.e. residues 13-24 of L35) and was used in an assay
CC to determine binding to the SH3 domains of c-src and other proteins.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX
SQ Sequence 12 AA;
Query Match 71.4%; Score 5; DB 17; Length 12;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 PPPLP 7
Db 4 PPPLP 8
RESULT 40
AAW25457
ID AAW25457 standard; peptide; 12 AA.
XX
XX AAW25457;
AC
XX
XX 27-MAR-1998 (first entry)
DT
XX
XX SH3 domain binding responsible peptide SEQ ID NO:251.
DE
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
OS
XX Unidentified.
XX
XX WO9730074-A1.
FN
XX
XX 21-AUG-1997.
PD
XX
XX 14-FEB-1997; 97WO-US02298.
PF
XX
XX 16-FEB-1996; 96US-0602999.
PR
XX
XX (CYTO-) CYTOGEN CORP.
PA (UYNC-) UNIV NORTH CAROLINA.
XX
XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
PI

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PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 XX
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 XX Claim 21; Page 85; 131pp; English.
 XX
 CC The present sequence represents a peptide responsible for Src homology
 CC region 3 (SH3) binding. SH3 binding peptides are selected from: (a)
 CC peptides which bind the SH3 domain of Cortactin; (b) peptides which bind
 CC the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of
 CC Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which
 CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain
 CC of p33bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC bind the SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 71.4%; Score 5; DB 18; Length 12;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 6 PPPLP 10
 RESULT 41
 AAW25468
 ID AAW25468 standard; peptide; 12 AA.
 AC
 AC AAW25468;
 XX
 XX 27-MAR-1998 (first entry)
 DT
 XX SH3 domain binding responsible peptide SEQ ID NO:266.
 DE
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 XX Synthetic.
 OS Unidentified.
 XX
 XX WO9730074-A1.
 PN
 XX 21-AUG-1997.
 FD
 XX 14-FEB-1997; 97WO-US02298.
 PF
 XX 16-FEB-1996; 96US-0602999.
 PR
 XX (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 DR
 XX

PT Src homology region 3 binding peptide - used to activate Src
 XX tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 XX Claim 21; Page 85; 131pp; English.
 XX
 CC The present sequence represents a peptide responsible for Src homology
 CC region 3 (SH3) binding. SH3 binding peptides are selected from: (a)
 CC peptides which bind the SH3 domain of Cortactin; (b) peptides which bind
 CC the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of
 CC Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which
 CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain
 CC of p33bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC bind the SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 71.4%; Score 5; DB 18; Length 12;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QPPPL 6
 DB 4 QPPPL 8
 RESULT 42
 AAB18002
 ID AAB18002 standard; Peptide; 12 AA.
 XX
 XX AAB18002;
 AC
 XX 31-OCT-2000 (first entry)
 DT
 XX Fc-TNF alpha peptide sequence SEQ ID NO:1116.
 DE
 XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 XX Synthetic.
 OS
 XX WO200024782-A2.
 PN
 XX 04-MAY-2000.
 PD
 XX 25-OCT-1999; 99WO-US25044.
 PF
 XX 23-OCT-1998; 98US-0105371.
 PR
 XX 22-OCT-1999; 99US-0428082.
 FR
 XX (AMGE-) AMGEN INC.
 PA
 XX Feige U, Liu C, Cheetham J, Boone TC;
 PI WPI; 2000-350702/30.
 DR
 XX Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and

PT autoimmune diseases -
XX Disclosure; Page 604; 608pp; English.
XX

CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-P1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, -(L4)f-P4
CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX

SQ Sequence 12 AA;
Query Match 71.4%; Score 5; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 8 PPPLP 12
|||||

RESULT 43
AAR84641
ID AAR84641 standard; Peptide; 13 AA.
AC AAR84641;
XX
XX 26-MAR-1996 (first entry)
DE
DE Grb2-SOS binding blocking peptide.
XX
XX SOS; Grb2; BCR-ABL; tyrosine kinase; transformation; Ras;
KW oncoprotein; leukaemia; Ras guanine nucleotide releasing protein.
XX
XX Synthetic.
OS
XX
XX CA2113494-A.
PN
XX
XX 15-JUL-1995.
PD
XX
XX 14-JAN-1994; 94CA-2113494.
PF
XX
XX 14-JAN-1994; 94CA-2113494.
PR
XX
XX (MOUN) MOUNT SINAI HOSPITAL CORP.
PA (TEXA) UNIV TEXAS.
XX
XX Arlinghaus R, Gish G, Liu J, Pawson A, Puil L;
PI
XX
XX WPI; 1995-302931/40.
DR
XX
XX Detection of agents that modify BCR-ABL mediated transformation -
PT useful in treatment of leukaemia and other malignancies
XX
XX Disclosure; Page 15; 106pp; English.
PS
XX Peptides (AAR84640-48) that block the binding of Grb2 (AAR84636) to
CC SOS Ras guanine nucleotide releasing protein are modelled on the
CC proline-rich motifs in the C-terminal region of mouse SOS1
CC (AAR84638) and SOS2 (AAR84639). The peptides can be used to screen
CC

CC for compounds that affect BCL-ABL mediated transformation. Such
CC compounds have value in the treatment of chronic, acute myelogenous
CC or acute lymphocytic leukaemia.
XX

SQ Sequence 13 AA;
Query Match 71.4%; Score 5; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 5 PPPLP 9
|||||

RESULT 44
AAB70928
ID AAB70928 standard; Protein; 13 AA.
XX
XX AAB70928;
AC
XX 30-JUL-2001 (first entry)
DT
XX
XX Polyoma virus VPI variant proline-rich peptide fragment.
DE
XX
XX VPI; Coat protein; WW domain; proline-rich; immobilization; biosensor;
KW bioreactor; protein packaging; PyVPI-WW150-D8C.
XX
XX Polyoma virus.
OS
XX
XX WO200132684-A2.
PN
XX
XX 10-MAY-2001.
PD
XX
XX 03-NOV-2000; 2000WO-EP10873.
PF
XX
XX 03-NOV-1999; 99DE-1052956.
PR
XX
XX (ACGT-) ACGT PROGENOMICS AG.
PA
XX
XX Boehm G, Schmidt U, Parthier C, Guenther C;
PI
XX
XX WPI; 2001-343471/36.
DR
XX
XX Linking two or more molecules through adapter sequences, useful e.g.
PT for purifying recombinant proteins, by exploiting interaction between
PT WW domain and proline-rich sequence -
XX
XX Example 5; Page 88; 100pp; German.
PS
XX
XX This invention describes a novel method (M1) for linking two or more
CC molecular substances (A) together via adapter sequences (AS). One (A) is
CC modified so that it contains, as AS, a WW domain or derived structure in
CC at least one region, and a second (A) is modified so that it contains,
CC as AS, a proline-rich sequence (PRS) able to bind to WW domain or its
CC derivative in at least one region and the modified components are
CC allowed to interact together through WW and PRS. The method is used to
CC provide permanent or temporary association between (A), e.g. temporary
CC immobilization, and matrix-assisted refolding, of recombinant proteins
CC from crude cell extracts or permanent immobilization in biosensors or
CC bioreactors, for directing packaging of proteins inside a virus-like
CC shell, or production of chimeric proteins (e.g. bispecific antibodies),
CC for medical, therapeutic, diagnostic or biotechnological use. Interaction
CC between WW and PRS is very strong (dissociation constant 20-100 nM) but
CC only temporary, and can be stabilized (e.g. against extremes of salt
CC concentration or temperature) by formation of disulfide bridges. Compared
CC with other systems with comparable properties, the WW/PRS system is
CC exceptionally small and compact and for many applications, e.g.
CC antibody-antigen interaction, is clearly superior to other ligand binding
CC domains. The system can only produce heterodimers. This sequence
CC represents a proline-rich peptide fragment from Polyoma virus coat
CC protein VPI which is used to illustrate the method of the invention.
XX

SQ Sequence 13 AA;
Query Match 71.4%; Score 5; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 9 PPPLP 13

RESULT 45
AAW05490
ID AAW05490 standard; Peptide; 14 AA.
XX AC
XX AAW05490;
XX
XX
DT 24-FEB-1998 (first entry)
DE SH3-binding peptide CRK.CON.
KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
KW cellular signalling element; cellular structural element; malignancy;
KW protein identification; functional domain; protein screening;
KW cellular signal transduction process; binding peptide.
XX
XX Synthetic.
XX
XX
PN WO9631625-A1.
XX
PD 10-OCT-1996.
XX
XX 04-APR-1996; 96WO-US04454.
XX
XX 03-APR-1996; 96US-0630915.
PR 07-APR-1995; 95US-0417872.
XX
XX (CYTO-) CYTOGEN CORP.
PA (UYNC-) UNIV NORTH CAROLINA.
XX
XX Fowlkes DM, Hoffman N, Kay BK, McConnell SJ, Sparks AB;
PI WPI; 1996-465045/46.
XX
XX Identifying polypeptide(s) having specific functional domain (esp.
PT SH3 domain) - comprises detecting selective binding to recognition
PT unit, regardless of sequence homology
XX
PS Example; Fig 13; 174pp; English.

XX AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding
CC peptides. These sequences were used as parts of multivalent recognition
CC unit complexes used in the method of the invention. The method of the
CC invention is for identifying polypeptides containing functional domains
CC of interest (especially SH3 domains). It comprises contacting a
CC multivalent recognition unit (RU) complex with a number of peptides and
CC identifying polypeptides having a selective binding affinity for the RU
CC complex. The method is based on functional similarities and does not
CC rely on sequence similarities. Prior methods only gave limited success
CC for identifying proteins containing an SH3 domain due to the minimal
CC sequence homology among known SH3 proteins. Multivalent RU complexes are
CC particularly suited to screening for polypeptides containing functional
CC domains that are similar to, but not identical in sequence to, the
CC original target functional domain. The new method enables proteins
CC having a common function to be identified. Identification of novel SH3
CC proteins will be useful for a better understanding of cell growth,
CC malignancy, signal transduction processes, etc. New candidate drugs can
CC be identified, and their specificities (e.g. pharmacological activities)
CC can be assessed using the method of the invention.

XX
XX
SQ Sequence 14 AA;
Query Match 71.4%; Score 5; DB 17; Length 14;

Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 5 PPPLP 9

RESULT 46
AAW38067
ID AAW38067 standard; Peptide; 14 AA.
XX AC
XX AAW38067;
XX
XX 23-APR-1998 (first entry)
XX
DE PPPPY motif containing peptide used to bind WW domains.
XX
KW Peptide recognition unit; WW domain; cell signalling; growth regulation;
KW cytoskeleton organisation; targeted drug screening; modulator;
KW WW domain interaction; YAP protein; dystrophin.
XX
XX Synthetic.
XX
XX WO9737223-A1.
XX
XX 09-OCT-1997.
XX
XX 03-APR-1997; 97WO-US05547.
XX
XX 03-APR-1996; 96US-0630916.
XX
XX (CYTO-) CYTOGEN CORP.
PA (UYNC-) UNIV NORTH CAROLINA.
XX
XX Fowlkes DM, Kay BK, Pirozzi G;
PI WPI; 1997-503234/46.
XX
XX Identifying cell signalling and growth regulatory polypeptides by
PT reaction with multivalent recognition complex - polypeptides are
PT useful in targeted drug selection
XX
PS Disclosure; Fig 15A; 220pp; English.

XX Peptides AAW38057-67 contain PPPPY-like motifs. The PPPY motif is
CC found in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides
CC containing this residue have been shown to bind the YAP WW domain, but
CC not the WW domain from dystrophin or to a panel of SH3 domains. Peptides
CC AAW38057-67 were biotinylated and complexed with alkaline streptavidin,
CC and used in a cross affinity mapping experiment. They were tested for
CC their ability to bind to the 12 individual novel WW domains of WWPI
CC (AAW36794), WWP2 (AAW36795), WWP3 (AAW37696) and WWP4 (AAW36797), which
CC were expressed as glutathione-S-transferase expression proteins. The
CC present peptide, derived from Crk protein, does not bind the WW domains
CC of the novel proteins. The WW domain is a small functional domain. Its
CC name is derived from the observation that two tryptophan residues, one in
CC the amino terminal portion of the WW domain and one in the carboxyl
CC terminal portion, are conserved. Most proteins containing WW domains have
CC a function involving cell signalling and growth regulation or the
CC organisation of the cytoskeleton. Polypeptides containing a WW domain
CC are identified by treating a multivalent recognition unit complex that
CC has selective binding affinity for a WW domain, with many polypeptides
CC and identifying those with selective affinity for the complex. Proteins
CC containing WW domains are used for targeted drug screening, i.e. to
CC identify potential modulators of specific WW domain interactions.

XX
XX
SQ Sequence 14 AA;
Query Match 71.4%; Score 5; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 5 PPPLP 9

RESULT 47

AAW38959
 ID AAW38959 standard; peptide; 15 AA.

XX AAW38959;

DT 27-MAR-1998 (first entry)

DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:356.

XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX Synthetic.

OS WO9730074-A1.

PN 21-AUG-1997.

PF 14-FEB-1997; 97WO-US02298.

PR 16-FEB-1996; 96US-0602999.

XX (CYTO-) CYTOGEN CORP.

PA (UYNC-) UNIV NORTH CAROLINA.

XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JB;

PI Sparks AB, Thorn JM;

XX WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1

PS Claim 22; Page 91; 131pp; English.

XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.

SQ Sequence 15 AA;

Query Match 71.4%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 7 PPPLP 11

RESULT 49

AAW39034
 ID AAW39034 standard; peptide; 15 AA.

XX AAW39034;

RESULT 48

AAW39050
 ID AAW39050 standard; peptide; 15 AA.

XX AAW39050;

XX 27-MAR-1998 (first entry)

DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:452.

XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX Synthetic.

PN WO9730074-A1.

XX 21-AUG-1997.

PF 14-FEB-1997; 97WO-US02298.

PR 16-FEB-1996; 96US-0602999.

XX (CYTO-) CYTOGEN CORP.

PA (UYNC-) UNIV NORTH CAROLINA.

XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JB;

PI Sparks AB, Thorn JM;

XX WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1

PS Claim 22; Page 94; 131pp; English.

XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.

SQ Sequence 15 AA;

Query Match 71.4%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 7 PPPLP 11

XX 27-MAR-1998 (first entry)
 XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:435.
 XX
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 XX Synthetic.
 XX
 XX WO9730074-A1.
 PN
 XX 21-AUG-1997.
 PD
 XX 14-FEB-1997; 97WO-US02298.
 XX
 XX 16-FEB-1996; 96US-0602999.
 PR
 XX (CYTO-) CYTOGEN CORP.
 PA
 XX (UYNC-) UNIV NORTH CAROLINA.
 XX
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 PI
 XX WPI; 1997-424972/39.
 DR
 XX
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 XX Claim 22; Page 94; 131pp; English.
 PS
 XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC peptides which bind their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 71.4%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 4 PPPLP 8
 RESULT 50
 AAW39040
 ID AAW39040 standard; peptide; 15 AA.
 AC
 XX AAW39040;
 XX
 XX 27-MAR-1998 (first entry)
 DT
 XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:441.
 DE
 XX

KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 XX Synthetic.
 XX
 XX WO9730074-A1.
 PN
 XX 21-AUG-1997.
 PD
 XX 14-FEB-1997; 97WO-US02298.
 XX
 XX 16-FEB-1996; 96US-0602999.
 PR
 XX (CYTO-) CYTOGEN CORP.
 PA
 XX (UYNC-) UNIV NORTH CAROLINA.
 XX
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 PI
 XX WPI; 1997-424972/39.
 DR
 XX
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 XX Claim 22; Page 94; 131pp; English.
 PS
 XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of p53bp2; (g) peptides which bind
 CC the SH3 domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 71.4%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 5 PPPLP 9
 RESULT 51
 AAW39005
 ID AAW39005 standard; peptide; 15 AA.
 XX
 XX AAW39005;
 AC
 XX 27-MAR-1998 (first entry)
 DT
 XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:404.
 DE
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 XX Synthetic.

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XX PN WO9730074-A1.
XX PD 21-AUG-1997.
XX PF 14-FEB-1997; 97WO-US02298.
XX PR 16-FEB-1996; 96US-0602999.
XX PA (CYTO-) CYTOGEN CORP.
XX PI (UYNC-) UNIV NORTH CAROLINA.
XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX PI Sparks AB, Thorn JM;
XX DR WPI; 1997-424972/39.
XX
XX Src homology region 3 binding peptide - used to activate Src
XX tyrosine kinase(s) and to stimulate immune response by increasing
XX production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 93; 131pp; English.
XX
XX The present sequence represents a peptide which resembles a Src homology
XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
XX peptides which bind the amino-terminal SH3 domain of Grb2. The purified
XX binding peptides can be used in the method to identify inhibitors of
XX their binding to their respective SH3 domains, which could be used to
XX modulate the pharmacological activity of proteins or polypeptide
XX containing the SH3 domain. The peptides can also be used to activate
XX Src or Src-related protein tyrosine kinases, to stimulate the immune
XX response by increasing the production of certain lymphokines, e.g.
XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX conjugated molecule to certain cellular compartments containing Src or
XX Src related proteins.
XX
XX Sequence 15 AA;
XX
Query Match 71.4%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 52
AAW39015
XX ID AAW39015 standard; peptide; 15 AA.
XX AC AAW39015;
XX
XX 27-MAR-1998 (first entry)
XX
DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:414.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX
XX WO9730074-A1.
XX PN 21-AUG-1997.
XX PD 14-FEB-1997; 97WO-US02298.
XX PR 16-FEB-1996; 96US-0602999.
XX PA (CYTO-) CYTOGEN CORP.
XX PI (UYNC-) UNIV NORTH CAROLINA.
XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX PI Sparks AB, Thorn JM;
XX DR WPI; 1997-424972/39.
XX
XX Src homology region 3 binding peptide - used to activate Src
XX tyrosine kinase(s) and to stimulate immune response by increasing
XX production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 93; 131pp; English.
XX
XX The present sequence represents a peptide which resembles a Src homology
XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
XX peptides which bind the amino-terminal SH3 domain of Grb2. The purified
XX binding peptides can be used in the method to identify inhibitors of
XX their binding to their respective SH3 domains, which could be used to
XX modulate the pharmacological activity of proteins or polypeptide
XX containing the SH3 domain. The peptides can also be used to activate
XX Src or Src-related protein tyrosine kinases, to stimulate the immune
XX response by increasing the production of certain lymphokines, e.g.
XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX conjugated molecule to certain cellular compartments containing Src or
XX Src related proteins.
XX
XX Sequence 15 AA;
XX
Query Match 71.4%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 53
AAW38988
XX ID AAW38988 standard; peptide; 15 AA.
XX AC AAW38988;
XX
XX 27-MAR-1998 (first entry)
XX
DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:385.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX
XX WO9730074-A1.
XX PN 21-AUG-1997.
XX PD 14-FEB-1997; 97WO-US02298.
XX PR 16-FEB-1996; 96US-0602999.
XX PA (CYTO-) CYTOGEN CORP.

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PF 14-FEB-1997; 97WO-US02298.
XX
XX 16-FEB-1996; 96US-0602999.
XX
XX (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX
XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX PI Sparks AB, Thorn JM;
XX DR WPI; 1997-424972/39.
XX
XX Src homology region 3 binding peptide - used to activate Src
XX tyrosine kinase(s) and to stimulate immune response by increasing
XX production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 93; 131pp; English.
XX
XX The present sequence represents a peptide which resembles a Src homology
XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
XX peptides which bind the amino-terminal SH3 domain of Grb2. The purified
XX binding peptides can be used in the method to identify inhibitors of
XX their binding to their respective SH3 domains, which could be used to
XX modulate the pharmacological activity of proteins or polypeptide
XX containing the SH3 domain. The peptides can also be used to activate
XX Src or Src-related protein tyrosine kinases, to stimulate the immune
XX response by increasing the production of certain lymphokines, e.g.
XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX conjugated molecule to certain cellular compartments containing Src or
XX Src related proteins.
XX
XX Sequence 15 AA;
XX
Query Match 71.4%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 53
AAW38988
XX ID AAW38988 standard; peptide; 15 AA.
XX AC AAW38988;
XX
XX 27-MAR-1998 (first entry)
XX
DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:385.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX
XX WO9730074-A1.
XX PN 21-AUG-1997.
XX PD 14-FEB-1997; 97WO-US02298.
XX PR 16-FEB-1996; 96US-0602999.
XX PA (CYTO-) CYTOGEN CORP.

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PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
PI Sparks AB, Thorn JM;
XX
XX WPI; 1997-424972/39.
XX
PT Src homology region 3 binding peptide - used to activate Src
PT tyrosine kinase(s) and to stimulate immune response by increasing
PT production of certain lymphokine(s), e.g. interleukin-1
XX
PS Claim 22; Page 92; 131pp; English.
XX
CC The present sequence represents a peptide which resembles a Src homology
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
CC binding peptides can be used in the method to identify inhibitors of
CC their binding to their respective SH3 domains, which could be used to
CC modulate the pharmacological activity of proteins or polypeptide
CC containing the SH3 domain. The peptides can also be used to activate
CC Src or Src-related protein tyrosine kinases, to stimulate the immune
CC response by increasing the production of certain lymphokines, e.g.
CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
CC conjugated molecule to certain cellular compartments containing Src or
CC Src related proteins.
XX
XX Sequence 15 AA;
SQ
    Query Match          71.4%; Score 5; DB 18; Length 15;
    Best Local Similarity 100.0%; Pred. No. 54;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 3 PPPLP 7
    Db 7 PPPLP 11
    |||||
    |||||

RESULT 54
AAW27070
ID AAW27070 standard; peptide; 15 AA.
XX
XX AC AAW27070;
XX
XX DT 19-MAR-1998 (first entry)
XX
XX DE Proline rich peptide.
XX
XX KW Proline rich; treatment; inflammation; septic shock;
XX rheumatoid arthritis; asthma; adult respiratory distress syndrome;
XX ischaemic heart disease; reperfusion injury;
XX inflammatory bowel disease.
XX
XX OS Homo sapiens.
XX
XX PN GB2311067-A.
XX
XX PD 17-SEP-1997.
XX
XX PF 08-JAN-1996; 96GB-0000307.
XX
XX PR 08-JAN-1996; 96GB-0000307.
XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX (YAMA ) YAMANOUCHI UK LTD.
XX
XX PI Finan P, Kellie S;
XX
XX DR WPI; 1997-427905/40.
XX
XX PT Proline rich peptides derived from a protein extracted from Namalwa
XX cells - for treating e.g. inflammatory diseases, rheumatoid and
XX other arthritides, asthma, adult respiratory distress syndrome,
XX ischaemic heart disease and inflammatory bowel disease
XX
XX PS Claim 2; Page 17; 28pp; English.
XX
XX CC The present proline rich peptide can be used to treat chronic and
XX acute inflammatory diseases and conditions, e.g. septic shock,
XX rheumatoid arthritis, asthma, adult respiratory distress syndrome,
XX ischaemic heart disease, reperfusion injury and inflammatory bowel
XX disease.
XX
XX Sequence 15 AA;
SQ
    Query Match          71.4%; Score 5; DB 18; Length 15;
    Best Local Similarity 100.0%; Pred. No. 54;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 2 QPPPL 6
    Db 6 QPPPL 10
    |||||
    |||||

RESULT 55
AAW27073
ID AAW27073 standard; peptide; 15 AA.
XX
XX AC AAW27073;
XX
XX DT 19-MAR-1998 (first entry)
XX
XX DE Proline rich peptide.
XX
XX KW Proline rich; treatment; inflammation; septic shock;
XX rheumatoid arthritis; asthma; adult respiratory distress syndrome;
XX ischaemic heart disease; reperfusion injury;
XX inflammatory bowel disease.
XX
XX OS Homo sapiens.
XX
XX PN GB2311067-A.
XX
XX PD 17-SEP-1997.
XX
XX PF 08-JAN-1996; 96GB-0000307.
XX
XX PR 08-JAN-1996; 96GB-0000307.
XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX (YAMA ) YAMANOUCHI UK LTD.
XX
XX PI Finan P, Kellie S;
XX
XX DR WPI; 1997-427905/40.
XX
XX PT Proline rich peptides derived from a protein extracted from Namalwa
XX cells - for treating e.g. inflammatory diseases, rheumatoid and
XX other arthritides, asthma, adult respiratory distress syndrome,
XX ischaemic heart disease and inflammatory bowel disease
XX
XX PS Claim 2; Page 17; 28pp; English.
XX
XX CC The present proline rich peptide can be used to treat chronic and
XX acute inflammatory diseases and conditions, e.g. septic shock,
XX rheumatoid arthritis, asthma, adult respiratory distress syndrome,
XX ischaemic heart disease, reperfusion injury and inflammatory bowel
XX disease.
XX
XX Sequence 15 AA;
SQ

```

Query Match 71.4%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPL 6
 DB 6 QPPPL 10

RESULT 56
 AAY41635
 ID AAY41635 standard; peptide; 15 AA.
 AC AAY41635;
 XX 02-DEC-1999 (first entry)
 DT
 DE Mammalian ion channel proline rich motif containing peptide #29.
 XX SH3 domain; binding motif; potassium channel; protein tyrosine kinase;
 KW proline rich.
 KW Homo sapiens.
 OS
 XX US955259-A.
 PN 21-SEP-1999.
 XX 19-DEC-1996; 96US-0769745.
 PF 19-DEC-1996; 96US-0769745.
 XX 19-DEC-1996; 96US-0769745.
 PR (UYBR-) UNIV BRANDEIS.
 PA Holmes TC, Levitan IB;
 PI WPI; 1999-560490/47.
 XX Identification of compounds that modulate potassium ion channel binding
 PT with protein tyrosine kinase SH3 domains -
 PT Disclosure; Column 8; 18pp; English.
 PS
 XX A method has been developed for determining if a compound modulates the
 CC binding of a potassium ion channel to the SH3 domain of a protein
 CC tyrosine kinase by contacting the channel with a polypeptide comprising
 CC the SH3 domain and the compound to be assessed and measuring channel-SH3
 CC binding. The method is useful for assessing the ability of a compound to
 CC modulate the formation of channel-SH3 domain complexes to improve the
 CC understanding of mechanisms of potassium channel blockage and assess the
 CC ability of potential therapeutics to inhibit blockage. AAY41607 to
 CC AAY41644 represent mammalian ion channel peptides with proline-rich
 CC motifs.
 XX
 SQ Sequence 15 AA;

Query Match 71.4%; Score 5; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPL 7
 DB 4 PPPPL 8

RESULT 57
 AAW25411
 ID AAW25411 standard; peptide; 16 AA.
 XX
 AC AAW25411;
 XX 27-MAR-1998 (first entry)
 DT
 XX

DE Crk N-terminal SH3 domain binding peptide SEQ ID NO:197.
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 PN WO9730074-A1.
 XX 21-AUG-1997.
 PD 14-FEB-1997; 97WO-US02298.
 XX 16-FEB-1996; 96US-0602999.
 PR (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 DR Src homology region 3 binding peptide - used to activate Src
 XX tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 PT Claim 18; Page 100; 131pp; English.
 PS
 XX The present sequence represents a Src homology region 3 (SH3) binding
 CC peptide. SH3 binding peptides are selected from: (a) peptides which
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 SQ Sequence 16 AA;

Query Match 71.4%; Score 5; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPPL 7
 DB 9 PPPPL 13

RESULT 58
 AAW38963
 ID AAW38963 standard; peptide; 17 AA.
 XX AAW38963;
 AC
 XX 27-MAR-1998 (first entry)
 DT Peptide resembling an SH3 domain binding peptide SEQ ID NO:360.
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW

KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX Synthetic.
 XX WO9730074-A1.
 XX 21-AUG-1997.
 XX 14-FEB-1997; 97WO-US02298.
 XX 16-FEB-1996; 96US-0602999.
 XX (CYTO-) CYTOGEN CORP.
 XX (UYNC-) UNIV NORTH CAROLINA.
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX Claim 22; Page 91; 131pp; English.
 XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC binding peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX SQ Sequence 17 AA;
 Query Match 71.4%; Score 5; DB 18; Length 17;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 9 PPPLP 13
 RESULT 59
 AAW38977
 ID AAW38977 standard; peptide; 17 AA.
 AC AAW38977;
 XX 27-MAR-1998 (first entry)
 XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:374.
 DE Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX Synthetic.
 XX WO9730074-A1.

XX 21-AUG-1997.
 XX 14-FEB-1997; 97WO-US02298.
 XX 16-FEB-1996; 96US-0602999.
 XX (CYTO-) CYTOGEN CORP.
 XX (UYNC-) UNIV NORTH CAROLINA.
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX Claim 22; Page 92; 131pp; English.
 XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC binding peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX SQ Sequence 17 AA;
 Query Match 71.4%; Score 5; DB 18; Length 17;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 9 PPPLP 13
 RESULT 60
 AAR91746
 ID AAR91746 standard; peptide; 18 AA.
 AC AAR91746;
 XX 14-AUG-1996 (first entry)
 XX Prolyl endopeptidase inhibitor peptide #1.
 DE Prolyl endopeptidase; PEP; inhibitory peptide; animal feed; therapy;
 KW prevention; dementia; human.
 XX Synthetic.
 XX JP08059697-A.
 XX 05-MAR-1996.
 XX 09-MAR-1995; 95JP-0079661.
 XX 15-JUN-1994; 94JP-0158031.

```
XX (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA (NIHA-) NIPPON HAM KK.
XX
XX WPI; 1996-184809/19.
XX
XX Prolyl:endo:peptidase inhibitory peptide(s) - useful as additives
PT for food and animal feed and to treat and prevent dementia
XX
XX Claim 1; Page 10; 11pp; Japanese.
XX
XX AAR91746-R91753 represent prolyl endopeptidase (PEP) inhibitory
CC peptides. These peptides are useful as PEP inhibitors in functional foods
CC and in animal feeds. They are used to prepare oral and parenteral
CC pharmaceutical preparations for the treatment and prevention of dementia
CC of animals, including humans. The advantage with using these peptides,
CC is that they are safe and easily absorbed.
XX
XX Sequence 18 AA;
SQ
Query Match 71.4%; Score 5; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 2 PPPLP 6

RESULT 61
AAR91750
ID AAR91750 standard; peptide; 18 AA.
XX
AC AAR91750;
XX
XX 14-AUG-1996 (first entry)
XX
DE Prolyl endopeptidase inhibitor peptide #5.
XX
XX Prolyl endopeptidase; PEP; inhibitory peptide; animal feed; therapy;
KW prevention; dementia; human.
XX
XX Synthetic.
XX
XX JP08059697-A.
XX
XX 05-MAR-1996.
XX
XX 09-MAR-1995; 95JP-0079661.
XX
XX 15-JUN-1994; 94JP-0158031.
XX
XX (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA (NIHA-) NIPPON HAM KK.
XX
XX WPI; 1996-184809/19.
XX
XX Prolyl:endo:peptidase inhibitory peptide(s) - useful as additives
PT for food and animal feed and to treat and prevent dementia
XX
XX Claim 1; Page 10; 11pp; Japanese.
XX
XX AAR91746-R91753 represent prolyl endopeptidase (PEP) inhibitory
CC peptides. These peptides are useful as PEP inhibitors in functional foods
CC and in animal feeds. They are used to prepare oral and parenteral
CC pharmaceutical preparations for the treatment and prevention of dementia
CC of animals, including humans. The advantage with using these peptides,
CC is that they are safe and easily absorbed.
XX
XX Sequence 18 AA;
SQ
Query Match 71.4%; Score 5; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 2 PPPLP 6

RESULT 62
AAW39010
ID AAW39010 standard; peptide; 18 AA.
XX
AC AAW39010;
XX
XX 27-MAR-1998 (first entry)
XX
DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:409.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX
XX WO9730074-A1.
XX
XX 21-AUG-1997.
XX
XX 14-FEB-1997; 97WO-US02298.
XX
XX 16-FEB-1996; 96US-0602999.
XX
XX (CVTO-) CYTOGEN CORP.
PA (UVNC-) UNIV NORTH CAROLINA.
XX
XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JB;
PI Sparks AB, Thorn JN;
XX
XX WPI; 1997-424972/39.
XX
XX Src homology region 3 binding peptide - used to activate Src
PT tyrosine kinase(s) and to stimulate immune response by increasing
PT production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 93; 131pp; English.
XX
XX The present sequence represents a peptide which resembles a Src homology
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
CC binding peptides can be used in the method to identify inhibitors of
CC their binding to their respective SH3 domains, which could be used to
CC modulate the pharmacological activity of proteins or polypeptide
CC containing the SH3 domain. The peptides can also be used to activate
CC Src or Src-related protein tyrosine kinases, to stimulate the immune
CC response by increasing the production of certain lymphokines, e.g.
CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
CC conjugated molecule to certain cellular compartments containing Src or
CC Src related proteins.
XX
XX Sequence 18 AA;
SQ
Query Match 71.4%; Score 5; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 11 PPPLP 15
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XX AC AAW05473;
XX DT 24-FEB-1998 (first entry)
XX DE XX
XX DE XX
XX KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
XX KW cellular signalling element; cellular structural element; malignancy;
XX KW protein identification; functional domain; protein screening;
XX KW cellular signal transduction process; binding peptide.
XX OS Synthetic.
XX PN W09G31625-A1.
XX PD 10-OCT-1996.
XX PF 04-APR-1996; 96WO-US04454.
XX PR 03-APR-1996; 96US-0630915.
XX PR 07-APR-1995; 95US-0417872.
XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX PI Fowlkes DM, Hoffman N, Kay BK, McConnell SJ, Sparks AB;
XX DR WPI; 1996-465045/46.
XX PT Identifying polypeptide(s) having specific functional domain (esp.
XX PT SH3 domain) - comprises detecting selective binding to recognition
XX PT unit, regardless of sequence homology
XX PS Example; Fig 13; 174pp; English.
XX CC AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding
XX CC peptides. These sequences were used as parts of multivalent recognition
XX CC unit complexes used in the method of the invention. The method of the
XX CC invention is for identifying polypeptides containing functional domains
XX CC of interest (especially SH3 domains). It comprises contacting a
XX CC multivalent recognition unit (RU) complex with a number of peptides and
XX CC identifying polypeptides having a selective binding affinity for the RU
XX CC complex. The method is based on functional similarities and does not
XX CC rely on sequence similarities. Prior methods only gave limited success
XX CC for identifying proteins containing an SH3 domain due to the minimal
XX CC sequence homology among known SH3 proteins. Multivalent RU complexes are
XX CC particularly suited to screening for polypeptides containing functional
XX CC domains that are similar to, but not identical in sequence to, the
XX CC original target functional domain. The new method enables proteins
XX CC having a common function to be identified. Identification of novel SH3
XX CC proteins will be useful for a better understanding of cell growth,
XX CC malignancy, signal transduction processes, etc. New candidate drugs can
XX CC be identified, and their specificities (e.g. pharmacological activities)
XX CC can be assessed using the method of the invention.
XX SQ Sequence 19 AA;
XX Query Match 71.4%; Score 5; DB 17; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 65;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 3 PPPLP 7
XX Db |||||
XX 2 PPPLP 6
XX RESULT 65
XX AAW38961
XX ID AAW38961 standard; peptide; 20 AA.
XX AC AAW38961;
XX XX

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XX AC AAW05473;
XX DT 24-FEB-1998 (first entry)
XX DE XX
XX DE XX
XX KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
XX KW cellular signalling element; cellular structural element; malignancy;
XX KW protein identification; functional domain; protein screening;
XX KW cellular signal transduction process; binding peptide.
XX OS Synthetic.
XX PN W09G31625-A1.
XX PD 10-OCT-1996.
XX PF 04-APR-1996; 96WO-US04454.
XX PR 03-APR-1996; 96US-0630915.
XX PR 07-APR-1995; 95US-0417872.
XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX PI Fowlkes DM, Hoffman N, Kay BK, McConnell SJ, Sparks AB;
XX DR WPI; 1996-465045/46.
XX PT Identifying polypeptide(s) having specific functional domain (esp.
XX PT SH3 domain) - comprises detecting selective binding to recognition
XX PT unit, regardless of sequence homology
XX PS Example; Fig 13; 174pp; English.
XX CC AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding
XX CC peptides. These sequences were used as parts of multivalent recognition
XX CC unit complexes used in the method of the invention. The method of the
XX CC invention is for identifying polypeptides containing functional domains
XX CC of interest (especially SH3 domains). It comprises contacting a
XX CC multivalent recognition unit (RU) complex with a number of peptides and
XX CC identifying polypeptides having a selective binding affinity for the RU
XX CC complex. The method is based on functional similarities and does not
XX CC rely on sequence similarities. Prior methods only gave limited success
XX CC for identifying proteins containing an SH3 domain due to the minimal
XX CC sequence homology among known SH3 proteins. Multivalent RU complexes are
XX CC particularly suited to screening for polypeptides containing functional
XX CC domains that are similar to, but not identical in sequence to, the
XX CC original target functional domain. The new method enables proteins
XX CC having a common function to be identified. Identification of novel SH3
XX CC proteins will be useful for a better understanding of cell growth,
XX CC malignancy, signal transduction processes, etc. New candidate drugs can
XX CC be identified, and their specificities (e.g. pharmacological activities)
XX CC can be assessed using the method of the invention.
XX SQ Sequence 19 AA;
XX Query Match 71.4%; Score 5; DB 17; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 65;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 3 PPPLP 7
XX Db |||||
XX 2 PPPLP 6
XX RESULT 65
XX AAW38961
XX ID AAW38961 standard; peptide; 20 AA.
XX AC AAW38961;
XX XX

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DT 27-MAR-1998 (first entry)
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:358.
 XX
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 OS Synthetic.
 XX
 XX WO9730074-A1.
 XX
 XX 21-AUG-1997.
 XX
 XX 14-FEB-1997; 97WO-US02298.
 XX
 XX 16-FEB-1996; 96US-0602999.
 XX
 XX (CYTO-) CYTOGEN CORP.
 XX (UNNC-) UNIV NORTH CAROLINA.
 PA
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 XX Sparks AB, Thorn JM;
 XX
 XX WPI; 1997-424972/39.
 XX
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 XX Claim 22; Page 91; 131pp; English.
 XX
 CC The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 XX Sequence 20 AA;
 SQ
 Query Match 71.4%; Score 5; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 12 PPPLP 16
 RESULT 66
 AAB39138
 ID AAB39138 standard; Protein; 20 AA.
 XX
 XX AAB39138;
 XX
 XX 02-FEB-2001 (first entry)
 XX
 XX Human secreted protein #46.
 DE
 XX Cytosolic; immunosuppressive; nootropic; neuroprotective; antiviral;

KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnerary; anticonvulsant; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 XX WO200058513-A1.
 XX
 XX 05-OCT-2000.
 XX
 XX 22-MAR-2000; 2000WO-US07506.
 XX
 XX 26-MAR-1999; 99US-0126505.
 XX 17-DEC-1999; 99US-0172412.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (ROSE/) ROSEN C A.
 XX
 XX Rosen CA, Ruben SM, Komatsoulis G;
 XX
 XX WPI; 2000-594649/56.
 XX N-Psdb; AAC73910.
 XX
 XX Forty-nine polynucleotide sequences, and their encoded secreted
 PT polypeptides, used in the treatment and diagnosis of cancers,
 PT autoimmune disorders, and skin disorders -
 XX
 XX Claim 11; Page 385; 413pp; English.
 XX
 CC Sequences AAB39093-B39141 represent the amino acid sequences of 49
 CC human secreted proteins encoded by the genes AAC73865-C73913. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and antagonists are useful in the
 CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, and ulcerative
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 XX
 XX Sequence 20 AA;
 SQ
 Query Match 71.4%; Score 5; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 13 PPPLP 17
 RESULT 67
 AAW65841
 ID AAW65841 standard; peptide; 5 AA.
 XX
 XX AAW65841;
 XX
 XX 19-OCT-1998 (first entry)
 XX
 XX Peptide #66 from pentapeptide combinatorial library #3.
 DE
 XX polyprolyl; cyclophilin; inhibitor; neurotrophic compound; ppi;
 KW piptidy-prolyl isomerase; rotamase; immunophilin protein; degeneration;
 KW neuronal damage; combinatorial library.
 XX
 OS Synthetic.

PA (YAMA) YAMANOUCHI UK LTD.
 XX Kellie S, Finan P;
 XX WPI; 2000-163495/15.
 XX Src homology 3 protein or fragment for preventing or treating
 PT proliferative disease, such as cancer or chronic inflammatory disease,
 PT comprises src homology 3 domain binding activity and nuclear
 PT localization activity -
 XX
 XX Claim 1; Page 34; 52pp; English.
 XX
 CC The invention provides a novel protein (np70) that has src homology 3
 CC (SH3) domain binding activity and nuclear localization activity. The
 CC proline-rich SH3 binding protein np70 or its fragments are useful for
 CC the prevention or treatment of proliferative disease, such as cancer and
 CC chronic inflammatory disease. Sequences AAY67443-464 represent peptide
 CC fragments of np70 that have SH3 domain binding activity.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 57.1%; Score 4; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPL 6
 DB 1 PPPL 4
 RESULT 70
 ID AAR53972 standard; peptide; 7 AA.
 XX
 AC AAR53972;
 XX
 DT 11-JAN-1995 (first entry)
 XX
 DE Neuropeptide (1).
 XX
 KW Neuropeptide; neurotransmitter; muscle; mussel; Mytilus edulis;
 KW constriction; anterior byssus retractor muscle; ABRM.
 XX
 OS Helix pomatia.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "pyroglutamic acid"
 FT Modified-site 7
 FT /note= "C-terminal is amidated"
 XX
 XX JP06107683-A.
 XX
 PD 19-APR-1994.
 XX
 PP 30-SEP-1992; 92JP-0300245.
 XX
 PR 30-SEP-1992; 92JP-0300245.
 XX
 XX (SUNR) SUNTORY LTD.
 XX
 XX WPI; 1994-163936/20.
 XX
 PT Neuro-peptide(s) isolated from Helix pomatia - useful in studying
 PT neuro-transmitting systems
 XX
 PS Claim 1; Page 2; 10pp; Japanese.
 XX
 CC The peptide inhibits strong constriction of the anterior byssus
 CC retractor muscle (ABRM) of Mytilus edulis induced by electrical
 CC irritation and is useful as biochemical reagent in the study of

CC the neurotransmitting system.
 XX Sequence 7 AA;
 SQ
 Query Match 57.1%; Score 4; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PPLP 7
 DB 2 PPLP 5
 RESULT 71
 AAW11128
 ID AAW11128 standard; peptide; 7 AA.
 XX
 AC AAW11128;
 XX
 DT 27-JUN-1997 (first entry)
 XX
 DE Src SH3 domain-binding peptide preferred core sequence.
 XX
 KW Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
 KW protein tyrosine kinase; signal transduction; RNA processing;
 KW trafficking; translation.
 XX
 OS Synthetic.
 XX
 XX WO9603649-A1.
 XX
 PD 08-FEB-1996.
 XX
 PF 24-JUL-1995; 95WO-US09382.
 XX
 PR 07-JUN-1995; 95US-0483555.
 PR 22-JUL-1994; 94US-0278865.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA.
 XX
 XX Der CU, Kay BK, Quilliam LA, Sparks AB, Thorn JM;
 XX WPI; 1996-117151/12.
 XX
 PT Peptide with binding affinity for Src homology region 3 (SH3)
 PT domains of proteins - useful for e.g. modulating signal transduction
 PT pathways at the cellular level, esp. protein tyrosine
 PT kinase-mediated
 XX
 PS Disclosure; Page 62; 116pp; English.
 XX
 CC AAW11128 represents a preferred core sequence of a set of peptides
 CC that bind to the Src SH3 domain. The SH3 binding peptides are useful in
 CC modulating signal transduction pathways at the cellular level
 CC (especially protein tyrosine kinase-mediated), modulating oncogenic
 CC protein activity, or providing compounds for the development of drugs
 CC with the ability to modulate broad classes, as well as specific classes,
 CC of proteins involved in signal transduction and also for regulating the
 CC processing, trafficking or translation of RNA. Conjugates of the peptides
 CC with detectable labels or imaging agents are useful for imaging cells,
 CC tissues and organs in which Src or Src-related proteins are expressed.
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 57.1%; Score 4; DB 17; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PPLP 7
 DB 4 PPLP 7

KW	Ab1; PLCgamma; p53bp2; Crk; Yes; Grb2.	
XX	Synthetic.	
OS	Unidentified.	
XX	W09730074-A1.	
XX	21-AUG-1997.	
XX	14-FEB-1997; 97WO-US02298.	
XX	16-FEB-1996; 96US-0602999.	
XX	(CYTO-) CYTOGEN CORP.	
PA	(UYN-) UNIV NORTH CAROLINA.	
XX		
PI	Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;	
PI	Sparks AB, Thorn JM;	
XX	WPI; 1997-424972/39.	
XX		
XX	Src homology region 3 binding peptide - used to activate Src	
PT	tyrosine kinase(s) and to stimulate immune response by increasing	
PT	production of certain lymphokine(s), e.g. interleukin-1	
XX	Disclosure; Page 8; 131pp; English.	
XX		
CC	The present sequence represents a Src homology region 3 (SH3) binding	
CC	peptide consensus motif. SH3 binding peptides are selected from: (a)	
CC	peptides which bind the SH3 domain of Cortactin; (b) peptides which bind	
CC	the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of	
CC	Ab1; (d) peptides which bind the SH3 domain of Src; (e) peptides which	
CC	bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain	
CC	of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;	
CC	(h) peptides which bind the SH3 domain of Yes; and (i) peptides which	
CC	bind the amino-terminal SH3 domain of Grb2. The purified binding	
CC	peptides can be used in the method to identify inhibitors of their	
CC	binding to their respective SH3 domains, which could be used to	
CC	modulate the pharmacological activity of proteins or polypeptide	
CC	containing the SH3 domain. The peptides can also be used to activate	
CC	Src or Src-related protein tyrosine kinases, to stimulate the immune	
CC	response by increasing the production of certain lymphokines, e.g.	
CC	tumour necrosis factor-alpha and interleukin-1, or to deliver a	
CC	conjugated molecule to certain cellular compartments containing Src or	
XX	Src related proteins.	
XX		
SQ	Sequence 7 AA;	
	Query Match 57.1%; Score 4; DB 18; Length 7;	
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;	
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	4 PPLP 7	
Db	4 PPLP 7	
RESULT 74		
AAW79781		
ID	AAW79781 standard; peptide; 7 AA.	
XX	AAW79781;	
XX		
DT	18-JAN-1999 (first entry)	
XX		
DE	Proline-rich peptide which binds with Src SH3 domain.	
XX		
KW	electrochemical; potentiometric; specific binding pair; assay;	
KW	competition; analysis; purification; proline-rich, Src SH3.	
XX	Unidentified.	
OS		
XX	WO9835232-A2.	
PN		

XX 13-AUG-1998.
 XX
 XX PF 06-FEB-1998; 98WO-US02440.
 XX
 PR 16-SEP-1997; 97US-0059049.
 PR 06-FEB-1997; 97US-0038919.
 XX
 XX (NOVA-) NOVALON PHARM CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 XX Fowlkes DM, Thorp HH;
 PI
 XX WPI; 1998-467163/40.
 XX
 XX Apparatus for electrochemically detecting binding - for use in
 PT biochemical analyses, drug development and protein purification
 PT assays
 XX
 PS Example 6; Page 55; 104pp; English.
 XX
 CC The invention relates to a method and apparatus for performing an
 CC electrochemical assay for detecting specific binding between members
 CC of a biological binding pair. The apparatus detects specific binding
 CC between a first member immobilised on an electrode and a second member
 CC which is biologically labelled, in the presence of an electrochemical
 CC mediator. The method may be used for performing binding and competitive
 CC binding assays. It may be used in performing high throughput screening
 CC assays for detecting inhibition of specific binding between the members
 CC of the binding pair for use in drug development, biochemical analyses
 CC and protein purification assays.
 CC The present sequence is an example of a peptide which is used in labelled
 CC form as a second binding member in the above assay. The peptide acts as a
 CC surrogate ligand for the first member. Specifically, the peptide
 CC is a proline-rich peptide which binds with Src SH3 domain.
 XX
 XX Sequence 7 AA;
 SQ

Query Match 57.1%; Score 4; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 ||||
 Db 4 PPLP 7

RESULT 75
 AAY04422
 ID AAY04422 standard; peptide; 7 AA.
 XX
 XX AC AAY04422;
 XX
 DT 25-JUN-1999 (first entry)
 XX
 XX Interleukin 6 binding peptide #17.
 DE
 XX Interleukin 6; IL-6; medicine; inhibition; interleukin 6 receptor;
 KW IL-6R; gp130 protein; stimulation; phase.
 KW
 XX Synthetic.
 OS
 XX JP11092498-A.
 XX
 XX PN
 XX PD 06-APR-1999.
 XX
 XX PF 22-SEP-1997; 97JP-0256604.
 XX
 XX PR 22-SEP-1997; 97JP-0256604.
 XX
 XX (TOYJ) TOSOH CORP.
 PA
 XX WP; 1999-283566/24.
 DR

XX Peptides specifically bind with IL-6 - useful for development of
 PT medicines with IL-6 inhibitory activity
 XX
 XX Example 3; Page 4; 5pp; Japanese.
 XX
 CC The present sequence represents a peptide which specifically binds and
 CC stimulates interleukin 6 (IL-6). The peptide was isolated with a phage
 CC display method. The peptide can be useful for development of medicines
 CC with IL-6 inhibitory activity and elucidation of binding form of IL-6,
 CC IL-6R and gp130 protein.
 XX
 XX Sequence 7 AA;
 SQ

Query Match 57.1%; Score 4; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 ||||
 Db 3 PPLP 6

Search completed: November 25, 2003, 18:15:37
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-641-801-1

Perfect score: 7

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Gapop 60.0 , Capext 60.0

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Maximum DB seq length: 20

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	5	71.4	9	9	US-09-835-232-11
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4	5	71.4	10	12	US-10-161-791-278
5	5	71.4	10	15	US-10-185-050-141
6	5	71.4	10	15	US-10-185-050-178
7	5	71.4	11	9	US-09-835-232-8
8	5	71.4	11	9	US-09-835-232-9
9	5	71.4	11	12	US-10-308-485-8
10	5	71.4	11	12	US-10-308-485-9
11	5	71.4	12	11	US-09-845-612B-9
12	5	71.4	12	12	US-10-161-791-251
13	5	71.4	12	12	US-10-161-791-266
14	5	71.4	12	12	US-10-161-791-267
15	5	71.4	13	11	US-09-945-917-13

Sequence 19, Appl	11	US-09-945-917-19	13	11	US-09-945-917-19
Sequence 21, Appl	13	US-09-945-917-21	13	11	US-09-945-917-21
Sequence 13, Appl	13	US-09-845-917A-13	13	12	US-09-845-917A-13
Sequence 19, Appl	13	US-09-845-917A-19	13	12	US-09-845-917A-19
Sequence 21, Appl	13	US-09-845-917A-21	13	12	US-09-845-917A-21
Sequence 11, Appl	13	US-10-067-668-11	13	15	US-10-067-668-11
Sequence 11, Appl	13	US-10-175-696-11	13	15	US-10-175-696-11
Sequence 186, Appl	14	US-09-879-957-186	14	9	US-09-879-957-186
Sequence 63, Appl	14	US-10-185-050-63	14	15	US-10-185-050-63
Sequence 3, Appl	14	US-10-148-936-3	14	15	US-10-148-936-3
Sequence 356, App	15	US-10-161-791-356	15	12	US-10-161-791-356
Sequence 385, App	15	US-10-161-791-385	15	12	US-10-161-791-385
Sequence 404, App	15	US-10-161-791-404	15	12	US-10-161-791-404
Sequence 414, App	15	US-10-161-791-414	15	12	US-10-161-791-414
Sequence 435, App	15	US-10-161-791-435	15	12	US-10-161-791-435
Sequence 441, App	15	US-10-161-791-441	15	12	US-10-161-791-441
Sequence 452, App	15	US-10-161-791-452	15	12	US-10-161-791-452
Sequence 197, App	16	US-10-161-791-197	16	12	US-10-161-791-197
Sequence 360, App	17	US-10-161-791-360	17	12	US-10-161-791-360
Sequence 374, App	17	US-10-161-791-374	17	12	US-10-161-791-374
Sequence 320, App	18	US-10-161-791-320	18	12	US-10-161-791-320
Sequence 409, App	18	US-10-161-791-409	18	12	US-10-161-791-409
Sequence 169, App	19	US-09-879-957-169	19	9	US-09-879-957-169
Sequence 358, App	20	US-10-161-791-358	20	12	US-10-161-791-358
Sequence 15, Appl	4	US-10-181-804A-15	4	12	US-10-181-804A-15
Sequence 3, Appl	4	US-10-192-985-3	4	15	US-10-192-985-3
Sequence 81, Appl	4	US-10-028-075B-81	4	15	US-10-028-075B-81
Sequence 81, Appl	4	US-10-029-206A-81	4	15	US-10-029-206A-81
Sequence 11, Appl	6	US-10-092-219-11	6	14	US-10-092-219-11
Sequence 14, Appl	6	US-10-028-075B-14	6	15	US-10-028-075B-14
Sequence 135, App	6	US-10-029-206A-135	6	15	US-10-029-206A-135
Sequence 4, Appl	7	US-09-019-679-4	7	9	US-09-019-679-4
Sequence 45, Appl	7	US-09-879-957-45	7	9	US-09-879-957-45
Sequence 17, Appl	7	US-09-731-242A-17	7	9	US-09-731-242A-17
Sequence 19, Appl	7	US-09-731-242A-19	7	9	US-09-731-242A-19
Sequence 20, Appl	7	US-09-731-242A-20	7	9	US-09-731-242A-20
Sequence 9, Appl	7	US-09-938-315-9	7	9	US-09-938-315-9
Sequence 9, Appl	7	US-10-161-791-9	7	12	US-10-161-791-9
Sequence 136, App	7	US-10-028-075B-136	7	15	US-10-028-075B-136
Sequence 137, App	7	US-10-028-075B-137	7	15	US-10-028-075B-137
Sequence 136, App	7	US-10-029-206A-136	7	15	US-10-029-206A-136
Sequence 137, App	7	US-10-029-206A-137	7	15	US-10-029-206A-137
Sequence 113, App	8	US-08-344-824-113	8	7	US-08-344-824-113
Sequence 329, App	8	US-08-344-824-329	8	7	US-08-344-824-329
Sequence 2749, Ap	8	US-10-224-999A-2749	8	12	US-10-224-999A-2749
Sequence 2750, Ap	8	US-10-224-999A-2750	8	12	US-10-224-999A-2750
Sequence 138, App	8	US-10-028-075B-138	8	15	US-10-028-075B-138
Sequence 138, App	8	US-10-029-206A-138	8	15	US-10-029-206A-138
Sequence 212, App	9	US-08-344-824-212	9	7	US-08-344-824-212
Sequence 8, Appl	9	US-09-938-315-8	9	9	US-09-938-315-8
Sequence 11, Appl	9	US-09-938-315-11	9	9	US-09-938-315-11
Sequence 34, Appl	9	US-09-945-917-34	9	11	US-09-945-917-34
Sequence 51, Appl	9	US-09-932-165-51	9	12	US-09-932-165-51
Sequence 66, Appl	9	US-09-932-165-66	9	12	US-09-932-165-66
Sequence 669, App	9	US-09-932-165-669	9	12	US-09-932-165-669
Sequence 1013, Ap	9	US-09-932-165-1013	9	12	US-09-932-165-1013
Sequence 1032, Ap	9	US-09-932-165-1032	9	12	US-09-932-165-1032
Sequence 1050, Ap	9	US-09-932-165-1050	9	12	US-09-932-165-1050
Sequence 1212, Ap	9	US-09-932-165-1212	9	12	US-09-932-165-1212
Sequence 1222, Ap	9	US-09-932-165-1222	9	12	US-09-932-165-1222
Sequence 34, Appl	9	US-09-845-917A-34	9	12	US-09-845-917A-34
Sequence 36, Appl	9	US-10-210-148-36	9	12	US-10-210-148-36
Sequence 2754, Ap	9	US-10-224-999A-2754	9	12	US-10-224-999A-2754
Sequence 2755, Ap	9	US-10-224-999A-2755	9	12	US-10-224-999A-2755
Sequence 2756, Ap	9	US-10-224-999A-2756	9	12	US-10-224-999A-2756
Sequence 8, Appl	9	US-10-161-791-8	9	12	US-10-161-791-8
Sequence 11, Appl	9	US-10-161-791-11	9	12	US-10-161-791-11
Sequence 152, App	10	US-09-932-165-152	10	12	US-09-932-165-152
Sequence 568, App	10	US-09-932-165-568	10	12	US-09-932-165-568
Sequence 1101, Ap	10	US-09-932-165-1101	10	12	US-09-932-165-1101
Sequence 1107, Ap	10	US-09-932-165-1107	10	12	US-09-932-165-1107
Sequence 1121, Ap	10	US-09-932-165-1121	10	12	US-09-932-165-1121

89 4 57.1 10 12 US-09-932-165-1309 Sequence 1309, Ap
90 4 57.1 10 12 US-09-932-165-1313 Sequence 1313, Ap
91 4 57.1 10 12 US-09-932-165-1343 Sequence 1343, Ap
92 4 57.1 10 12 US-09-932-165-1398 Sequence 1398, Ap
93 4 57.1 10 12 US-10-192-381-60 Sequence 60, Appl
94 4 57.1 10 12 US-10-192-381-61 Sequence 61, Appl
95 4 57.1 10 12 US-10-224-999A-2760 Sequence 2760, Ap
96 4 57.1 10 12 US-10-224-999A-2761 Sequence 2761, Ap
97 4 57.1 10 12 US-10-224-999A-2762 Sequence 2762, Ap
98 4 57.1 10 12 US-10-224-999A-2763 Sequence 2763, Ap
99 4 57.1 10 12 US-10-200-708-126 Sequence 126, App
100 4 57.1 10 12 US-10-200-708-232 Sequence 232, App

ALIGNMENTS

RESULT 1
US-10-281-652-1
; Sequence 1, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-1

Query Match 100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
 |||||
DB 1 MQPPPLP 7

RESULT 2
US-09-835-232-11
; Sequence 11, Application US/09835232
; Patent No. US20020098489A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leder, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/09/835,232
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT

; ORGANISM: Mus musculus
US-09-835-232-11
Query Match 71.4%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
DB 4 PPPLP 8

RESULT 3
US-10-308-485-11
; Sequence 11, Application US/10308485
; Publication No. US20030170683A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leder, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/10/308,485
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/835,232
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-308-485-11

Query Match 71.4%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
DB 4 PPPLP 8

RESULT 4
US-10-161-791-278
; Sequence 278, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 278:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-278

Query Match 71.4%; Score 5; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 2 PPPLP 6

RESULT 5
US-10-185-050-141
; Sequence 141, Application US/10185050
; Publication No. US20030077577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid

; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 141:
US-10-185-050-141
Query Match 71.4%; Score 5; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 PPPLP 7
Db 5 PPPLP 9
RESULT 6
US-10-185-050-178
; Sequence 178, Application US/10185050
; Publication No. US20030077577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 178:
US-10-185-050-178

Query Match 71.4%; Score 5; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 PPPLP 7
Db 5 PPPLP 9
RESULT 7

US-09-835-232-8
 ; Sequence 8, Application US/09835232
 ; Patent No. US20020098489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leder, Philip
 ; APPLICANT: Leder, Benjamin
 ; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: 00383/052002
 ; CURRENT APPLICATION NUMBER: US/09/835,232
 ; CURRENT FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: US 60/196,811
 ; PRIOR FILING DATE: 2000-04-13
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 1
 ; OTHER INFORMATION: Xaa=Met or Val
 US-09-835-232-8

Query Match 71.4%; Score 5; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 6 PPPLP 10

RESULT 8
 US-09-835-232-9
 ; Sequence 9, Application US/09835232
 ; Patent No. US20020098489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leder, Philip
 ; APPLICANT: Leder, Benjamin
 ; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: 00383/052002
 ; CURRENT APPLICATION NUMBER: US/09/835,232
 ; CURRENT FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: US 60/196,811
 ; PRIOR FILING DATE: 2000-04-13
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-835-232-9

Query Match 71.4%; Score 5; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 7 PPPLP 11

RESULT 9
 US-10-308-485-8
 ; Sequence 8, Application US/10308485
 ; Publication No. US20030170683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leder, Philip
 ; APPLICANT: Leder, Benjamin
 ; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: 00383/052002
 ; CURRENT APPLICATION NUMBER: US/10/308,485
 ; CURRENT FILING DATE: 2002-12-03
 ; PRIOR APPLICATION NUMBER: US/09/835,232
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: US 60/196,811
 ; PRIOR FILING DATE: 2000-04-13
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 1
 ; OTHER INFORMATION: Xaa=Met or Val
 US-10-308-485-8

Query Match 71.4%; Score 5; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 6 PPPLP 10

RESULT 10
 US-10-308-485-9
 ; Sequence 9, Application US/10308485
 ; Publication No. US20030170683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leder, Philip
 ; APPLICANT: Leder, Benjamin
 ; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: 00383/052002
 ; CURRENT APPLICATION NUMBER: US/10/308,485
 ; CURRENT FILING DATE: 2002-12-03
 ; PRIOR APPLICATION NUMBER: US/09/835,232
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: US 60/196,811
 ; PRIOR FILING DATE: 2000-04-13
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-308-485-9

Query Match 71.4%; Score 5; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 7 PPPLP 11

RESULT 11
 US-09-845-612B-9
 ; Sequence 9, Application US/09845612B
 ; Publication No. US20030083261A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YU, HONGTAO
 ; APPLICANT: TANG, ZHANYUN
 ; APPLICANT: LUO, XUELIAN
 ; APPLICANT: RIZO-REV, JOSE
 ; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MI
 ; TITLE OF INVENTION: POINT PROTEIN MAD2

FILE REFERENCE: UTSD:795
CURRENT APPLICATION NUMBER: US/09/845,612B
BEST FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)..(12)
OTHER INFORMATION: synthetic peptide
US-09-845-612B-9

Query Match 71.4%; Score 5; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPL 6
Db 6 QPPPL 10

RESULT 12

US-10-161-791-251
Sequence 251, Application US/10161791
Publication No. US20030186863A1

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999

FILING DATE: 16-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-202

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 251:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-10-161-791-251

Query Match 71.4%; Score 5; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 6 PPPLP 10

RESULT 13

US-10-161-791-266
Sequence 266, Application US/10161791
Publication No. US20030186863A1

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/602,999

FILING DATE: 16-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-202

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 266:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-10-161-791-266

Query Match 71.4%; Score 5; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPL 6
Db 4 QPPPL 8

RESULT 14

US-10-161-791-267
Sequence 267, Application US/10161791
Publication No. US20030186863A1

```
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 267:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-267

Query Match 71.4%; Score 5; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 6 PPPLP 10

RESULT 15
US-09-945-917-13
; Sequence 13, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-945-917-21

Query Match 71.4%; Score 5; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 6 PPPLP 10

RESULT 17
US-09-945-917-21
; Sequence 21, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-945-917-21

Query Match 71.4%; Score 5; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 5 PPPLP 9

RESULT 16
US-09-945-917-19
; Sequence 19, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-945-917-19

Query Match 71.4%; Score 5; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 5 PPPLP 9

RESULT 16
US-09-945-917-19
; Sequence 19, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-945-917-19

Query Match 71.4%; Score 5; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 5 PPPLP 9

RESULT 16
US-09-945-917-19
; Sequence 19, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-945-917-19

Query Match 71.4%; Score 5; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 5 PPPLP 9
```



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; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-21

Query Match          71.4%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 5 PPPLP 9

RESULT 21
US-10-067-668-11
; Sequence 11, Application US/10067668
; Publication No. US20030022334A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN
; TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-136001
; CURRENT APPLICATION NUMBER: US/10/067,668
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US-10-067-668-11

Query Match          71.4%; Score 5; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 22
US-10-175-696-11
; Sequence 11, Application US/10175696
; Publication No. US20030092658A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-193001
; CURRENT APPLICATION NUMBER: US/10/175,696
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/067,668
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720

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; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-13

Query Match          71.4%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 5 PPPLP 9

RESULT 19
US-09-845-917A-19
; Sequence 19, Application US/09845917A
; Publication No. US20030167538A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-19

Query Match          71.4%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 6 PPPLP 10

RESULT 20
US-09-845-917A-21
; Sequence 21, Application US/09845917A
; Publication No. US20030167538A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND

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; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19319
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,727
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-175-696-11

Query Match 71.4%; Score 5; DB 15; Length 13;
Best Local Similarity 100.0%; Pred.No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 23

US-09-879-957-186
; Sequence 186, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 186:
US-09-879-957-186

Query Match 71.4%; Score 5; DB 9; Length 14;
Best Local Similarity 100.0%; Pred.No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 5 PPPLP 9

RESULT 24

US-10-185-050-63
; Sequence 63, Application US/10185050
; Publication No. US20030077577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-185-050-63

Query Match 71.4%; Score 5; DB 15; Length 14;
Best Local Similarity 100.0%; Pred.No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      3 PPPLP 7
Db      5 PPPLP 9

RESULT 25
US-10-148-936-3
; Sequence 3, Application US/10148936
; Publication No. US20030113819A1
; GENERAL INFORMATION:
; APPLICANT: Horton, Jeffrey
; APPLICANT: Smith, John
; APPLICANT: Teear, Michelle
; APPLICANT: Kendall, Jonathan
; APPLICANT: Michael, Nigel
; TITLE OF INVENTION: Reagent and Method for Delivery of Molecules into Cells
; FILE REFERENCE: PA9963
; CURRENT APPLICATION NUMBER: US/10/148,936
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04593
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: GB 9928674.2
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligomer
US-10-148-936-3

Query Match      71.4%; Score 5; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPLP 7
Db      5 PPPLP 9

RESULT 26
US-10-161-791-356
; Sequence 356, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
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```
QY      3 PPPLP 7
Db      7 PPPLP 11

RESULT 27
US-10-161-791-385
; Sequence 385, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
```

```
QY      3 PPPLP 7
Db      7 PPPLP 11

RESULT 28
US-10-161-791-356
; Sequence 356, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
```

```
QY      3 PPPLP 7
Db      7 PPPLP 11

RESULT 29
US-10-161-791-356
; Sequence 356, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
```

```
QY      3 PPPLP 7
Db      7 PPPLP 11

RESULT 30
US-10-161-791-356
; Sequence 356, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
```

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QY      3 PPPLP 7
Db      7 PPPLP 11

RESULT 31
US-10-161-791-356
; Sequence 356, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
```

; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-385

Query Match 71.4%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 7 PPPLP 11

RESULT 28

US-10-161-791-404
; Sequence 404, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 404:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-404

Query Match 71.4%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 29

US-10-161-791-414
; Sequence 414, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-414

Query Match 71.4%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 30

US-10-161-791-435
; Sequence 435, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME

```
/
/ NUMBER OF SEQUENCES: 467
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/161,791
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/602,999
/ FILING DATE: 16-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mistrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 1101-202
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 435:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ US-10-161-791-435

Query Match 71.4%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 31
US-10-161-791-441
/ Sequence 441, Application US/10161791
/ Publication No. US2003018683A1
/ GENERAL INFORMATION:
/ APPLICANT: SPARKS, Andrew B.
/ APPLICANT: KAY, Brian K.
/ APPLICANT: THORN, Judith M.
/ APPLICANT: QUILLIAM, Lawrence A.
/ APPLICANT: DER, Channing J.
/ APPLICANT: FOWLKES, Dana M.
/ APPLICANT: RIDER, James E.
/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
/ ISOLATING AND USING SAME
/ NUMBER OF SEQUENCES: 467
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
```

```
/
/ APPLICATION NUMBER: US/10/161,791
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/602,999
/ FILING DATE: 16-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mistrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 1101-202
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 441:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ US-10-161-791-441

Query Match 71.4%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 5 PPPLP 9

RESULT 32
US-10-161-791-452
/ Sequence 452, Application US/10161791
/ Publication No. US2003018683A1
/ GENERAL INFORMATION:
/ APPLICANT: SPARKS, Andrew B.
/ APPLICANT: KAY, Brian K.
/ APPLICANT: THORN, Judith M.
/ APPLICANT: QUILLIAM, Lawrence A.
/ APPLICANT: DER, Channing J.
/ APPLICANT: FOWLKES, Dana M.
/ APPLICANT: RIDER, James E.
/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
/ ISOLATING AND USING SAME
/ NUMBER OF SEQUENCES: 467
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/161,791
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/602,999
/ FILING DATE: 16-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mistrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 1101-202
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
```

INFORMATION FOR SEQ ID NO: 452:

SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-10-161-791-452

Query Match 71.4%; Score 5; DB 12; Length 15;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 |||||

Db 7 PPPLP 11

RESULT 33

US-10-161-791-197
 ; Sequence 197, Application US/10161791
 ; Publication No. US20030186863A1

GENERAL INFORMATION:
 APPLICANT: SPARKS, Andrew B.
 APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.
 APPLICANT: QUILLIAM, Lawrence A.
 APPLICANT: DER, Channing J.

APPLICANT: FOWLKES, Dana M.
 APPLICANT: RIDER, James E.

TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 TITLE OF INVENTION: ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 467
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York

STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/161,791

FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/602,999

FILING DATE: 16-FEB-1996
 ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie
 REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-202
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 197:

SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid

TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-10-161-791-197

Query Match 71.4%; Score 5; DB 12; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 |||||

Db 9 PPPLP 13

RESULT 34

US-10-161-791-360

; Sequence 360, Application US/10161791
 ; Publication No. US20030186863A1

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
 APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.
 APPLICANT: QUILLIAM, Lawrence A.

APPLICANT: DER, Channing J.
 APPLICANT: FOWLKES, Dana M.

APPLICANT: RIDER, James E.
 TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

TITLE OF INVENTION: ISOLATING AND USING SAME
 NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York

STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/161,791

FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/602,999

FILING DATE: 16-FEB-1996
 ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie
 REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-202
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 360:

SEQUENCE CHARACTERISTICS:
 LENGTH: 17 amino acids
 TYPE: amino acid

TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-10-161-791-360

Query Match 71.4%; Score 5; DB 12; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 |||||

Db 9 PPPLP 13

RESULT 35

US-10-161-791-374

; Sequence 374, Application US/10161791
 ; Publication No. US20030186863A1

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
 APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.
 APPLICANT: QUILLIAM, Lawrence A.

APPLICANT: DER, Channing J.
 APPLICANT: FOWLKES, Dana M.

```

; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 374:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-374

Query Match 71.4% Score 5; DB 12: Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPLP 7
Db 9 PPLP 13

RESULT 36
US-10-161-791-320
; Sequence 320, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 374:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-374
```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 320:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-320

Query Match 71.4% Score 5; DB 12: Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPLP 7
Db 10 PPLP 14

RESULT 37
US-10-161-791-409
; Sequence 409, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 409:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-409

Query Match          71.4%; Score 5; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPLP 7
DB      11 PPPLP 15

RESULT 38
US-09-879-957-169
; Sequence 169, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-09-879-957-169

Query Match          71.4%; Score 5; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
```

```
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPLP 7
DB      2 PPPLP 6

RESULT 39
US-10-161-791-358
; Sequence 358, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 358:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-358

Query Match          71.4%; Score 5; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPLP 7
DB      12 PPPLP 16

RESULT 40
US-10-181-804A-15
; Sequence 15, Application US/10181804A
; Publication No. US20030162220A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, HARUO
; APPLICANT: KIM, EUI HO
```



```
; TITLE OF INVENTION: WT1 INTERACTING PROTEIN WTIP
; FILE REFERENCE: 053466/0335
; CURRENT APPLICATION NUMBER: US/10/181,804A
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: PCT/JP01/00461
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: JP 2000-14949
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: motif
US-10-181-804A-15

Query Match          57.1%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 41
US-10-192-985-3
; Sequence 3, Application US/10192985
; Publication No. US20030084483A1
; GENERAL INFORMATION:
; APPLICANT: Simpson, Gordon G
; APPLICANT: Dean, Caroline
; APPLICANT: Dijkwel, Paul
; TITLE OF INVENTION: Methods and Means for Modification of Plant
; TITLE OF INVENTION: Characteristics
; FILE REFERENCE: 0380-P02932US0
; CURRENT APPLICATION NUMBER: US/10/192,985
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: GB 0117054.7
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif
US-10-192-985-3

Query Match          57.1%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 42
US-10-028-075B-81
; Sequence 81, Application US/10028075B
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
```

```
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pdb/1RLQ/1RLQ-R; swissnew/P01229/LSHB HUMAN
US-10-028-075B-81

Query Match          57.1%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 43
US-10-029-206A-81
; Sequence 81, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pdb/1RLQ/1RLQ-R; swissnew/P01229/LSHB HUMAN
US-10-029-206A-81

Query Match          57.1%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 44
US-10-092-219-11
; Sequence 11, Application US/10092219
; Publication No. US20020115114A1
; GENERAL INFORMATION:
; APPLICANT: Domin, Jan
; TITLE OF INVENTION: No. US20020115114A1 Lipid Kinase
; FILE REFERENCE: 1064HG/50947
; CURRENT APPLICATION NUMBER: US/10/092,219
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/355,160
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-219-11

Query Match
  57.1%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 45
US-10-029-115-14
; Sequence 14, Application US/10029115
; Publication No. US20030077597A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Fu, Alan C
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: No. US20030077597A1 Germinal Center Kinase Cell Cycle Proteins,
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: A-70229/RXS/DHR
; CURRENT APPLICATION NUMBER: US/10/029,115
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-115-14

Query Match
  57.1%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 46
US-10-028-075B-135
; Sequence 135, Application US/10028075B
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-028-075B-135

Query Match
  57.1%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 47
US-10-029-206A-135
; Sequence 135, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-029-206A-135

Query Match
  57.1%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 4 PPLP 7
Db 3 PPLP 6

RESULT 48
US-09-019-679-4
; Sequence 4, Application US/09019679
; Patent No. US20020012943A1
; GENERAL INFORMATION:
; APPLICANT: Fowkes, Dana M
; APPLICANT: Thorp, H. Holden
; TITLE OF INVENTION: Electrochemical Probes for Detection of Molecular
; TITLE OF INVENTION: Interactions and Drug Discovery
; FILE REFERENCE: 97082-B
; CURRENT APPLICATION NUMBER: US/09/019,679
; CURRENT FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: 60/036,919
; EARLIER FILING DATE: 1997-02-06
; EARLIER APPLICATION NUMBER: 60/059,049
; EARLIER FILING DATE: 1997-09-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Src SH3
; OTHER INFORMATION: binding motif
US-09-019-679-4

Query Match
  57.1%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 4 PPLP 7
Db 4 PPLP 7
```

```

RESULT 49
US-09-879-957-45
; Sequence 45, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-879-957-45

Query Match 57.1%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 4 PPLP 7

RESULT 50
US-09-731-242A-17
; Sequence 17, Application US/09731242A
; Patent No. US20020058253A1
; GENERAL INFORMATION:
; APPLICANT: KRANZ, DAVID
; APPLICANT: WITTRUP, K. DANE
; APPLICANT: HOLLER, PHILLIP
; TITLE OF INVENTION: HIGH AFFINITY TCR PROTEINS AND METHODS
; FILE REFERENCE: 89-99
; CURRENT APPLICATION NUMBER: US/09/731,242A
; CURRENT FILING DATE: 2000-12-06

Query Match 57.1%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 4 PPLP 7

RESULT 51
US-09-731-242A-19
; Sequence 19, Application US/09731242A
; Patent No. US20020058253A1
; GENERAL INFORMATION:
; APPLICANT: KRANZ, DAVID
; APPLICANT: WITTRUP, K. DANE
; APPLICANT: HOLLER, PHILLIP
; TITLE OF INVENTION: HIGH AFFINITY TCR PROTEINS AND METHODS
; FILE REFERENCE: 89-99
; CURRENT APPLICATION NUMBER: US/09/731,242A
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/169,179
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/009,388
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..(..)
; OTHER INFORMATION: CDR3alpha sequence
US-09-731-242A-19

Query Match 57.1%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 6
Db 3 PPPL 6

RESULT 52
US-09-731-242A-20
; Sequence 20, Application US/09731242A
; Patent No. US20020058253A1
; GENERAL INFORMATION:
; APPLICANT: KRANZ, DAVID
; APPLICANT: WITTRUP, K. DANE
; APPLICANT: HOLLER, PHILLIP
; TITLE OF INVENTION: HIGH AFFINITY TCR PROTEINS AND METHODS
; FILE REFERENCE: 89-99
; CURRENT APPLICATION NUMBER: US/09/731,242A
; CURRENT FILING DATE: 2000-12-06

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Query Match          57.1%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 P L P L 7
Db      4 P L P L 7

RESULT 54
US-10-161-791-9
; Sequence 9, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNTE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-9

Query Match          57.1%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 P L P L 7
Db      4 P L P L 7

RESULT 55
US-10-028-075B-136
; Sequence 136, Application US/10028075B
; Publication No. US2003011373A1
; GENERAL INFORMATION:

```

```
/ APPLICANT: Khan, Nisar A.
/ APPLICANT: Benner, Robert
/ TITLE OF INVENTION: Gene regulator
/ FILE REFERENCE: 2183-5223US
/ CURRENT APPLICATION NUMBER: US/10/028,075B
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: EP 01203748.7
/ PRIOR FILING DATE: 2001-10-04
/ NUMBER OF SEQ ID NOS: 175
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 136
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-028-075B-136

Query Match          57.1%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 3 PPLP 6

RESULT 56
US-10-028-075B-137
/ Sequence 137, Application US/10028075B
/ Publication No. US20030113733A1
/ GENERAL INFORMATION:
/ APPLICANT: Khan, Nisar A.
/ APPLICANT: Benner, Robert
/ TITLE OF INVENTION: Gene regulator
/ FILE REFERENCE: 2183-5223US
/ CURRENT APPLICATION NUMBER: US/10/028,075B
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: EP 01203748.7
/ PRIOR FILING DATE: 2001-10-04
/ NUMBER OF SEQ ID NOS: 175
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 137
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-028-075B-137

Query Match          57.1%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 4 PPLP 7

RESULT 57
US-10-029-206A-136
/ Sequence 136, Application US/10029206A
/ Publication No. US20030119720A1
/ GENERAL INFORMATION:
/ APPLICANT: Khan, Nisar A.
/ APPLICANT: Benner, Robert
/ TITLE OF INVENTION: Oligopeptide treatment of anthrax
/ FILE REFERENCE: 2183-5222US
/ CURRENT APPLICATION NUMBER: US/10/029,206A
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: US/10/029,206A
/ CURRENT FILING DATE: 2001-12-21
/ NUMBER OF SEQ ID NOS: 175
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 137
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-029-206A-136

Query Match          57.1%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 4 PPLP 7

RESULT 58
US-10-029-206A-137
/ Sequence 137, Application US/10029206A
/ Publication No. US20030119720A1
/ GENERAL INFORMATION:
/ APPLICANT: Khan, Nisar A.
/ APPLICANT: Benner, Robert
/ TITLE OF INVENTION: Oligopeptide treatment of anthrax
/ FILE REFERENCE: 2183-5222US
/ CURRENT APPLICATION NUMBER: US/10/029,206A
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 09/821,380
/ PRIOR FILING DATE: 2001-03-29
/ NUMBER OF SEQ ID NOS: 175
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 137
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-029-206A-137

Query Match          57.1%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 4 PPLP 7

RESULT 59
US-08-344-824-113
/ Sequence 113, Application US/08344824
/ Publication No. US20030152580A1
/ GENERAL INFORMATION:
/ APPLICANT: SETTE, Alessandro
/ APPLICANT: SIDNEY, John
/ TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
/ NUMBER OF SEQUENCES: 399
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Kourie and Crew
/ STREET: One Market Plaza, Steuart Street Tower, 20th
/ STREET: Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94105
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-113

Query Match          57.1%; Score 4; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 1 PPLP 4

RESULT 60
US-08-344-824-329
; Sequence 329, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 329:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-329

Query Match          57.1%; Score 4; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 2 PPLP 5

RESULT 61
US-10-224-999A-2749
; Sequence 2749, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2749
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Hepatitis E virus
US-10-224-999A-2749

Query Match          57.1%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 5 PPLP 8

RESULT 62
US-10-224-999A-2750
; Sequence 2750, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2750
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Hepatitis E virus
US-10-224-999A-2750

Query Match          57.1%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 5 PPLP 8
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
| | | |
Db 4 PPLP 7

RESULT 63
US-10-028-075B-138
; Sequence 138, Application US/10028075B
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 138
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-028-075B-138

Query Match 57.1%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
| | | |
Db 4 PPLP 7

RESULT 64
US-10-029-206A-138
; Sequence 138, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 138
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-029-206A-138

Query Match 57.1%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
| | | |
Db 4 PPLP 7

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-344-824-212
; Sequence 212, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-212

Query Match 57.1%; Score 4; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
| | | |
Db 2 PPLP 5

RESULT 66
US-09-938-315-8
; Sequence 8, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; SPARKS, ANDREW B.
; THORN, JUDITH M.
; QUILLIAM, LAWRENCE A.
; DER, CHANNING J.
; TITLE OF INVENTION: Src SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia

```

; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "hydrophobic residue"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-938-315-8

Query Match          57.1%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 4 PPLP 7

RESULT 68
US-09-945-917-34
; Sequence 34, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-34

Query Match          57.1%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 3 PPLP 6

RESULT 69
US-09-932-165-51
; Sequence 51, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83p2H3 and Cat-P2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00

```


; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-51

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 6
| | | |
Db 4 PPPL 7

RESULT 70
US-09-932-165-66
; Sequence 66, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-66

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPP 5
| | | |
Db 3 QPPP 6

RESULT 71
US-09-932-165-669
; Sequence 669, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS

; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 669
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-669

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPP 5
| | | |
Db 3 QPPP 6

RESULT 72
US-09-932-165-1013
; Sequence 1013, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1013
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1013

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPP 5
| | | |
Db 5 QPPP 8

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RESULT 73
US-09-932-165-1032
; Sequence 1032, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2e11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1032
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1032

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PPPL 6
Db      1 PPPL 4

RESULT 74
US-09-932-165-1050
; Sequence 1050, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2e11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1050
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1050

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PPPL 6
Db      1 PPPL 4
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Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PPPL 6
Db      6 PPPL 9

RESULT 75
US-09-932-165-1212
; Sequence 1212, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2e11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1212
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1212

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QPPP 5
Db      1 QPPP 4

Search completed: November 25, 2003, 20:25:24
Job time : 14.9255 secs
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GenCore version 5.1.6
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 OM protein - protein search, using sw model
 Run on: November 25, 2003, 19:27:29 : Search time 7.63298 Seconds
 (without alignments)
 38.802 Million cell updates/sec

Title: US-09-641-801-1

Perfect score: 7

Sequence: 1 MQPPPLP 7

Scoring table: OLIGO

Gapex 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

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Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	4	US-09-641-801-1
2	5	71.4	7	1	US-08-230-047-40
3	5	71.4	7	5	PCT-US94-01840-11
4	5	71.4	8	1	US-09-641-640-11
5	5	71.4	8	2	US-08-612-857-8
6	5	71.4	10	1	US-08-230-047-12
7	5	71.4	10	1	US-08-230-047-14
8	5	71.4	10	1	US-08-212-190A-8
9	5	71.4	10	2	US-08-900-321-8
10	5	71.4	10	3	US-08-348-518C-26
11	5	71.4	10	3	US-08-476-509B-26
12	5	71.4	10	3	US-08-899-595-8
13	5	71.4	10	3	US-08-602-999A-278
14	5	71.4	10	4	US-09-500-124-278
15	5	71.4	10	5	PCT-US95-03610-8
16	5	71.4	11	1	US-08-336-343A-25
17	5	71.4	11	3	US-08-652-877-22
18	5	71.4	11	3	US-08-652-877-32
19	5	71.4	11	3	US-08-476-515A-22
20	5	71.4	11	3	US-08-476-515A-32
21	5	71.4	12	1	US-08-230-047-17
22	5	71.4	12	3	US-08-602-999A-251
23	5	71.4	12	3	US-08-602-999A-266
24	5	71.4	12	3	US-08-602-999A-267
25	5	71.4	12	4	US-09-500-124-251
26	5	71.4	12	4	US-09-500-124-266
27	5	71.4	12	4	US-09-500-124-267
28	5	71.4	14	3	US-08-185-432-12
29	5	71.4	14	3	US-08-630-916A-63
30	5	71.4	14	4	US-08-630-915A-186
31	5	71.4	15	1	US-08-185-432-10
32	5	71.4	15	2	US-08-769-745-31
33	5	71.4	15	3	US-08-602-999A-356
34	5	71.4	15	3	US-08-602-999A-385
35	5	71.4	15	3	US-08-602-999A-404
36	5	71.4	15	3	US-08-602-999A-414
37	5	71.4	15	3	US-08-602-999A-435
38	5	71.4	15	3	US-08-602-999A-441
39	5	71.4	15	3	US-08-602-999A-452
40	5	71.4	15	4	US-09-500-124-385
41	5	71.4	15	4	US-09-500-124-404
42	5	71.4	15	4	US-09-500-124-414
43	5	71.4	15	4	US-09-500-124-435
44	5	71.4	15	4	US-09-500-124-441
45	5	71.4	15	4	US-09-500-124-452
46	5	71.4	16	1	US-08-185-432-9
47	5	71.4	16	1	US-08-185-432-14
48	5	71.4	16	3	US-08-602-999A-197
49	5	71.4	16	4	US-09-500-124-197
50	5	71.4	17	1	US-08-320-047-10
51	5	71.4	17	3	US-08-602-999A-360
52	5	71.4	17	3	US-08-602-999A-374
53	5	71.4	17	4	US-09-500-124-360
54	5	71.4	17	4	US-09-500-124-374
55	5	71.4	17	4	US-08-602-999A-320
56	5	71.4	18	3	US-08-602-999A-409
57	5	71.4	18	4	US-09-500-124-320
58	5	71.4	18	4	US-09-500-124-409
59	5	71.4	19	4	US-08-630-915A-169
60	5	71.4	20	3	US-08-602-999A-358
61	5	71.4	20	4	US-09-006-428A-25
62	5	71.4	20	4	US-09-195-868-19
63	4	57.1	6	3	US-08-664-962B-18
64	4	57.1	6	3	US-09-311-743-18
65	4	57.1	6	3	US-08-743-168B-38
66	4	57.1	6	4	US-09-355-160D-11
67	4	57.1	6	4	US-09-119-507B-117
68	4	57.1	6	4	US-09-645-791-36
69	4	57.1	6	4	US-08-081-539-113
70	4	57.1	6	4	US-08-466-647-113
71	4	57.1	6	4	US-08-602-999A-9
72	4	57.1	6	4	US-08-630-915A-45
73	4	57.1	7	1	US-08-185-883-6
74	4	57.1	7	3	US-09-203-921-6
75	4	57.1	7	3	US-08-424-414C-8
76	4	57.1	7	4	US-08-615-181-97
77	4	57.1	7	4	US-08-586-234-77
78	4	57.1	7	4	US-08-602-999A-8
79	4	57.1	8	3	US-08-652-877-21
80	4	57.1	8	3	US-08-185-883-8
81	4	57.1	8	3	US-08-185-883-11
82	4	57.1	8	3	US-08-476-515A-21
83	4	57.1	9	3	US-09-203-921-8
84	4	57.1	9	3	US-09-203-921-10
85	4	57.1	9	3	US-09-424-414C-13
86	4	57.1	9	3	US-08-278-865-8
87	4	57.1	9	3	US-08-278-865-11
88	4	57.1	9	3	US-09-500-124-8
89	4	57.1	9	3	US-09-023-905A-19
90	4	57.1	9	3	US-09-023-905A-20
91	4	57.1	9	3	US-09-023-905A-38
92	4	57.1	9	3	Sequence 1, Appl
93	4	57.1	9	3	Sequence 40, Appl
94	4	57.1	9	3	Sequence 11, Appl
95	4	57.1	9	3	Sequence 8, Appl
96	4	57.1	9	3	Sequence 13, Appl
97	4	57.1	9	3	Sequence 8, Appl
98	4	57.1	9	3	Sequence 11, Appl
99	4	57.1	9	3	Sequence 8, Appl
100	4	57.1	9	3	Sequence 21, Appl

Sequence 12, Appl
 Sequence 63, Appl
 Sequence 186, Appl
 Sequence 10, Appl
 Sequence 31, Appl
 Sequence 356, Appl
 Sequence 385, Appl
 Sequence 404, Appl
 Sequence 414, Appl
 Sequence 435, Appl
 Sequence 441, Appl
 Sequence 452, Appl
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 Sequence 385, Appl
 Sequence 404, Appl
 Sequence 414, Appl
 Sequence 435, Appl
 Sequence 441, Appl
 Sequence 452, Appl
 Sequence 9, Appl
 Sequence 14, Appl
 Sequence 197, Appl
 Sequence 10, Appl
 Sequence 360, Appl
 Sequence 374, Appl
 Sequence 360, Appl
 Sequence 374, Appl
 Sequence 320, Appl
 Sequence 320, Appl
 Sequence 409, Appl
 Sequence 409, Appl
 Sequence 169, Appl
 Sequence 358, Appl
 Sequence 358, Appl
 Sequence 25, Appl
 Sequence 19, Appl
 Sequence 18, Appl
 Sequence 18, Appl
 Sequence 38, Appl
 Sequence 11, Appl
 Sequence 117, Appl
 Sequence 36, Appl
 Sequence 36, Appl
 Sequence 113, Appl
 Sequence 113, Appl
 Sequence 9, Appl
 Sequence 9, Appl
 Sequence 45, Appl
 Sequence 6, Appl
 Sequence 6, Appl
 Sequence 8, Appl
 Sequence 77, Appl
 Sequence 77, Appl
 Sequence 8, Appl
 Sequence 11, Appl
 Sequence 21, Appl
 Sequence 8, Appl
 Sequence 21, Appl
 Sequence 11, Appl
 Sequence 10, Appl
 Sequence 10, Appl
 Sequence 13, Appl
 Sequence 8, Appl
 Sequence 11, Appl
 Sequence 8, Appl
 Sequence 11, Appl
 Sequence 19, Appl
 Sequence 20, Appl
 Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-09-641-803-1
; Sequence 1, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-1

Query Match 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
Db 1 MQPPPLP 7

RESULT 2
US-08-230-047-40
; Sequence 40, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashchenko, Yuri D.
; APPLICANT: Jays, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817

; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-230-047-40

Query Match 71.4%; Score 5; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 1 PPPLP 5

RESULT 3
PCT-US94-01840-11
; Sequence 11, Application PC/TUS9401840
; GENERAL INFORMATION:
; APPLICANT: Christopher E. Rudd
; APPLICANT: Prasad Kanteti
; APPLICANT: Lewis Cantley
; TITLE OF INVENTION: CD4 MEDIATED MODULATION OF
; TITLE OF INVENTION: LIPID KINASES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/023,915
; FILING DATE: February 26, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/063001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; PCT-US94-01840-11

Query Match 71.4%; Score 5; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 1 PPPLP 5

RESULT 4

US-09-641-640-8
; Sequence 8, Application US/09641640
; Patent No. RE37952
; GENERAL INFORMATION:
; APPLICANT: SCHWEIGHOFFER, Fabien
; TOCQUE, Bruno
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 15-Aug-2000
; APPLICATION NUMBER: US/09/641.640
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,857
; FILING DATE: <Unknown>
; APPLICATION NUMBER: WO PCT/FR94/00542
; FILING DATE: 09-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST93044-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..8
; OTHER INFORMATION: /note= "3BP1 peptide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-641-640-8

Query Match 71.4%; Score 5; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 1 PPPLP 5

RESULT 5
US-08-612-857-8
; Sequence 8, Application US/08612857
; Patent No. 5831048
; GENERAL INFORMATION:
; APPLICANT: SCHWEIGHOFFER, Fabien
; TOCQUE, Bruno
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047

STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,857
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93-10971
FILING DATE: 15-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00542
FILING DATE: 09-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: 38,619
REFERENCE/DOCKET NUMBER: ST93044-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..8
OTHER INFORMATION: /note= "3BP1 peptide"
US-08-612-857-8

Query Match 71.4%; Score 5; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 1 PPPLP 5

RESULT 6
US-08-230-047-12
; Sequence 12, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashenko, Yuri D.
; APPLICANT: Jaye, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047

;/ FILING DATE: 19-APR-1994
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Goodman, Rosanne
;/ REGISTRATION NUMBER: 32,534
;/ REFERENCE/DOCKET NUMBER: A1465-US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (610) 454-3817
;/ TELEFAX: (610) 454-3808
;/ INFORMATION FOR SEQ ID NO: 12:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 10 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
US-08-230-047-12

Query Match 71.4%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 7
US-08-230-047-14
;/ Sequence 14, Application US/08230047
;/ Patent No. 5541109
;/ GENERAL INFORMATION:
;/ APPLICANT: Searfoss III, George H.
;/ APPLICANT: Ivashchenko, Yuri D.
;/ APPLICANT: Jaye, Michael C.
;/ TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
;/ TITLE OF INVENTION: PROTEIN
;/ NUMBER OF SEQUENCES: 40
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Rhone-Poulenc Rorer Inc.
;/ STREET: 500 Arcoia Road, 3C43
;/ CITY: Collegeville
;/ STATE: PA
;/ COUNTRY: USA
;/ ZIP: 19426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.0 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/230,047
FILING DATE: 19-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: A1465-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3817
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

Query Match 71.4%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7

Db
|||||
6 PPPLP 10

RESULT 8
US-08-212-190A-8
;/ Sequence 8, Application US/08212190A
;/ Patent No. 5652223
;/ GENERAL INFORMATION:
;/ APPLICANT: KOHN, Elise C.
;/ APPLICANT: LIOTTA, Lance A.
;/ APPLICANT: KIM, Young Sook
;/ TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
;/ TITLE OF INVENTION: USES THEREOF
;/ NUMBER OF SEQUENCES: 10
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew
;/ STREET: Steuart Street Tower, One Market Plaza
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: US
;/ ZIP: 94105-1493

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,190A
FILING DATE: 14-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15280-204US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-212-190A-8

Query Match 71.4%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 9
US-08-900-321-8
;/ Sequence 8, Application US/08900321
;/ Patent No. 5981712
;/ GENERAL INFORMATION:
;/ APPLICANT: Kohn, Elise C.
;/ APPLICANT: Liotta, Lance A.
;/ APPLICANT: Kim, Young S.
;/ TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
;/ TITLE OF INVENTION: Uses Thereof
;/ NUMBER OF SEQUENCES: 10
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, Eighth Floor
;/ CITY: San Francisco
;/ STATE: California

; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; BEST Local Similarity 71.4%; Score 5; DB 2; Length 10;
; Mismatches 0; Conservative 0; Indels 0; Gaps 0;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,321
; FILING DATE: 25-JUL-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-204100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-900-321-8

Query Match 71.4%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 10
US-08-348-518C-26
; Sequence 26, Application US/08348518C
; Patent No. 6022740
; GENERAL INFORMATION:
; APPLICANT: SUDOL, MARIUS
; APPLICANT: PEER, BORK
; APPLICANT: HENRY, CHEN
; TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A
; TITLE OF INVENTION: SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
; TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,518C
; FILING DATE: 01-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-101
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-348-518C-26

Query Match 71.4%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPL 6
Db 4 QPPPL 8

RESULT 11
US-08-476-509B-26
; Sequence 26, Application US/08476509B
; Patent No. 6034212
; GENERAL INFORMATION:
; APPLICANT: SUDOL, MARIUS
; APPLICANT: PEER, BORK
; APPLICANT: HENRY, CHEN
; TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A
; TITLE OF INVENTION: SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
; TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,509B
; FILING DATE: 01-DEC-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-101 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-476-509B-26

Query Match 71.4%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPL 6
 Db 4 QPPL 8

RESULT 12

US-08-899-595-8
 ; Sequence 8, Application US/08899595
 ; Patent No. 6111072
 ; GENERAL INFORMATION:
 ; APPLICANT: Narumiya, Shuh
 ; APPLICANT: Takahashi, No. 6111072uaki
 ; TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
 ; TITLE OF INVENTION: ENCODING SAME
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/899,595
 ; FILING DATE: 24-JUL-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 8-242701
 ; FILING DATE: 26-AUG-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 9-90170
 ; FILING DATE: 25-MAR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stephen A. Bent
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 049441/0112
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 10
 ; OTHER INFORMATION: /product= "G/S/A/V"
 ; US-08-899-595-8

Query Match 71.4%; Score 5; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 7
 Db 4 PPPL 8

RESULT 13

US-08-602-999A-278
 ; Sequence 278, Application US/08602999A
 ; Patent No. 6184205
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; TITLE OF INVENTION: ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,999A
 ; FILING DATE: 16-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 278:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-602-999A-278

Query Match 71.4%; Score 5; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 7
 Db 2 PPPL 6

RESULT 14

US-09-500-124-278
 ; Sequence 278, Application US/09500124
 ; Patent No. 6432920
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; TITLE OF INVENTION: ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mirock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 278:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-09-500-124-278

Query Match 71.4%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
|
|
|
|
|
Db 2 PPPLP 6

RESULT 15
PCT-US95-03610-8
;; Sequence 8, Application PC/TUS9503610
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
;; NUMBER OF SEQUENCES: 10
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/03610
;; FILING DATE: 14-MAR-1995
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/212,190
;; FILING DATE: 14-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weber, Kenneth A.
;; REGISTRATION NUMBER: 31,677
;; REFERENCE/DOCKET NUMBER: 15280-204000PC
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
PCT-US95-03610-8

Query Match 71.4%; Score 5; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
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|
|
Db 5 PPPLP 9

RESULT 16
US-08-336-343A-25
;; Sequence 25, Application US/08336343A
;; Patent No. 5677144
;; GENERAL INFORMATION:
;; APPLICANT: Ullrich, Axel
;; TITLE OF INVENTION: CKK-2, A No. 5677144el Receptor Tyrosine Kinase
;; NUMBER OF SEQUENCES: 43
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/336,343A
;; FILING DATE: 08-NOV-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7693-065
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-336-343A-25

Query Match 71.4%; Score 5; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
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|
|
Db 4 PPPLP 8

RESULT 17
US-08-652-877-22
;; Sequence 22, Application US/08652877
;; Patent No. 6187548
;; GENERAL INFORMATION:
;; APPLICANT: Akerstrom, Goran
;; APPLICANT: Juhlin, Claes
;; APPLICANT: Rask, Lars
;; APPLICANT: Crumley, Gregg R.
;; APPLICANT: Morse, Clarence C.
;; APPLICANT: Murray, Edward M.
;; APPLICANT: Hjalms, Goran
;; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
;; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 106
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Rd., 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426-0107
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.5.1
 ; SOFTWARE: Word 6.0 (Patentin)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/652,877
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/15203
 ; FILING DATE: 22-NOV-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/344,836
 ; FILING DATE: 23-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/487,314
 ; FILING DATE: 07-JUNE-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Savitzky, Martin
 ; REGISTRATION NUMBER: 29,699
 ; REFERENCE/DOCKET NUMBER: A1355E-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-454-3816
 ; TELEFAX: 610-454-3808
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE: internal
 ; US-08-652-877-22

Query Match 71.4%; Score 5; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred.No. 9.3;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 Db 4 PPPLP 8

RESULT 18
 US-08-652-877-32
 ; Sequence 32, Application US/08652877
 ; Patent No. 6187548
 ; GENERAL INFORMATION:
 ; APPLICANT: Akerstrom, Goran
 ; APPLICANT: Juhlin, Claes
 ; APPLICANT: Rask, Lars
 ; APPLICANT: Crumley, Gregg R.
 ; APPLICANT: Morse, Clarence C.
 ; APPLICANT: Murray, Edward M.
 ; APPLICANT: Hjaln, Goran
 ; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
 ; TITLE OF INVENTION: Thereof and DNA Encoding Same
 ; NUMBER OF SEQUENCES: 106
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Rd., 3C43
 ; CITY: Collegeville
 ; STATE: PA

; COUNTRY: USA
 ; ZIP: 19426-0107
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.5.1
 ; SOFTWARE: Word 6.0 (Patentin)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/652,877
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/15203
 ; FILING DATE: 22-NOV-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/344,836
 ; FILING DATE: 23-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/487,314
 ; FILING DATE: 07-JUNE-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Savitzky, Martin
 ; REGISTRATION NUMBER: 29,699
 ; REFERENCE/DOCKET NUMBER: A1355E-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-454-3816
 ; TELEFAX: 610-454-3808
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE: internal
 ; US-08-652-877-32

Query Match 71.4%; Score 5; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred.No. 9.3;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 Db 4 PPPLP 8

RESULT 19
 US-08-476-515A-22
 ; Sequence 22, Application US/08476515A
 ; Patent No. 6239270
 ; GENERAL INFORMATION:
 ; APPLICANT: Akerstrom, Goran
 ; APPLICANT: Juhlin, Claes
 ; APPLICANT: Rask, Lars
 ; APPLICANT: Crumley, Gregg R.
 ; APPLICANT: Morse, Clarence C.
 ; APPLICANT: Murray, Edward M.
 ; APPLICANT: Hjaln, Goran
 ; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
 ; TITLE OF INVENTION: Thereof and DNA Encoding Same
 ; NUMBER OF SEQUENCES: 84
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Martin Savitzky
 ; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426-0107
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Compaq PC

```

; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)
; CURRENT APPLICATION DATA: US/08/476,515A
; APPLICATION NUMBER: US/08/476,515A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00483
; FILING DATE: 24-MAY-1994
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-08-476-515A-22

```

```

Query Match 71.4%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 3 PPPLP 7
Db 4 PPPLP 8

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```

RESULT 20
US-08-476-515A-32
; Sequence 32, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akersstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Raak, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalms, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
; STREET: 3C43,
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,515A
; FILING DATE: 07-JUN-1995

```

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00483
; FILING DATE: 24-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-08-476-515A-32

```

```

Query Match 71.4%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 3 PPPLP 7
Db 4 PPPLP 8

```

```

RESULT 21
US-08-230-047-17
; Sequence 17, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashenko, Yuri D.
; APPLICANT: Jaye, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:

```

```
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-230-047-17

Query Match          71.4%; Score 5; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 22
US-08-602-999A-251
; Sequence 251, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-266

Query Match          71.4%; Score 5; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPL 6
Db 4 QPPPL 8

RESULT 24
US-08-602-999A-267
; Sequence 267, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
```

```
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 267:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-267

Query Match 71.4%; Score 5; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 6 PPPLP 10

RESULT 25
US-09-500-124-251
; Sequence 251, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
```

```
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-251

Query Match 71.4%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 6 PPPLP 10

RESULT 26
US-09-500-124-266
; Sequence 266, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 266:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-266
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Query Match 71.4%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPL 6
| | | | |
Db 4 QPPL 8

RESULT 27
US-09-500-124-267
; Sequence 267, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09500,124
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 267:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-267

Query Match 71.4%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
| | | | |
Db 6 PPPLP 10

RESULT 28
US-08-185-432-12
; Sequence 12, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:

; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Busseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEx PROTEINS, NUCLEIC ACIDS, AND
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/185,432
; APPLICATION NUMBER: 08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-185-432-12

Query Match 71.4%; Score 5; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
| | | | |
Db 4 PPPLP 8

RESULT 29
US-08-630-916A-63
; Sequence 63, Application US/08630916A
; Patent No. 601137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 866-8864/9741
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-916A-63

Query Match 71.4%; Score 5; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
|||||
Db 5 PPPLP 9

RESULT 30
US-08-630-915A-186
Sequence 186, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: McCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-630-915A-186

Query Match 71.4%; Score 5; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
|||||
Db 5 PPPLP 9

RESULT 31
US-08-185-432-10
Sequence 10, Application US/08185432
Patent No. 5750652
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Xu, Tian
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-185-432-10

Query Match 71.4%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
|||||
Db 5 PPPLP 9

RESULT 32
US-08-769-745-31
Sequence 31, Application US/08769745
Patent No. 595259
GENERAL INFORMATION:
APPLICANT: Holmes, Todd C.
APPLICANT: Levitan, Irwin B.
APPLICANT: Brandeis University

; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-08-769-745-31

Query Match 71.4%; Score 5; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 33
US-08-602-999A-356
; Sequence 356, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 356:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-356

Query Match 71.4%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 34
US-08-602-999A-385
; Sequence 385, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-385

Query Match 71.4%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 7 PPPLP 11

QY 3 PPPLP 7
Db 7 PPPLP 11

RESULT 35
US-08-602-999A-404
; Sequence 404, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-385

Query Match 71.4%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 7 PPPLP 11

RESULT 35
US-08-602-999A-404
; Sequence 404, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-385

Query Match 71.4%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 404:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-404

Query Match 71.4%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 36
US-08-602-999A-414
; Sequence 414, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-435
```

```
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-414

Query Match 71.4%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 37
US-08-602-999A-435
; Sequence 435, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-435
```

Query Match 71.4%; Score 5; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;

Qy 3 PPPLP 7
 Db 4 PPPLP 8

RESULT 38

US-08-602-999A-441
 ; Sequence 441, Application US/08602999A
 ; Patent No. 6184205
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,999A
 ; FILING DATE: 16-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 441:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-602-999A-441

Query Match 71.4%; Score 5; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;

Qy 3 PPPLP 7
 Db 5 PPPLP 9

RESULT 39

US-08-602-999A-452
 ; Sequence 452, Application US/08602999A
 ; Patent No. 6184205
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,999A
 ; FILING DATE: 16-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 452:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-602-999A-452

Query Match 71.4%; Score 5; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 Db 7 PPPLP 11

RESULT 40

US-09-500-124-356
 ; Sequence 356, Application US/09500124
 ; Patent No. 6432920
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/602,999
APPLICATION NUMBER:
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 356:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-356

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 7 PPPLP 11

RESULT 41
US-09-500-124-385
Sequence 385, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 385:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-385

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 7 PPPLP 11

RESULT 42
US-09-500-124-404
Sequence 404, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 404:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-404

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
|||||
Db 4 PPPLP 8

RESULT 43

US-09-500-124-414
; Sequence 414, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-414

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
|||||
Db 4 PPPLP 8

RESULT 44

US-09-500-124-435
; Sequence 435, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-435

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
|||||
Db 4 PPPLP 8

RESULT 45

US-09-500-124-441
; Sequence 441, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

```
;
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/500,124
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 441:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-441

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 5 PPPLP 9

RESULT 46
US-09-500-124-452 Application US/09500124
; Sequence 452
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
```

```
;
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 452:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-452

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 7 PPPLP 11

RESULT 47
US-08-185-432-9
; Sequence 9, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Busseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-185-432-9

Query Match 71.4%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 3 PPPLP 7
 |||||
 Db 6 PPPLP 10

RESULT 48

US-08-185-432-14
 ; Sequence 14, Application US/08185432
 ; Patent No. 5750652
 ; GENERAL INFORMATION:
 ; APPLICANT: Artavanis-Tsakonas, Spyridon
 ; APPLICANT: Busseau, Isabelle
 ; APPLICANT: Diederich, Robert J.
 ; APPLICANT: Xu, Tian
 ; APPLICANT: Matsuno, Kenji
 ; TITLE OF INVENTION: DELTA PROTEINS, NUCLEIC ACIDS, AND
 ; ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PENNIE & EDMONDS
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/185,432
 ; FILING DATE: 21-JAN-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 7326-006
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-185-432-14

Query Match 71.4%; Score 5; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 |||||
 Db 6 PPPLP 10

RESULT 49

US-08-602-999A-197
 ; Sequence 197, Application US/08602999A
 ; Patent No. 6184205
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,999A
 ; FILING DATE: 16-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 197:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: Peptide
 ; US-08-602-999A-197

Query Match 71.4%; Score 5; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 |||||
 Db 9 PPPLP 13

RESULT 50

US-09-500-124-197
 ; Sequence 197, Application US/09500124
 ; Patent No. 6432920
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/500,124
 ; FILING DATE:
 ; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mirock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 197:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; US-09-500-124-197

Query Match 71.4%; Score 5; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 9 PPPLP 13

;; RESULT 51
;; US-08-230-047-10
;; Sequence 10, Application US/08230047
;; Patent No. 5541109
;; GENERAL INFORMATION:
;; APPLICANT: Seafross III, George H.
;; APPLICANT: Ivashchenko, Yuri D.
;; APPLICANT: Jaye, Michael C.
;; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
;; TITLE OF INVENTION: PROTEIN
;; NUMBER OF SEQUENCES: 40
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Rhone-Poulenc Rorer Inc.
;; STREET: 500 Arcola Road, 3043
;; CITY: Collegeville
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19426

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Macintosh
;; OPERATING SYSTEM: System 7.1
;; SOFTWARE: Word 5.0 (patentin)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/230,047
;; FILING DATE: 19-APR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goodman, Rosanne
;; REGISTRATION NUMBER: 32,534
;; REFERENCE/DOCKET NUMBER: A1465-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (610) 454-3817
;; TELEFAX: (610) 454-3808
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-230-047-10

Query Match 71.4%; Score 5; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 5 PPPLP 9

;; RESULT 52
;; US-08-602-999A-360
;; Sequence 360, Application US/08602999A
;; Patent No. 6184205
;; GENERAL INFORMATION:
;; APPLICANT: SPARKS, Andrew B.
;; APPLICANT: KAY, Brian K.
;; APPLICANT: THORN, Judith M.
;; APPLICANT: QUILLIAM, Lawrence A.
;; APPLICANT: DER, Channing J.
;; APPLICANT: FOWLKES, Dana M.
;; APPLICANT: RIDER, James B.
;; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;; TITLE OF INVENTION: ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/602,999A
;; FILING DATE: 16-FEB-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mirock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 360:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; US-08-602-999A-360

Query Match 71.4%; Score 5; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 9 PPPLP 13

;; RESULT 53
;; US-08-602-999A-374
;; Sequence 374, Application US/08602999A
;; Patent No. 6184205
;; GENERAL INFORMATION:
;; APPLICANT: SPARKS, Andrew B.
;; APPLICANT: KAY, Brian K.
;; APPLICANT: THORN, Judith M.
;; APPLICANT: QUILLIAM, Lawrence A.
;; APPLICANT: DER, Channing J.
;; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 374:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-374

Query Match 71.4%; Score 5; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 3 PPPLP 7
Db 9 PPPLP 13

RESULT 54
US-09-500-124-360
; Sequence 360, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 360:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-360

Query Match 71.4%; Score 5; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 3 PPPLP 7
Db 9 PPPLP 13

RESULT 55
US-09-500-124-374
; Sequence 374, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 374;
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-374

Query Match 71.4%; Score 5; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 9 PPPLP 13

RESULT 56
US-08-602-999A-320
Sequence 320, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 320:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-320

Query Match 71.4%; Score 5; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 10 PPPLP 14

RESULT 57
US-08-602-999A-409
Sequence 409, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 409:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-409

Query Match 71.4%; Score 5; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 11 PPPLP 15

RESULT 58
US-09-500-124-320
Sequence 320, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds

```

; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 320:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-320

Query Match 71.4%; Score 5; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 10 PPPLP 14

RESULT 59
US-09-500-124-409
; Sequence 409, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 409:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-409

Query Match 71.4%; Score 5; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 11 PPPLP 15

RESULT 60
US-08-630-915A-169
; Sequence 169, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

```

US-08-630-915A-169

Query Match 71.4%; Score 5; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 2 PPPLP 6

RESULT 61

US-08-602-999A-358
; Sequence 358, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602.999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 358:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-358

Query Match 71.4%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 12 PPPLP 16

RESULT 62

US-09-500-124-358
; Sequence 358, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500.124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 358:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-358

Query Match 71.4%; Score 5; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 12 PPPLP 16

RESULT 63

US-09-006-428A-25
; Sequence 25, Application US/09006428A
; Patent No. 6444439
; GENERAL INFORMATION:
; APPLICANT: Jing Li
; APPLICANT: Kazuhisa Nishizawa
; APPLICANT: Wenqian An
; APPLICANT: Ellis L. Reinherz
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A
; TITLE OF INVENTION: cdc15-LIKE ADAPTOR PROTEIN (CD2BP1)
; FILE REFERENCE: 1062.1020-000
; CURRENT APPLICATION NUMBER: US/09/006.428A
; CURRENT FILING DATE: 1998-01-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens

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;
; FEATURE:
; OTHER INFORMATION: polypeptide
US-09-006-428A-25

Query Match          57.1%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 64
US-09-195-868-19
; Sequence 19, Application US/09195868
; Patent No. 6090621
; GENERAL INFORMATION:
; APPLICANT: KAVANAUGH MD, MICHAEL
; APPLICANT: POT PH.D., DAVID
; APPLICANT: WILLIAMS MDPHD, LEWIS T.
; TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE
; TITLE OF INVENTION: 5-PHOSPHATASES (SIPs)
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 HORTON STREET
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/195,868
; FILING DATE:
; CLASSIFICATION:
; APPLICATION NUMBER: US/09/195,868
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FIRESTONE, LEIGH H.
; REGISTRATION NUMBER: 36,831
; REFERENCE/DOCKET NUMBER: 1182.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-923-2707
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-195-868-19

Query Match          57.1%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 3 PPLP 6

RESULT 65
US-08-664-962B-18
; Sequence 18, Application US/08664962B
; Patent No. 6218162
; GENERAL INFORMATION:
; APPLICANT: Krystal, Gerald
```

```
;
; TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MERCHANT & GOULD
; STREET: 3100 NO. 6218162west Center, 90 South Seventh Street
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: U.S.A.
; ZIP: 55402-4131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/664,962B
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Douglas P.
; REGISTRATION NUMBER: 30,300
; REFERENCE/DOCKET NUMBER: M&G 7933.49-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-664-962B-18

Query Match          57.1%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 66
US-09-311-743-18
; Sequence 18, Application US/09311743
; Patent No. 6238903
; GENERAL INFORMATION:
; APPLICANT: Krystal, Gerald
; TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,743
; FILING DATE: 14-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 7771-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 416-364-7311
```

```

; TELEFAX: 416-361-1398
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-311-743-18

Query Match          57.1%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPLP 7
Db      1 PPLP 4

RESULT 67
US-08-743-168B-38
; Sequence 38, Application US/08743168B
; Patent No. 6271015
; GENERAL INFORMATION:
; APPLICANT: Gilula, No. 6271015ton B
; APPLICANT: Cravatt, Benjamin F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10550 No. 6271015th Torrey Pines Road
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,168B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/489,535
; FILING DATE: 12-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 485.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
;
US-08-743-168B-38

Query Match          57.1%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPLP 7
Db      1 PPLP 4

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; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: A-68344/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/645,456A
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US/09/425,324
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-645-456A-36

Query Match 57.1%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
|||
Db 1 PPLP 4

RESULT 71
US-09-425-324A-36
; Sequence 36, Application US/09425324A
; Patent No. 6562591
; GENERAL INFORMATION:
; APPLICANT: Fu, C. Alan
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: A-68344/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/425,324A
; CURRENT FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-425-324A-36

Query Match 57.1%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
|||
Db 1 PPLP 4

RESULT 72
US-09-645-791-36
; Sequence 36, Application US/09645791
; Patent No. 6563658
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Fu, Alan C
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: A-68344-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/645,791
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 09/425,324
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-645-791-36

Query Match 57.1%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
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Db 1 PPLP 4

RESULT 73
US-08-081-539-113
; Sequence 113, Application US/08081539
; Patent No. 5501962
; GENERAL INFORMATION:
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
; TITLE OF INVENTION: Chimeric Hybrid Polypeptides
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
; ADDRESS: Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,539
; FILING DATE: 19930621
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanady, Mary J.
; REGISTRATION NUMBER: 28623
; REFERENCE/DOCKET NUMBER: 2724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-081-539-113

Query Match 57.1%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
|||
Db 2 PPLP 5

RESULT 74
US-08-466-647-113
; Sequence 113, Application US/08466647

Patent No. 5543141
GENERAL INFORMATION:
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Ollins, Peter O.
TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
TITLE OF INVENTION: ChimERIC Hybrid Polypeptides
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
ADDRESSEE: Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,647
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,539
FILING DATE: 21-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kanady, Mary J.
REGISTRATION NUMBER: 28623
REFERENCE/DOCKET NUMBER: 2724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-647-113

Query Match 57.1%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 2 PPLP 5

RESULT 75
US-08-602-999A-9
Sequence 9, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-9

Query Match 57.1%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 4 PPLP 7

Search completed: November 25, 2003, 20:15:56
Job time : 9.63298 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 15.6436 Seconds
(without alignments)
104.507 Million cell updates/sec

Title: US-09-641-801-2

Perfect score: 17

Sequence: 1 LQTPQPLQVMMEPQGD 17

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	23.5	10	2	PQ0788
2	4	23.5	14	2	OMD2 dehydrogenase
3	4	23.5	15	2	Omega-gliadine 1 a
4	4	23.5	15	2	alpha-1-antitrypsin
5	4	23.5	20	2	IG heavy chain V r
6	4	23.5	20	2	antifungal 2S stor
7	4	23.5	20	2	flagellar motor sw
8	3	17.6	8	2	interphotoreceptor
9	3	17.6	9	2	neutral proteinase
10	3	17.6	9	2	231K exoantigen -
11	3	17.6	10	2	calliFWRamide 1 -
12	3	17.6	10	2	alpha-2-macroglobu
13	3	17.6	10	2	hypothetical 1.3K
14	3	17.6	10	2	vitellogenin, 190K
15	3	17.6	11	2	hypothetical prote
16	3	17.6	11	2	cycloinulooligosac
17	3	17.6	11	2	Achatina cardio-ex
18	3	17.6	11	2	acetylcholinestera
19	3	17.6	12	2	transcription fact
20	3	17.6	12	2	napin - rape (frag
21	3	17.6	13	2	actin 7 - soybean
22	3	17.6	13	2	neural cell adhesi
23	3	17.6	13	2	2S albumin large c
24	3	17.6	14	2	deoxynucleotidyltr
25	3	17.6	14	2	hypothetical prote
26	3	17.6	14	2	ovostatin - duck (
27	3	17.6	14	2	alpha-2-macroglobu
28	3	17.6	14	2	cerebrin 30 - huma
29	3	17.6	14	2	fibroblast-activat
					IG heavy chain DJ

30	17.6	14	2	PN0666	dystrophin-associat
31	17.6	14	2	PC7075	guanilate cyclase
32	17.6	15	2	PA0021	protein QA300016 -
33	17.6	15	2	PN0148	omega-gliadine 3 -
34	17.6	15	2	A41436	alpha-macroglobuli
35	17.6	15	2	PN0665	dystrophin-associat
36	17.6	15	2	PH0789	T-cell receptor al
37	17.6	16	2	B42324	cytochrome B450c27
38	17.6	16	2	C49048	T-cell receptor be
39	17.6	16	2	PH0763	T-cell receptor be
40	17.6	16	2	PH0767	T-cell receptor be
41	17.6	16	2	A46236	transforming prote
42	17.6	16	2	D83794	hypothetical prote
43	17.6	17	2	S15754	actin 6 - soybean
44	17.6	17	2	S40530	aleurone protein -
45	17.6	17	2	C43599	hypothetical prote
46	17.6	17	2	S05033	photosystem II pro
47	17.6	17	2	S41207	F420-non-reducing-
48	17.6	17	2	S21289	glutathione transf
49	17.6	18	2	B24735	glutathione transf
50	17.6	18	2	S52614	u-plasminogen acti
51	17.6	18	2	S46418	NHL protein - cur
52	17.6	18	2	S55002	protein 1 - legion
53	17.6	18	2	S10452	hypothetical prote
54	17.6	18	2	B48408	21K high mobility
55	17.6	18	2	A61392	brain-associated s
56	17.6	18	2	D85601	hypothetical prote
57	17.6	18	4	S56393	lacZ/isl mutant fu
58	17.6	19	2	C32735	thyroglobulin - pi
59	17.6	19	2	B32735	thyroglobulin - sh
60	17.6	19	2	P00548	capsid protein VP2
61	17.6	19	2	S29766	cytochrome c(EDH)
62	17.6	19	2	S63489	dissimilatory sulf
63	17.6	19	2	A48408	21K high mobility
64	17.6	19	2	I39327	pre-T/NK cell-asso
65	17.6	19	2	A34467	36K microfibril-as
66	17.6	20	2	A60822	Cytochrome P450 PB
67	17.6	20	2	A39328	notochis II-5b non
68	17.6	20	2	PH0111	style glycoprotein
69	17.6	20	2	A05313	apolipoprotein A-I
70	17.6	20	2	JN0252	water-soluble 35K
71	17.6	20	2	S08605	hypothetical prote
72	17.6	20	2	PL0039	outer membrane pro
73	17.6	20	2	I64036	hypothetical prote
74	17.6	20	2	S63490	dissimilatory sulf
75	17.6	20	2	D56046	urinary tract ston
76	17.6	20	2	A42865	Ca2+/calmodulin-de
77	17.6	20	2	S65884	translation initia
78	17.6	20	2	S33291	lipopolysaccharide
79	17.6	20	2	A53592	H+-exporting ATPas
80	11.8	3	3	A23751	spinal cord peptid
81	11.8	3	3	B23751	spinal cord peptid
82	11.8	3	3	A33802	thyrotropin-releas
83	11.8	4	1	ECXAA	tyrosine-melanocyt
84	11.8	4	2	A32039	gamma subunit of p
85	11.8	4	2	A48360	22K superhelical D
86	11.8	4	2	A61300	D-mannosate hydrol
87	11.8	4	2	S17745	ribosomal protein
88	11.8	4	2	S17255	auto-RF amide neu
89	11.8	4	2	A25844	synaptosomal-assoc
90	11.8	4	2	E44823	T-cell receptor be
91	11.8	4	2	PT0711	globulin IV alpha
92	11.8	4	2	S09478	hypothetical prote
93	11.8	5	2	T10954	photosystem I 10.4
94	11.8	5	2	PQ0689	acid proteinase li
95	11.8	5	2	B37988	T-cell receptor be
96	11.8	5	2	PT0513	T-cell receptor be
97	11.8	5	2	PT0625	T-cell receptor be
98	11.8	5	2	PT0538	T-cell receptor be
99	11.8	5	2	PT0703	T-cell receptor be
100	11.8	5	2	PT0690	T-cell receptor be

ALIGNMENTS

RESULT 1

PQ0788
 NADH2 dehydrogenase (EC 1.6.99.3) 20K chain - fava bean mitochondrion (fragment)
 N:Alternate names: complex I 20K chain; NADH-ubiquinone reductase 20K chain
 C:Species: mitochondrion Vicia faba (fava bean)
 C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 03-Jun-2002
 C:Accession: PQ0788
 R:Letterme, S.; Boutry, M.
 Plant Physiol. 102, 435-443, 1993
 A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH-ubiquinone reductase)
 A:Reference number: PQ0775; MUID:94151437; PMID:8108509
 A:Accession: PQ0788
 A:Molecule type: protein
 A:Residues: 1-10 <DET>
 C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the three complexes in the mitochondrial electron transport chain, ranging from 5K to 75K.
 C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by a series of redox reactions.
 C:Genetics:
 A:Genome: mitochondrion
 C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 23.5%; Score 4; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
 ||||
 DB 7 LLQV 10

RESULT 2

PN0147
 omega-gliadine 1 and 2 - Aegilops longissima (fragment)
 C:Species: Aegilops longissima
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PN0147; PN0146
 R:Odintsova, T.I.; Egorov, T.A.
 Biokhimiia 55, 509-516, 1990
 A:Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of the N-terminal amino group
 A:Reference number: PN0146; MUID:90283493; PMID:2354218
 A:Accession: PN0147
 A:Molecule type: protein
 A:Residues: 1-14 <ODI>
 A:Experimental source: strain K-202
 A>Note: omega-gliadine 2 (amino-terminal fragment)
 A:Accession: PN0146
 A:Molecule type: Protein
 A:Residues: 1-9 <OD2>
 A:Experimental source: strain K-202
 A>Note: omega-gliadine 1 (amino-terminal fragment)

Query Match 23.5%; Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
 ||||
 DB 11 LQTP 14

RESULT 3

A61391
 alpha-1-antitrypsin homolog - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 17-Mar-1999
 C:Accession: A61391
 R:Tanaka, N.; Sekiya, S.; Takamizawa, H.; Kato, N.; Moriyama, Y.; Fujimura, S.
 Jpn. J. Cancer Res. 82, 693-700, 1991
 A:Title: Characterization of a 54 kDa, alpha-1-antitrypsin-like protein isolated from ascaris suum
 A:Reference number: A61391; MUID:91310496; PMID:1906855

A:Accession: A61391
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <PAN>

Query Match 23.5%; Score 4; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17
 ||||
 DB 3 PQGD 6

RESULT 4

A42413
 Ig heavy chain V region (UBL-copurifying) - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
 C:Accession: A42413
 R:Bao, Z.; Muschler, J.; Horwitz, A.F.
 J. Biol. Chem. 267, 4974-4980, 1992
 A:Title: LBL, a novel, developmentally regulated, laminin-binding lectin.
 A:Reference number: A42413; MUID:92165867; PMID:1531660
 A:Accession: A42413
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <BAO>
 C:Keywords: heterotetramer; immunoglobulin

Query Match 23.5%; Score 4; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
 ||||
 DB 11 LQTP 14

RESULT 5

D42842
 antifungal 2S storage albumin large chain - radish (fragment)
 C:Species: Raphanus sativus (radish)
 C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
 C:Accession: D42842
 R:Terras, F.R.; Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderleyde, J. Biol. Chem. 267, 15301-15309, 1992
 A:Title: Analysis of two novel classes of plant antifungal proteins from radish (Raphanus sativus)
 A:Reference number: A42842; MUID:92348373; PMID:1639777
 A:Accession: D42842
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <TER>
 A:Experimental source: seed
 A>Note: sequence extracted from NCBI backbone (NCBIP:109925)
 C:Superfamily: wheat alpha-amylase inhibitor

Query Match 23.5%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
 ||||
 DB 9 PLLQ 12

RESULT 6

PS0028
 flagellar motor switch protein flbD - Escherichia coli (fragment)
 C:Species: Escherichia coli
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1993
 C:Accession: PS0028
 R:Malakooti, J.; Kameda, Y.; Matsumura, P.

J. Bacteriol. 171, 2728-2734, 1989
 A>Title: DNA sequence analysis, gene product identification, and localization of flagellin
 A:Reference number: PS0027; MUID:89213963; PMID:2651416
 A:Accession: PS0028
 A:Molecule type: DNA
 A:Residues: 1-20 <MAL>
 C:Genetics:
 A:Gene: fibD

Query Match 23.5%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
 ||||
 Db 17 PLLQ 20

RESULT 7
 F24417
 N:Interphotoreceptor retinoid-binding protein - bush baby (fragment)
 N:Alternate names: interstitial retinol-binding protein
 C:Species: Galago sp. (bush baby)
 C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 18-Jun-1993
 C:Accession: F24417
 R:Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
 FEBS Lett. 205, 309-312, 1986
 A>Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10
 A:Reference number: A91365; MUID:86301171; PMID:3743780
 A:Accession: F24417
 A:Molecule type: protein
 A:Residues: 1-20 <PON>

Query Match 23.5%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLL 8
 ||||
 Db 5 QPLL 8

RESULT 8
 A35180
 neutral proteinase (EC 3.4.1.-), calcium-activated - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
 C:Accession: A35180
 R:Yoshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Satoh, M.
 J. Biol. Chem. 265, 5809-5815, 1990
 A>Title: Purification of a novel type of calcium-activated neutral protease from rat bra
 A:Reference number: A35180; MUID:90202830; PMID:2318836
 A:Accession: A35180
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <YOS>
 C:Keywords: hydrolase

Query Match 17.6%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
 ||||
 Db 1 PLL 3

RESULT 9
 B33098
 231K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
 C:Species: Plasmodium falciparum
 C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C:Accession: B33098

R:Nichols, J.H.; Hager, L.P.
 submitted to the Protein Sequence Database, May 1990
 A:Reference number: A33098
 A:Accession: B33098
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <NIC>

Query Match 17.6%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3
 ||||
 Db 2 LQT 4

RESULT 10
 A41978
 callipemrfamide 1 - bluebottle fly (Calliphora vomitoria)
 C:Species: Calliphora vomitoria
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
 C:Accession: A41978
 R:Dube, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Tho;
 Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
 A>Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (d
 A:Reference number: A41978; MUID:92196111; PMID:1549595
 A:Accession: A41978
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <DUV>
 C:Keywords: amidated carboxyl end; neuropeptide
 F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 17.6%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQ 5
 ||||
 Db 1 TPQ 3

RESULT 11
 S33844
 alpha-2-macroglobulin - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 22-Nov-1993 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C:Accession: S33844
 R:Warburton, M.J.; Coles, B.; Dundas, S.R.; Gusterson, B.A.; O'Hare, M.J.
 Eur. J. Biochem. 214, 803-809, 1993
 A>Title: Hydrocortisone induces the synthesis of alpha(2)-macroglobulin by rat mamma
 A:Reference number: S33843; MUID:93307297; PMID:7686489
 A:Accession: S33844
 A:Molecule type: protein
 A:Residues: 1-10 <WAR>
 A:Superfamily: alpha-2-macroglobulin
 C:Keywords: glycoprotein; plasma; proteinase inhibitor; thiolester bond

Query Match 17.6%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
 ||||
 Db 6 EPQ 8

RESULT 12
 JQ0943
 hypothetical 1.3K protein - infectious bursal disease virus (strain 52/70)
 C:Species: infectious bursal disease virus
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 08-Oct-1999

C;Accession: JQ0943
R;Bayliss, C.D.; Spies, U.; Shaw, K.; Peters, R.W.; Papageorgiou, A.; Mueller, H.; Bourne J. Gen. Virol. 71, 1303-1312, 1990
A;Title: A comparison of the sequences of segment A of four infectious bursal disease viruses
A;Reference number: JQ0941; MUID:90278420; PMID:2161902
A;Accession: JQ0943
A;Status: translation not shown
A;Molecule type: genomic RNA
A;Residues: 1-10 <BAV>
A;Cross-references: GB:D00869; NID:g221038; PIDN:BAA00743.1; PID:di001203; PID:g221039

Query Match 17.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LQ 9
|||
DB 5 LQ 7

RESULT 13
A61622
vitellogenin, 190k chain - gypsy moth (fragment)
N;Contains: vitellin
C;Species: Lymantria dispar (gypsy moth)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 15-Oct-1999
C;Accession: A61622
R;Hiremath, S.; Eshita, S.
Insect Biochem. Mol. Biol. 22, 605-611, 1992
A;Title: Purification and characterization of vitellogenin from the gypsy moth, Lymantria dispar
A;Reference number: A61622
A;Accession: A61622
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <HIR>
C;Keywords: egg yolk; hemolymph

Query Match 17.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
|||
DB 5 EPQ 7

RESULT 14
E86128
hypothetical protein Z5903 [imported] - Escherichia coli (strain O157:H7, substrain EDL958)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: E86128
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lw, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E86128
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-10 <STO>
A;Cross-references: GB:AE005174; NID:gi2519314; PIDN:AA059489.1; GSPDB:GN00145; UNGWP:Z5903
A;Experimental source: strain O157:H7, substrain EDL958
C;Genetics:
A;Gene: Z5903

Query Match 17.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LQV 10
|||
DB 5 LQV 7

RESULT 15
PC2330
cycloinulooligosaccharide fructanotransferase (EC 2.4.-.-) - Bacillus circulans (MCI-102)
C;Species: Bacillus circulans
C;Date: 21-Mar-1995 #sequence_revision 26-May-1995 #text_change 07-May-1999
C;Accession: PC2330
R;Kushibe, S.; Mitsui, K.; Yamagishi, M.; Yamada, K.; Morimoto, Y.
Biosci. Biotechnol. Biochem. 59, 31-34, 1995
A;Title: Purification and characterization of cycloinulooligosaccharide fructanotransferase
A;Reference number: PC2330; MUID:95201377; PMID:7765973
A;Accession: PC2330
A;Molecule type: protein
A;Residues: 1-11 <KUS>
C;Comment: This enzyme hydrolyzes beta-(2-1) glycosidic linkages and acts in intermol.
C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 17.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16
|||
DB 9 PQG 11

RESULT 16
A34662
Achatina cardio-excitatory peptide-1 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 11-Jul-1997
C;Accession: A34662
R;Fujiimoto, K.; Ohta, N.; Yoshida, M.; Kubota, I.; Muneoka, Y.; Kobayashi, M.
Biochem. Biophys. Res. Commun. 167, 777-783, 1990
A;Title: A novel cardio-excitatory peptide isolated from the atria of the African giant snail
A;Reference number: A34662; MUID:90211261; PMID:2322251
A;Accession: A34662
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <FUU>
C;Keywords: amidated carboxyl end
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 17.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16
|||
DB 7 PQG 9

RESULT 17
S68637
acetylcholinesterase (EC 3.1.1.7) P chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 30-Jan-1998
C;Accession: S68637
R;Boschetti, N.; Brodbeck, U.
FEBS Lett. 380, 133-136, 1996
A;Title: The membrane anchor of mammalian brain acetylcholinesterase consists of a signal peptide
A;Reference number: S68637; MUID:96181683; PMID:8603722
A;Accession: S68637
A;Molecule type: protein
A;Residues: 1-11 <BOS>
A;Experimental source: brain
C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein

Query Match 17.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 BPQ 15
|||
Db 1 BPQ 3

RESULT 18

S25485
transcription factor NF1 - rat
N/Alternate names: HNF1 protein; LFBI protein
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Oct-1999
R/Tomei, L.; Piaggio, G.; Toniatti, C.; Lazaro, D.; de Francesco, R.; Pozzi, L.; Gerstner, J.; Cortese, R.
A/Accession: S25485; S50121
A/Residues: 1-12 <TOM>
A/Description: LFBI/HNF1 acts as a repressor of its own transcription.
A/Reference number: S25485
A/Accession: S25485
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-12 <TOM>
A/Cross-references: EMBL:X67649; NID:G56575; PIDN:CAA47891.1; PID:G56576
R/Piaggio, G.; Tomei, L.; Toniatti, C.; de Francesco, R.; Gerstner, J.; Cortese, R.
Nucleic Acids Res. 22, 4284-4290, 1994
A/Title: LFBI/HNF1 acts as a repressor of its own transcription.
A/Reference number: S50121; MUID:95023202; PMID:7937157
A/Accession: S50121
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-12 <PTA>
A/Cross-references: EMBL:X67649; NID:G56575; PIDN:CAA47891.1; PID:G56576
C/Suprafamily: transcription factor HNF-1; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 17.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3
|||
Db 8 LQT 10

RESULT 19

S67528
napin - rape (fragments)
C/Species: Brassica napus (rape)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C/Accession: S67528
R/Muren, E.; Ek, B.; Rask, L.
Eur. J. Biochem. 227, 316-321, 1995
A/Title: Processing of the 2S storage protein pronapin in Brassica napus and in transfor
A/Reference number: S67528; MUID:95154306; PMID:7851402
A/Accession: S67528
A/Status: Preliminary
A/Molecule type: protein
A/Residues: 1-6; 7-12 <MUR>

Query Match 17.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16
|||
Db 7 PQG 9

RESULT 20

S15755
actin 7 - soybean (fragment)
C/Species: Glycine max (soybean)
C/Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
C/Accession: S15755
R/Pearson, L.; Meagher, R.B.

Query Match 17.6%; Score 3; DB 2; Length 13;

Plant Mol. Biol. 14, 513-526, 1990
A/Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
A/Reference number: S15754; MUID:91346640; PMID:2102831
A/Accession: S15755
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-13 <PEA>
A/Cross-references: EMBL:X17120; NID:G18527; PIDN:CAA34980.1; PID:G18528
C/Suprafamily: actin
C/Keywords: cytoskeleton; structural protein

Query Match 17.6%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
|||
Db 8 QPL 10

RESULT 21

D39690
neural cell adhesion molecule, cardiac splice form +,-,+ - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C/Accession: D39690
R/Keyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A/Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule
A/Reference number: A39690; MUID:91141516; PMID:1996115
A/Accession: D39690
A/Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual
A/Molecule type: mRNA
A/Residues: 1-13 <REY>
A/Cross-references: GB:M63970
C/Suprafamily: neural cell adhesion molecule; fibronectin type III repeat homology; ir
C/Keywords: cardiac muscle; cell adhesion; heart

Query Match 17.6%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16
|||
Db 8 PQG 10

RESULT 22

S09716
2S albumin large chain (1 and 2) nII - rape (fragments)
N/Alternate names: 2S albumin large chain nIII
C/Species: Brassica napus (rape)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Aug-1998
C/Accession: S09716; S09718; S09717
R/Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A/Title: Beta-turns as structural motifs for the proteolytic processing of seed protei
A/Reference number: S09720; MUID:9042974; PMID:2185951
A/Accession: S09716
A/Molecule type: protein
A/Residues: 1-9;10-13 <MON>
A/Experimental source: seed
A/Note: 3-Ser was also found
A/Accession: S09718
A/Molecule type: protein
A/Residues: 1-9;10-13 <MO2>
A/Experimental source: seed
A/Accession: S09717
A/Molecule type: protein
A/Residues: 1-9;10-13 <MO3>
A/Experimental source: seed

Query Match 17.6%; Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 14 PQG 16
|||

Db 1 PQG 3
|||

RESULT 23

I84603
deoxynucleotidyltransferase - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
R;Koizumi, O.; Kaneda, T.; Morishita, R.
Biochem. Biophys. Res. Commun. 144, 185-190, 1987
A>Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in man
A;Reference number: 145884; MUID:87213162; PMID:3579900
A;Accession: I84603
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-13 <RES>
A;Cross-references: GB:M26144; MID:g951194; PIDN:AAA74588.1; PID:g951195
C;Genetics:
A;Gene: GDB:DNMT
A;Cross-references: GDB:119100; OMTM:187410
A;Map position: 10q23-10q24

Query Match 17.6%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
|||

Db 8 QPL 10
|||

RESULT 24

A35105
hypothetical protein - Neurospora crassa mitochondrion (fragment)
C:Species: mitochondrion Neurospora crassa
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Dec-1999
C;Accession: A35105
R;Saville, B.J.; Collins, R.A.
Cell 61, 685-696, 1990
A>Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora
A;Reference number: A35105; MUID:90263093; PMID:2160856
A;Accession: A35105
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-14 <SAV>
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC3
C;Keywords: mitochondrion

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
|||

Db 7 LLQ 9
|||

RESULT 25

S00150
ovostatin - duck (fragment)
R;Alternate names: ovomacroglobulin
C:Species: Anas platyrhynchos (domestic duck)
C>Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
C;Accession: S00150
R;Nagase, H.; Harris Jr., E.D.; Brew, K.

J. Biol. Chem. 261, 1421-1426, 1986
A>Title: Evidence for a thiol ester in duck ovostatin (ovomacroglobulin).
A;Reference number: S00150; MUID:86111792; PMID:3511043
A;Accession: S00150
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <NAG>
A;Note: part of this sequence, including the amino end of the mature chicken and duck

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
|||

Db 4 EPQ 6
|||

RESULT 26

B20872
alpha-2-macroglobulin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C;Accession: B20872
R;Nagase, H.; Harris Jr., E.D.; Woessner Jr., J.F.; Brew, K.
J. Biol. Chem. 258, 7481-7489, 1983
A>Title: Ovostatin: a novel proteinase inhibitor from chicken egg white. I. Purificat
A;Reference number: A92427; MUID:83238315; PMID:6408074
A;Accession: B20872
A;Molecule type: protein
A;Residues: 1-14 <NAG>

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
|||

Db 5 EPQ 7
|||

RESULT 27

PH1566
cerebrin 30 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C;Accession: PH1566
R;Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.
J. Neurochem. 61, 533-540, 1993
A>Title: Micropurification of two human cerebrospinal fluid proteins by high performa
A;Reference number: PH1566; MUID:93329419; PMID:8336140
A;Accession: PH1566
A;Molecule type: protein
A;Residues: 1-14 <LEO>

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
|||

Db 9 QPL 11
|||

RESULT 28

B61235
fibroblast-activating factor 35K precursor - human (fragments)
C:Species: Homo sapiens (man)
C>Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 12-May-1994
C;Accession: B61235
R;Deneter, J.; Medzihradsky, D.; Kha, H.; Goetzl, E.J.; Turck, C.W.
Immunology 72, 350-354, 1991
A>Title: Isolation and partial characterization of the structures of fibroblast activ

A:Reference number: A61235; MUID:91224664; PMID:2026444
 A:Accession: B61235
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <DEM>

Query Match 17.6%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
 |||
 Db 6 LLQ 8
 |||

RESULT 29

PHI327
 Ig heavy chain DJ region (clone C113-105) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PHI327
 R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
 A:Reference number: PHI302; MUID:93094761; PMID:1460419
 A:Accession: PHI327
 A:Molecule type: DNA
 A:Residues: 1-14 <NAS>
 C:Keywords: heterotetramer; immunoglobulin

Query Match 17.6%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VNM 12
 |||
 Db 3 VNM 5
 |||

RESULT 30

PN0666
 dystrophin-associated glycoprotein A3a-V - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
 C:Accession: PN0666
 R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
 J. Biochem. 114, 634-639, 1993
 A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in dystrophic muscle
 A:Reference number: PN0662; MUID:94156881; PMID:8113213
 A:Accession: PN0666
 A:Molecule type: protein
 A:Residues: 1-14 <YOS>
 C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
 C:Keywords: glycoprotein; skeletal muscle

Query Match 17.6%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
 |||
 Db 3 PLL 5
 |||

RESULT 31

PC7075
 Guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C:Accession: PC7075
 R:Tsuigita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
 Electrophoresis 21, 1853-1871, 2000
 A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of b

A:Reference number: PC7072
 A:Accession: PC7075
 A:Molecule type: protein
 A:Residues: 1-14 <TSU>
 A:Experimental source: strain C57BL/6Cr Slc, male; brain, striatum
 C:Keywords: brain; phosphorus-oxygen lyase

Query Match 17.6%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16
 |||
 Db 9 PQG 11
 |||

RESULT 32

PA0021
 protein QA300016 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C:Accession: PA0021
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JTPID, July 1994
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
 A:Reference number: PA0001
 A:Accession: PA0021
 A:Molecule type: protein
 A:Residues: 1-15 <KAM>
 A:Experimental source: leaf

Query Match 17.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
 |||
 Db 9 EPQ 11
 |||

RESULT 33

PN0148
 omega-gliadine 3 - Aegilops longissima (fragment)
 C:Species: Aegilops longissima
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PN0148
 R:Odintsova, T.I.; Egorov, T.A.
 Biokhimiia 55, 509-516, 1990
 A:Title: N-terminal sequences of omega-gliadins of Aegilops longissima: On the origin of the omega-gliadins
 A:Reference number: PN0146; MUID:90283493; PMID:2354218
 A:Accession: PN0148
 A:Molecule type: protein
 A:Residues: 1-15 <ODI>
 A:Experimental source: strain K-202
 A:Note: 11-Gln was also found

Query Match 17.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQ 5
 |||
 Db 13 TPQ 15
 |||

RESULT 34

A41436
 alpha-macroglobulin - green sea turtle (fragment)
 C:Species: Chelonia mydas (green sea turtle)
 C>Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 18-Jun-1993
 C:Accession: A41436
 R:Osada, T.; Sasaki, T.; Ikai, A.
 J. Biochem. 103, 212-217, 1988

A;Title: Purification and characterization of alpha-macroglobulin and ovomacroglobulin d
 A;Reference number: A41436; MUID:88227890; PMID:2453503
 A;Accession: A41436
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <OSA>

Query Match 17.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPQ 15
 |||
 Db 3 EPQ 5

RESULT 35

PN0665
 dystrophin-associated glycoprotein A3a-IV - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
 C;Accession: PN0665

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993
 A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
 A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0665

A;Molecule type: protein

A;Residues: 1-15 <YOS>

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 17.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLL 8
 |||
 Db 3 PLL 5

RESULT 36

PH0789
 T-cell receptor alpha chain (E22 V-alpha-4.delta-7R) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PH0789

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0789

A;Molecule type: mRNA

A;Residues: 1-15 <CAS>

A;Cross-references: EMBL:X60894

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 17.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQT 3
 |||
 Db 10 LQT 12

RESULT 37

B42324
 cytochrome P450c27/25 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Mar-1999

C;Accession: B42324
 R;Shayiq, R.M.; Avadhani, N.G.
 J. Biol. Chem. 267, 2421-2428, 1992
 A;Title: Sequence complementarity between the 5'-terminal regions of mRNAs for rat mi-
 ap.

A;Reference number: A42324; MUID:92129322; PMID:1733943

A;Accession: B42324

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-16 <SHA>

A;Note: sequence extracted from NCBI backbone (NCBIN:78408, NCBIP:88990)

C;Superfamily: human cytochrome P450 CYP11B1; cytochrome P450 homology

C;Keywords: heme; transmembrane protein

Query Match 17.6%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 QVM 11
 |||
 Db 3 QVM 5

RESULT 38

C49048
 T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragmen-
 C;Species: Homo sapiens (man)
 C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
 C;Accession: C49048

R;Sloud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.

Eur. J. Immunol. 22, 2413-2419, 1992

A;Title: Limited heterogeneity of T cell receptor variable region gene usage in juven
 A;Reference number: A49048; MUID:92387250; PMID:1387614

A;Accession: C49048

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-16 <SIO>

A;Experimental source: patient EV, IL-2R+ synovial T-cells

A;Note: sequence extracted from NCBI backbone (NCBIP:113265)

C;Keywords: T-cell receptor

Query Match 17.6%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQ 9
 |||
 Db 6 LLQ 8

RESULT 39

PH0763
 T-cell receptor beta chain (F15) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
 C;Accession: PH0763

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility comple
 allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0763

A;Molecule type: mRNA

A;Residues: 1-16 <CAS>

A;Cross-references: EMBL:X60857; NID:G50933; PIDN:CAA43247.1; PID:G50934

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 17.6%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 PQG 16

A;Cross-references: GB:AP001511; GB:BA000004; NID:gi0173727; PIDN:BA04875.1; GSPDB:GN
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH1156

Query Match 17.6%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 MME 13
 Db 10 MME 12

RESULT 43
 S15754
 actin 6 - soybean (fragment)
 C;Species: Glycine max (soybean)
 C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999
 C;Accession: S15754; S08049
 R;Pearson, L.; Meagher, R.B.
 Plant Mol. Biol. 14, 513-526, 1990
 A;Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
 A;Reference number: S15754; MUID:91346640; PMID:2102831
 A;Accession: S15754
 A;Molecule type: DNA
 A;Residues: 1-17 <PEA>
 A;Cross-references: EMBL:X17119; NID:gi18525; PIDN:CAA34979.1; PID:gi18526
 A;Superfamily: actin
 C;Keywords: cytoskeleton

Query Match 17.6%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPL 7
 Db 8 QPL 10

RESULT 44
 S40530
 aleurone protein - barley
 C;Species: Hordeum vulgare (barley)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jan-2000
 C;Accession: S40530
 R;Yupanis, T.; Burgess, S.R.; Jackson, P.J.; Shewry, P.R.
 J. Exp. Bot. 41, 385-392, 1990
 A;Title: Characterization of the major protein component from aleurone cells of barley
 A;Reference number: S40530
 A;Accession: S40530
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-17 <YUP>
 C;Superfamily: glycinin

Query Match 17.6%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 QGD 17
 Db 3 QGD 5

RESULT 45
 C43599
 hypothetical protein (cylIIA 3' region) - Actinobacillus pleuropneumoniae (serotype 9)
 N;Alternate names: CylII-B (truncated)
 C;Species: Actinobacillus pleuropneumoniae
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 08-Oct-1999
 C;Accession: C43599; S18854
 R;Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, A.L.J.

Db 6 PQG 8
 RESULT 40
 PH0767
 T-cell receptor beta chain (J5) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
 C;Accession: PH0767
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-x-
 allelic exclusion and antigen-specific repertoire.
 A;Reference number: PH0746; MUID:92078946; PMID:1836010
 A;Accession: PH0767
 A;Molecule type: mRNA
 A;Residues: 1-16 <CAS>
 A;Cross-references: EMBL:X60861; NID:g52752; PIDN:CAA43251.1; PID:g52753
 A;Experimental source: T lymphocyte
 C;Keywords: T-cell receptor

Query Match 17.6%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 PQG 16
 Db 6 PQG 8

RESULT 41
 A46236
 transforming protein myc, form 1 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
 C;Accession: A46236
 R;Hann, S.R.; Sloan-Brown, K.; Spotts, G.D.
 Genes Dev. 6, 1229-1240, 1992
 A;Title: Translational activation of the non-AUG-initiated c-myc 1 protein at high cell
 A;Reference number: A46236; MUID:92331929; PMID:1628829
 A;Accession: A46236
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-16 <HAN>
 A;Cross-references: GB:X01023
 C;Genetics:
 A;Start codon: CTG
 C;Keywords: alternative initiators

Query Match 17.6%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TPQ 5
 Db 9 TPQ 11

RESULT 42
 D83794
 hypothetical protein BH1156 [imported] - Bacillus halodurans (strain C-125)
 C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: D83794
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-16 <STO>

Infect. Immun. 59, 4497-4504, 1991
 A;Title: Cytolysins of *Actinobacillus pleuropneumoniae* serotype 9.
 A;Reference number: A43599; MUID:92040145; PMID:1937809
 A;Accession: C43599
 A;Molecule type: DNA
 A;Residues: 1-17 <SMI>
 A;Cross-references: GB:X61111; NID:g38939; PIDN:CRA43424.1; PID:g38942

Query Match 17.6%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MEP 14
 |||
 Db 1 MEP 3

RESULT 46

S05033
 photosystem II protein psbL - *Synechococcus* sp. (strain Copeland) (fragment)
 N;Alternate names: photosystem II 5K protein
 C;Species: *Synechococcus* sp.
 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
 C;Accession: S05033
 R;Keuchi, M.; Koike, H.; Inoue, Y.
 FEBS Lett. 251, 155-160, 1989

A;Title: Identification of psbI and psbL gene products in cyanobacterial photosystem II
 A;Reference number: S05030
 A;Accession: S05033
 A;Molecule type: protein
 A;Residues: 1-17 <IKE>
 A;Note: the source is designated as *Synechococcus vulcanus*
 C;Genetics:
 A;Gene: psbL
 C;Keywords: photosynthesis; photosystem II; thylakoid

Query Match 17.6%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MEP 14
 |||
 Db 1 MEP 3

RESULT 47

S41207
 F420-non-reducing-hydrogenase (EC 1.12.99.-) 51K chain - *Methanobacterium thermoautotrophicum*
 C;Species: *Methanobacterium thermoautotrophicum*
 A;Variety: strain Marburg
 C;Date: 06-Feb-1995 #sequence_revision 17-Jul-1998 #text_change 07-May-1999
 C;Accession: S41207
 R;Setzke, E.; Hedderich, R.; Heiden, S.; Thauer, R.K.
 Eur. J. Biochem. 220, 139-149, 1994

A;Title: H(2): heterodisulfide oxidoreductase complex from *Methanobacterium thermoautotrophicum*
 A;Reference number: S41204; MUID:94164153; PMID:8119281
 A;Accession: S41207
 A;Molecule type: protein
 A;Residues: 1-17 <SET>
 A;Experimental source: strain Marburg

C;Complex: membrane-associated complex; holoenzyme is the hydrogen:heterodisulfide oxidoreductase (EC 1.12.99.-) and a F420-non-reducing-hydrogenase (EC 1.12.99.-) subcomplex; each of the subcomplexes is a F420-non-reducing-hydrogenase (EC 1.12.99.-)
 C;Function:
 A;Description: reduction of coenzyme M-N-7-mercaptoheptanoylthreonine phosphate heterodisulfide (EC 1.12.99.2)

C;Keywords: membrane-associated complex; oxidoreductase

Query Match 17.6%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MEP 14
 |||

Db 5 MEP 7

RESULT 48

S21289
 glutathione transferase (EC 2.5.1.18) - rat
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
 C;Accession: S21289
 R;Meyer, D.J.; Gilmore, K.S.; Coles, B.; Dalton, K.; Hulbert, P.B.; Ketterer, B.
 Biochem. J. 283, 919, 1992
 A;Title: Corrigendum. Structural distinction of rat GSH transferase subunit 10.
 A;Reference number: S21289; MUID:92272699; PMID:1590780
 A;Accession: S21289
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-17 <MEY>
 C;Keywords: transferase

Query Match 17.6%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3
 |||
 Db 13 LQT 15

RESULT 49

B24735
 glutathione transferase (EC 2.5.1.18) 1-2 - rat (fragment)
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993
 C;Accession: B24735
 R;Mannervik, B.; Alin, P.; Guthenberg, C.; Jansson, H.; Tahir, M.K.; Warholm, M.; Jor. Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985

A;Title: Identification of three classes of cytosolic glutathione transferase common to rat liver and placenta

A;Reference number: A24735; MUID:86042634; PMID:3864155
 A;Accession: B24735
 A;Molecule type: protein
 A;Residues: 1-18 <MAN>
 C;Superfamily: glutathione transferase
 C;Keywords: transferase

Query Match 17.6%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MEP 14
 |||
 Db 15 MEP 17

RESULT 50

I52614
 u-plasminogen activator receptor precursor - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
 C;Accession: I52614
 R;Soravia, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.
 Blood 86, 624-635, 1995
 A;Title: A conserved TATA-less proximal promoter drives basal transcription from the u-plasminogen activator receptor

A;Reference number: I52614; MUID:95329719; PMID:7605992
 A;Accession: I52614
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-18 <RES>

A;Cross-references: GB:S78532; NID:g999307; PIDN:AAD14289.1; PID:g4261989
 C;Genetics:
 A;Gene: uPAR
 C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 17.6%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
|||
Db 5 PLL 7

RESULT 51
S46418
NTL1 protein - curled-leaved tobacco
C:Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 02-Aug-2002
C:Accession: S46418
R:Daniel-Vedele, F.; Caboche, M.
Mol. Gen. Genet. 240, 365-373, 1993
A:Title: A tobacco cDNA clone encoding a GATA-1 zinc finger protein homologous to regula
A:Reference number: S46418; MUID:94019241; PMID:8413186
A:Accession: S46418
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-18 <DNA>
A:Cross-references: EMBL:S65745
C:Superfamily: Arabidopsis thaliana GATA transcription factor 4

Query Match 17.6%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQ 5
|||
Db 5 TPQ 7

RESULT 52
S55002
protein 1 - Legionella pneumophila (fragment)
C:Species: Legionella pneumophila
C:Date: 23-Aug-1995 #sequence_revision 12-Apr-1996 #text_change 07-May-1999
C:Accession: S55002
R:Waik, Y.A.; Eisenstein, B.I.; Engleberg, N.C.
Infect. Immun. 61, 1320-1329, 1993
A:Title: Phenotypic modulation by Legionella pneumophila upon infection of macrophages.
A:Reference number: S55002; MUID:93202732; PMID:8454334
A:Accession: S55002
A:Molecule type: protein
A:Residues: 1-18 <KWA>

Query Match 17.6%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
|||
Db 10 PLL 12

RESULT 53
S10452
hypothetical protein (bpha 5' region) - Aspergillus niger
C:Species: Aspergillus niger
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1997
C:Accession: S10452
R:van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.; van Balken
submitted to the EMBL Data Library, March 1990
A:Reference number: S10452
A:Accession: S10452
A:Molecule type: DNA
A:Residues: 1-18 <VAN>
A:Cross-references: EMBL:X52521; NID:g2336; PID:g2337

Query Match 17.6%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
|||
Db 4 QPL 6

RESULT 54
B48408
21K high mobility group protein, hepatic (isoform 2) - Atlantic salmon (fragment)
C:Species: Salmo salar (Atlantic salmon)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 07-Feb-1997
C:Accession: B48408
R:Waters, S.; Khamis, M.; Von Der Decken, A.
Cell. Mol. Biol. 38, 783-789, 1992
A:Title: Purification of the Atlantic salmon hepatic 21 kDa protein and classification
A:Reference number: A48408
A:Accession: B48408
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <WAT>
C:Keywords: liver

Query Match 17.6%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
|||
Db 13 EPQ 15

RESULT 55
A61392
brain-associated small cell lung cancer antigen - human (fragment)
N:Alternate names: BASCA
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Sep-1994
C:Accession: A61392
R:Umezawa, Y.; Kuge, S.; Kikyo, N.; Shirai, T.; Watanabe, J.; Fujiwara, M.; Okabe, T.
Jpn. J. Clin. Oncol. 21, 251-255, 1991
A:Title: Identity of brain-associated small cell lung cancer antigen and the CD56 (NK)
A:Reference number: A61392; MUID:92046737; PMID:1719260
A:Accession: A61392
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <UME>

Query Match 17.6%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LQV 10
|||
Db 1 LQV 3

RESULT 56
D85601
hypothetical protein z1127 [imported] - Escherichia coli (strain O157:H7, substrain EI
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: D85601; E85652
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodac
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85601
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <STO>
A:Cross-references: GB:AE005174; NID:g12513923; PIDN:AA05272.1; GSPDB:GN00145; UWGP:Z

A;Experimental source: strain O157:H7, substrain EDL933
 A;Accession: E85652
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-18 <ST2>
 A;Cross-references: GB:AE005174; NID:g12514440; PIDN:AAG55681.1; GSPDB:GNO0145; UWGP:Z15
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: Z1127; Z1566

Query Match 17.6%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9

Db 3 LLQ 5

RESULT 57

I56393
 lacZ/IS1 mutant fusion protein - Escherichia coli (fragment)
 C;Species: Escherichia coli
 C;Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 19-May-2000
 C;Accession: I56393
 R;Malamy, M.H.; Rahaim, P.T.; Hoffman, C.S.; Baghdoyan, D.; O'Connor, M.B.; Miller, J.F.
 J. Mol. Biol. 181, 551-555, 1985
 A;Title: A frameshift mutation at the junction of an IS1 insertion within lacZ restores
 A;Reference number: I56393; MUID:85210885; PMID:2987506
 A;Accession: I56393
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-18 <MAL>
 A;Cross-references: GB:K03504; NID:g146583; PIDN:AAA24058.1; PID:g146584
 C;Keywords: fusion protein

Query Match 17.6%; Score 3; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QVM 11

Db 12 QVM 14

RESULT 58

C32735
 thyroglobulin - pig (fragment)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Apr-1997
 C;Accession: C32735
 R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.
 Biochem. Biophys. Res. Commun. 118, 423-429, 1984
 A;Title: The isolation of identical thyroxine containing amino acid sequences from bovin
 A;Reference number: C32735; MUID:84153804; PMID:6704086
 A;Accession: C32735
 A;Status: preliminary
 A;Molecule type: protein

A;Residues: 1-19 <RAW>
 C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homol
 C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
 F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 17.6%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7

Db 10 QPL 12

RESULT 59

B32735
 thyroglobulin - sheep (fragment)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Apr-1997
 C;Accession: B32735
 R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.
 Biochem. Biophys. Res. Commun. 118, 423-429, 1984
 A;Title: The isolation of identical thyroxine containing amino acid sequences from bo
 A;Reference number: A32735; MUID:84153804; PMID:6704086
 A;Accession: B32735
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-19 <RAW>
 C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat ho
 C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
 F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 17.6%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7

Db 10 QPL 12

RESULT 60

PQ0548
 capsid protein VP26 - human herpesvirus 1 (fragment)
 C;Species: human herpesvirus 1
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C;Accession: PQ0548
 R;Davison, M.D.; Rixon, F.J.; Davison, A.J.
 J. Gen. Virol. 73, 2709-2713, 1992
 A;Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herp
 A;Reference number: PQ0544; MUID:93019027; PMID:1328483
 A;Accession: PQ0548
 A;Molecule type: protein
 A;Residues: 1-19 <DAV>
 A;Experimental source: strain 17
 C;Genetics:
 A;Gene: UL35
 C;Keywords: capsid protein

Query Match 17.6%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16

Db 15 PQG 17

RESULT 61

S29766
 cytochrome c (EDH) - Pseudomonas aeruginosa
 C;Species: Pseudomonas aeruginosa
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
 C;Accession: S29766
 R;Schrover, J.M.J.; Frank, J.; van Wierlink, J.E.; Duine, J.A.
 Biochem. J. 290, 123-127, 1993
 A;Title: Quaternary structure of quinoprotein ethanol dehydrogenase from Pseudomonas
 A;Reference number: S29766; MUID:93176105; PMID:8382472
 A;Accession: S29766
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-19 <SCH>

Query Match 17.6%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPG 5

```

Db          |||
           5 TPQ 7

Query Match      17.6%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 62
S63489
disseminatory sulfite reductase alpha chain, membrane-bound - Desulfovibrio desulfuricans
C:Species: Desulfovibrio desulfuricans
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S63489
R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
Eur. J. Biochem. 233, 873-879, 1995
A:Title: Molecular properties of the disseminatory sulfite reductase from Desulfovibrio
A:Reference number: S63489; MUID:96085152; PMID:8521853
A:Accession: S63489
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <STE>

Query Match      17.6%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          6 PLL 8
           |||
           6 PLL 8

RESULT 63
A48408
21K high mobility group protein, hepatic (isoform 1) - Atlantic salmon (fragment)
C:Species: Salmo salar (Atlantic salmon)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 07-Feb-1997
C:Accession: A48408
R:Waters, S.; Khamis, M.; Von Der Decken, A.
Cell. Mol. Biol. 38, 783-789, 1992
A:Title: Purification of the Atlantic salmon hepatic 21 kDa protein and classification a
A:Reference number: A48408
A:Accession: A48408
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <WAT>
C:Keywords: liver

Query Match      17.6%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          13 EPQ 15
           |||
           14 EPQ 16

RESULT 64
I39327
pre-T/NK cell-associated protein 1D12A2 - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I39327
R:Panes-Goldberg, M.G.; Hori, T.; Mohan-Peterson, S.; Spits, H.
J. Immunol. 151, 5810-5821, 1993
A:Title: Identification of human pre-T/NK cell-associated genes.
A:Reference number: I39327; MUID:94044805; PMID:8228263
A:Accession: I39327
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:I17325; NID:g306322; PIDN:AAA16780.1; PID:g306323
C:Genetics:
A:Gene: GDB:PTNKAP1
A:Cross-references: GDB:5507882
A:Map position: 8p21-8p11.2

```

```

Query Match      17.6%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 LQT 3
           |||
           14 LQT 16

RESULT 65
A34467
36K microfibril-associated protein - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 18-Jun-1993
C:Accession: A34467
R:Kobayashi, R.; Tashima, Y.; Masuda, H.; Shozawa, T.; Nunata, Y.; Miyauchi, K.; Hayak
J. Biol. Chem. 264, 17437-17444, 1989
A:Title: Isolation and characterization of a new 36-kDa microfibril-associated glycop
A:Reference number: A34467; MUID:90008913; PMID:2793866
A:Accession: A34467
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <KOB>

Query Match      17.6%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          5 QPL 7
           |||
           16 QPL 18

RESULT 66
A60822
cytochrome P450 PB-3a - rat (fragment)
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Jun-1999
C:Accession: A60822; 155191
R:Ameliazad, Z.; Narbonne, J.F.; Wolf, C.R.; Robertson, L.W.; Oesch, F.
Biochem. Pharmacol. 37, 3245-3249, 1988
A:Title: Effect of nutritional imbalances on cytochrome P-450 isozymes in rat liver.
A:Reference number: A60822; MUID:88293549; PMID:3041969
A:Accession: A60822
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <AME>
R:Hashimoto, T.; Matsumoto, T.; Nishizawa, M.; Kawabata, S.
J. Biochem. 103, 487-492, 1988
A:Title: A mutant rat strain deficient in induction of a phenobarbital-inducible form
A:Reference number: 155191; MUID:88273074; PMID:2839467
A:Accession: 155191
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-20 <RES>
A:Cross-references: GB:D00250; NID:g220727; PIDN:BAA00181.1; PID:g220728
C:Superfamily: human cytochrome P450 CYP2B6; cytochrome P450 homology
C:Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane prot

Query Match      17.6%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          12 MEP 14
           |||
           1 MEP 3

RESULT 67
A39328
norechis II-5b nontoxic venom protein - common tiger snake (fragment)
C:Species: Notechis scutatus scutatus (common tiger snake, mainland tiger snake)

```

C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 30-Sep-1993
 C;Accession: A39328
 R;fang, C.C.; Chang, L.S.; Wu, F.S.
 Toxicon 29, 1337-1344, 1991
 A;Title: Venom constituents of Notochis scutatus (Australian tiger snake) from
 A;Reference number: A39328; PMID:92263371; PMID:1814009
 A;Accession: A39328
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <YAN>
 C;Superfamily: phospholipase A2

Query Match 17.6%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
 |||
 Db 17 QPL 19

RESULT 68
 PH0111

style glycoprotein S3 - garden petunia (fragment)
 C;Species: Petunia x hybrida (garden petunia)
 C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 20-Apr-2001
 C;Accession: PH0111
 R;Broothaerts, W.J.; van Laere, A.; Witters, R.; Preaux, G.; Decock, B.; van Damme, J.;
 Plant Mol. Biol. 14, 93-102, 1990
 A;Title: Purification and N-terminal sequencing of style glycoproteins associated with s
 A;Reference number: PH0109; PMID:91322492; PMID:2101314
 A;Accession: PH0111
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <BRO>
 C;Superfamily: Enterobacter ribonuclease

Query Match 17.6%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
 |||
 Db 4 LLQ 6

RESULT 69

A05313
 apolipoprotein A-I - red quonon (fragment)
 N;Alternate names: apo-A-I
 C;Species: Erythrocebus patas (red quonon, hussar)
 C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 11-May-2000
 C;Accession: A05313
 R;Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.
 Biochemistry 15, 1928-1933, 1976
 A;Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus
 A;Reference number: A90395; PMID:76184721; PMID:178359
 A;Accession: A05313
 A;Molecule type: protein
 A;Residues: 1-20 <MAH>
 C;Superfamily: apolipoprotein A-I
 C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipop

Query Match 17.6%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTP 4
 |||
 Db 5 QTP 7

RESULT 70

JN0252

water-soluble 35K protein - soybean (fragment)
 C;Species: Glycine max (soybean)
 C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 23-Mar-1995
 C;Accession: JN0252
 R;Akhtaruzzaman, M.; Kimura, Y.; Takagi, S.
 Biosci. Biotechnol. Biochem. 56, 873-878, 1992
 A;Title: Glycinin A4A5 subunit digesting protease in soybean seeds.
 A;Reference number: JN0252
 A;Accession: JN0252
 A;Molecule type: protein
 A;Residues: 1-20 <AKH>
 A;Experimental source: seed
 C;Superfamily: glycinin

Query Match 17.6%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
 |||
 Db 16 EPQ 18

RESULT 71

S08605
 hypothetical protein 1 estrogen receptor 5'-region - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 18-Aug-2000
 C;Accession: S08605
 R;Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.
 EMBO J. 5, 891-897, 1986
 A;Title: The chicken estrogen receptor sequence: homology with v-erbA and the human
 A;Reference number: S07192; PMID:86247578; PMID:3755102
 A;Accession: S08605
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-20 <KRU>
 A;Cross-references: EMBL:X03805; NID:G63378; PIDN:CAA27431.1; PID:G63379
 A;Note: the authors translated the codon TTT for residue 5 as Gly and TTC for residue
 C;Superfamily: unassigned leader peptides

Query Match 17.6%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
 |||
 Db 11 EPQ 13

RESULT 72

PL0039
 outer membrane protein C class 5 - Neisseria meningitidis (fragment)
 C;Species: Neisseria meningitidis
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1993
 C;Accession: PL0039
 R;Achtman, M.; Neibert, M.; Crowe, B.A.; Strittmatter, W.; Kusecek, B.; Weyse, E.; Wa
 J. Exp. Med. 168, 507-525, 1988
 A;Title: Purification and characterization of eight class 5 outer membrane protein va
 A;Reference number: PL0038; PMID:88316168; PMID:2457646
 A;Accession: PL0039
 A;Molecule type: protein
 A;Residues: 1-20 <ACH>
 A;Note: residues 17-18 are probably Lys-Ser
 C;Comment: The Neisseria meningitidis class 5 proteins are proposed to correspond to
 C;Keywords: membrane protein

Query Match 17.6%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3

Query Match 17.6%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTP 4
|||
Db 8 QTP 10

Search completed: November 25, 2003, 18:28:13
Job time : 17.6436 secs

Db 4 LQT 6
|||
RESULT 73
I64036
Hypothetical protein HI1571 - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998
C/Accession: I64036
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
R/Fleischmann, R.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:95350630; PMID:7542800
A/Accession: I64036
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-20 <TIGR>
A/Cross-references: GB:U32831; GB:L42023; NID:G1574407; PID:G1574420; TIGR:HI1571
C/Genetics:
A/Start codon: GTG

Query Match 17.6%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPQ 15
|||
Db 16 EPQ 18

RESULT 74
S63490
dissimilatory sulfite reductase alpha chain, soluble - Desulfovibrio desulfuricans (frag
C/Species: Desulfovibrio desulfuricans
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C/Accession: S63490
R/Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
Eur. J. Biochem. 233, 873-879, 1995
A/Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio
A/Reference number: S63489; MUID:96085152; PMID:8521853
A/Accession: S63490
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-20 <STE>

Query Match 17.6%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLL 8
|||
Db 6 PLL 8

RESULT 75
D56046
urinary tract stone matrix protein 6, 15K - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 12-Apr-1995
C/Accession: D56046
R/Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.
submitted to the Protein Sequence Database, February 1995
A/Description: Isolation, characterization and sequence of stone proteins.
A/Reference number: A56046
A/Accession: D56046
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-20 <BIN>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 8.22872 Seconds
(without alignments)
97.154 Million cell updates/sec

Title: US-09-641-801-2

Perfect score: 17

Sequence: 1 LQTQPQLQVMMEPQGD 17

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	17.6	9	1	AL10 CARMA
2	3	17.6	9	1	FAR1 CALVO
3	3	17.6	9	1	OXYT_RAJCL
4	3	17.6	9	1	RT33_BOVIN
5	3	17.6	10	1	FAR6_PANRE
6	3	17.6	10	1	RT02_BOVIN
7	3	17.6	11	1	CEPI_ACHFU
8	3	17.6	11	1	RANC_RANPI
9	3	17.6	12	1	FIFI_SARBU
10	3	17.6	13	1	ACT7_SOYEN
11	3	17.6	13	1	CRBL_ICASP
12	3	17.6	13	1	LPAA_PORGI
13	3	17.6	15	1	ARCA_STRP5
14	3	17.6	15	1	UC30_MAIZE
15	3	17.6	16	1	PA21_TPIST
16	3	17.6	17	1	ACT6_SOYEN
17	3	17.6	17	1	B29K_PORGI
18	3	17.6	17	1	PSBL_SYNYU
19	3	17.6	18	1	ALBG_EQUAS
20	3	17.6	20	1	AP1G_EQUAS
21	3	17.6	20	1	APAI_ERYPA
22	3	17.6	20	1	OMPW_VIBAL
23	3	17.6	20	1	SCBI_CANFA
24	3	17.6	20	1	OCPI_OCTMI
25	2	11.8	4	1	RM01_YEAST
26	2	11.8	5	1	UXA4_CHLTR
27	2	11.8	6	1	ACPI_RABIT
28	2	11.8	6	1	VP19_HSVIK
29	2	11.8	7	1	ALL3_CARMA
30	2	11.8	7	1	E105_LITRU
31	2	11.8	7	1	FAR1_HELTI
32	2	11.8	7	1	GFRP_MOUSE
33	2	11.8	7	1	LANC_CARUI

34	2	11.8	7	1	MNP1_LEPDE
35	2	11.8	7	1	PPH2_LYCES
36	2	11.8	7	1	UH11_RAT
37	2	11.8	7	1	ACI_THUAL
38	2	11.8	8	1	AKHG_GRYBI
39	2	11.8	8	1	AKH_LIBAU
40	2	11.8	8	1	AKH_TABAT
41	2	11.8	8	1	ALL6_CYDPO
42	2	11.8	8	1	COM2_CONPU
43	2	11.8	8	1	CPD1_ENTFA
44	2	11.8	8	1	FAR1_PENMO
45	2	11.8	8	1	HTF1_PERAM
46	2	11.8	8	1	HTF2_PERAM
47	2	11.8	8	1	LCK3_LEUMA
48	2	11.8	8	1	LMT2_LOCMI
49	2	11.8	8	1	LPK_LEUMA
50	2	11.8	8	1	NFB_BOVIN
51	2	11.8	8	1	UC26_MAIZE
52	2	11.8	8	1	UF06_MOUSE
53	2	11.8	8	1	WP1_PERAT
54	2	11.8	8	1	BUK_CLOPA
55	2	11.8	9	1	CONV_CONVE
56	2	11.8	9	1	COKE_THUOB
57	2	11.8	9	1	DSIP_RABIT
58	2	11.8	9	1	FAR2_CALVO
59	2	11.8	9	1	FAR3_PENMO
60	2	11.8	9	1	FAR4_PENMO
61	2	11.8	9	1	FAR9_ASCSU
62	2	11.8	9	1	FARA_CALVO
63	2	11.8	9	1	FRP1_SARBU
64	2	11.8	9	1	KNL3_BOMVA
65	2	11.8	9	1	LMT3_LOCMI
66	2	11.8	9	1	MGMT_BOVIN
67	2	11.8	9	1	OXYA_SQUAC
68	2	11.8	9	1	OXYT_RABIT
69	2	11.8	9	1	PPH1_LYCES
70	2	11.8	9	1	RE42_LITRU
71	2	11.8	9	1	TAL1_PICUA
72	2	11.8	9	1	TAL3_PICUA
73	2	11.8	9	1	THYF_PIG
74	2	11.8	9	1	UF02_MOUSE
75	2	11.8	9	1	ULAD_HUMAN
76	2	11.8	9	1	UPA3_HUMAN
77	2	11.8	9	1	UPA6_HUMAN
78	2	11.8	10	1	AKHX_LOCMI
79	2	11.8	10	1	BPE2_BOTIN
80	2	11.8	10	1	BPE2_BOTJA
81	2	11.8	10	1	BPP_VIPAS
82	2	11.8	10	1	BRK_ONCMY
83	2	11.8	10	1	COMX_RAT
84	2	11.8	10	1	COXQ_RABIT
85	2	11.8	10	1	COXQ_SHEEP
86	2	11.8	10	1	CU30_LOCMI
87	2	11.8	10	1	FAR5_MACRS
88	2	11.8	10	1	FAR7_MACRS
89	2	11.8	10	1	FARP_MYTED
90	2	11.8	10	1	GONI_ILLMI
91	2	11.8	10	1	HTF1_ROMMI
92	2	11.8	10	1	HTF2_CARMO
93	2	11.8	10	1	HTF_NAUCI
94	2	11.8	10	1	HTF_TABAT
95	2	11.8	10	1	LPK2_LOCMI
96	2	11.8	10	1	NSI_MYCTU
97	2	11.8	10	1	PNEU_HUMAN
98	2	11.8	10	1	PNEU_RAT
99	2	11.8	10	1	TEMK_RANTE
100	2	11.8	10	1	TKL2_LOCMI

ALIGNMENTS

RESULT 1

```
AL10_CARMA
ID AL10_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas (Common shore crab) (Green crab).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RX "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
R Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 963 MW; 372D79CDBC4776C7 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQP 6
DB 2 PQP 4

RESULT 2
FARI_CALVO
ID FARI_CALVO STANDARD; PRT; 9 AA.
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliphorFamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX TIGSUB=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Renfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliphorFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARI (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW PIR; A41978; A41978.
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQ 5

AL10_CARMA
ID AL10_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas (Common shore crab) (Green crab).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RX "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
R Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 963 MW; 372D79CDBC4776C7 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQP 6
DB 2 PQP 4

RESULT 2
FARI_CALVO
ID FARI_CALVO STANDARD; PRT; 9 AA.
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliphorFamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX TIGSUB=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Renfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliphorFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARI (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW PIR; A41978; A41978.
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQ 5

us-09-641-801-2.oligo.rsp
Db 1 TPQ 3

RESULT 3
OXYT_RAJCL
ID OXYT_RAJCL STANDARD; PRT; 9 AA.
AC P42994;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glumitocin.
OS Raja clavata (Thornback ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hymnosqualea; Pristiogaster; Batoidea;
OC Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=7781;
RN [1]
RP SEQUENCE.
RX MEDLINE=66123415; PubMed=5880565;
RX Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RA "Phylogeny of neurophyseal peptides: isolation of a new hormone,
RT glumitocin (Ser 4-Gln 8-cytocin) present in a cartilaginous fish,
RT the ray (Raja clavata).";
RL Biochim. Biophys. Acta 107:393-396(1965).
CC -!- FUNCTION: ANTIDIURETIC HORMONE
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
KW PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 984 MW; 17E9C76EB455B04B CRC64;

Query Match 17.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQQ 16
DB 7 PQQ 9

RESULT 4
RT33_BOVIN
ID RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRPS33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrion.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;
```


Query Match 17.6%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
 Db 5 QPL 7

RESULT 5

ID FAR6 PANRE STANDARD; PRT; 10 AA.
 AC P82650;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of RMRamide-related
 RT peptides (FARs) from free-living nematode, Panagrellus redivivus.";
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.
 CC -!- FUNCTION: MYOACTIVE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMR/AMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 10 10
 FT SEQUENCE 10 AA; 1132 NW; CB13E4C9D776C76D CRC64;

Query Match 17.6%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQP 6
 Db 4 PQP 6

RESULT 6

ID RT02 BOVIN STANDARD; PRT; 10 AA.
 AC P82923;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).
 GN MRPS2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Liver;
 RX MEDLINE=21276436; PubMed=11279123;
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
 RT "The small subunit of the mammalian mitochondrial ribosome:
 RT identification of the full complement of ribosomal proteins present.";
 RL J. Biol. Chem. 276:119363-119374(2001).
 CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR001865; Ribosomal_S2.
 DR Pfam: PF00318; Ribosomal_S2; PARTIAL.

DR PROSITE; PS00962; RIBOSOMAL S2 1; PARTIAL.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1246 MW; 6A7A6679C04B476B CRC64;

Query Match 17.6%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MEP 14
 Db 2 MEP 4

RESULT 7

CEPI1 ACHFV STANDARD; PRT; 11 AA.
 ID CEPI1 ACHFV STANDARD; PRT; 11 AA.
 AC P22750;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Cardio-excitatory peptide-1 (ACEP-1).
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Ferussac; TISSUE=Heart atrium;
 RX MEDLINE=90211261; PubMed=2322251;
 RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
 RT "A novel cardio-excitatory peptide isolated from the atria of the
 RT African giant snail, Achatina fulica.";
 RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
 CC -!- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
 CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
 CC MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE
 CC MOVEMENT OF ACHATINA.
 CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
 DR PIR; A34662; A34662.
 KW Hormone; Amidation.
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 POG 16
 Db 7 POG 9

RESULT 8

RANC_RANPI STANDARD; PRT; 11 AA.
 ID RANC_RANPI STANDARD; PRT; 11 AA.
 AC P08951;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ranatensin-C.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=84131098; PubMed=6141890;
 RA Nakajima T.;
 RL Unpublished results, cited by:
 RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;

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RL Comp. Biochem. Physiol. 77C:99-108(1984).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY
DR InterPro: IPR000874; Bombesin.
DR Pfam: PF02044; Bombesin; 1.
DR PROSITE: PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation.
FT MOD_RES 11
FT SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;
SQ
Query Match 17.6%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TPQ 5
Db 2 TPQ 4
RESULT 9
FIFI_SARBU STANDARD; PRT; 12 AA.
ID -FIFI_SARBU
AC P83349;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FIRamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
CC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=2242733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRFamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FPRP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 12
FT SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;
SQ
Query Match 17.6%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PQP 6
Db 3 PQP 5
RESULT 10
ACT7_SOYBN STANDARD; PRT; 13 AA.
ID -ACT7_SOYBN
AC P15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 7 (Fragment).
GN SAC7.
OS Glycine max (Soybean).
CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wayne;
RX MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5',
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: Belongs to the actin family.
CC
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CC
CC EMBL: X17120; CAA34980.1; -
CC PIR: S15755; S15755.
CC InterPro: IPR004001; Actin.
CC InterPro: IPR004000; Actin_like.
CC PROSITE: PS00406; ACTINS 1; PARTIAL.
CC PROSITE: PS00432; ACTINS 2; PARTIAL.
CC PROSITE: PS01132; ACTINS_ACT LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON_TER 13
FT SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;
SQ
Query Match 17.6%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QPL 7
Db 8 QPL 10
RESULT 11
CRBL_ICASP STANDARD; PRT; 13 AA.
ID -CRBL_ICASP
AC P17237;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chemotactic peptide (I-CPI).
OS Icaria sp. (Ropalidian wasp).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
CC Vespidae; Polistinae; Icaria.
OX NCBI_TaxID=7495;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RA (In) Izumiya N. (eds.);
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,
RL Osaka (1985).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
CC Mast cell degranulation; Chemotaxis; Amidation.
KW MOD_RES 13
FT MOD_RES 13

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SQ SEQUENCE 13 AA; 1353 MW; 348DBC7AA30A3768 CRC64;
Query Match 17.6%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
Db |||
7 PLL 9

RESULT 12
LPAA_PORGI
ID LPAA_PORGI STANDARD; PRT; 13 AA.
AC P81411;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Lipid-A-associated protein (Fragment).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE.
RC STRAIN=W50;
RX MEDLINE=99061194; PubMed=9846737;
RA Sharp L., Poole S., Reddi K., Fletcher J., Nair S., Wilson M.,
RA Curtis M., Henderson B., Tabona P.;
RT "A lipid A-associated protein of Porphyromonas gingivalis, derived
RT from the haemagglutinating domain of the RI protease gene family, is
RT a potent stimulator of interleukin 6 synthesis.";
RL Microbiology 144:3019-3026(1998).
CC -!- FUNCTION: IS ASSOCIATED WITH LIPID A, A PHOSPHORYLATED GLYCOLIPID
CC THAT ANCHORS THE LIPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE
CC CELL.
FT VARIANT 12 12 G -> F.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1346 MW; 38EA796EAF6A63AB7 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QGD 17
Db |||
2 QGD 4

RESULT 13
ARCA_STRF5
ID ARCA_STRF5 STANDARD; PRT; 15 AA.
AC P58827;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD)
DE (Streptococcal acid glycoprotein) (Fragment).
GN ARCA OR SAGP.
OS Streptococcus pyogenes (serotype M5).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=160491;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=Manfredo / Serotype M5;
RX MEDLINE=98298018; PubMed=9632565;
RA Degnan B.A., Palmer J.M., Robson T., Jones C.B.D., Fischer M.,
RA Glanville M., Mellor G.D., Diamond A.G., Kehoe M.A., Goodacre J.A.;
RT "Inhibition of human peripheral blood mononuclear cell proliferation
RT by Streptococcus pyogenes cell extract is associated with arginine
RT deiminase activity.";
RL Infect. Immun. 66:3050-3058(1998).

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CC -!- FUNCTION: Antitumor protein. Has a powerful and dose-dependent
CC inhibitory effect on antigen, superantigen, or mitogen-stimulated
CC human peripheral blood mononuclear cell (PBMC) proliferation. It
CC may inhibit cell proliferation by arresting cell cycle and
CC inducing apoptosis.
CC -!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).
CC -!- PATHWAY: Arginine degradation via arginine deiminase; first step.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the arginine deiminase family.
DR HAMAP; MF_00242; -; 1.
KW Hydrolase; Arginine metabolism; Glycoprotein.
FT INIT_MET 0
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1657 MW; D21150201B00EB46 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTP 4
Db |||
3 QTP 5

RESULT 14
UC30_MAIZE
ID UC30_MAIZE STANDARD; PRT; 15 AA.
AC P80636;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 662)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 32.3 kDa.
DR Maize-2DPAGE; P80636; COLEOPTILE.
DR MaizeDB; 123961; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1545 MW; 3485190F4EF38018 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
Db |||
5 PLL 7

RESULT 15
PA21_TRIST
ID PA21_TRIST STANDARD; PRT; 16 AA.
AC P82892;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2, basic 1 (EC 3.1.1.4) (PA2-I) (PLA2-I)
DE (Phosphatidylcholine 2-acylhydrolase) (Fragment).

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OS Trimeresurus stejnegeri (Chinese green tree viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OC NCBI_TaxID=39682;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Li S.Y., Wang W.Y., Xiong Y.L.;
 RT "Isolation, sequence and characterization of five variants of
 RT phospholipase A2 from venom of snake Trimeresurus stejnegeri.";
 RL Submitted (DEC-2000) to the SWISS-PROT data bank.
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP II
 CC SUBFAMILY.
 DR InterPro: IPR001211; PhospholipaseA2.
 DR PROSITE: PS00119; PA2 ASP; PARTIAL.
 DR PROSITE: PS00118; PA2 HIS; PARTIAL.
 KW Hydrolase; Lipid degradation; Calcium; Multigene family.
 FT NON TER 16 16
 SQ SEQUENCE 16 AA; 2012 MW; 4EF2D4959E981117 CRC64;
 Query Match 17.6%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 LLQ 9
 Db 2 LLQ 4
 RESULT 16
 ID ACT6_SOYEN STANDARD; PRT; 17 AA.
 AC P15986;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Actin 6 (Fragment).
 GN SAG6.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OC NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Wayne;
 RX MEDLINE=91346640; PubMed=2102831;
 RA Pearson L., Meagher R.B.;
 RT "Diverse soybean actin transcripts contain a large intron in the 5'
 RT untranslated leader: structural similarity to vertebrate muscle actin
 RT genes.";
 RL Plant Mol. Biol. 14:513-526(1990).
 CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
 CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
 CC IN ALL EUKARYOTIC CELLS.
 CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
 CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
 CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
 CC -!- SIMILARITY: Belongs to the actin family.
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 CC -----
 CC EMBL; X17119; CAA34979.1; -.
 DR DR PIR; S15754; S15754.
 DR InterPro: IPR004001; Actin.
 DR InterPro: IPR004000; Actin_like.
 DR Pfam: PF00022; actin; 1.
 DR PROSITE: PS00406; ACTINS_1; PARTIAL.
 DR PROSITE: PS00432; ACTINS_2; PARTIAL.
 DR PROSITE: PS01132; ACTINS_ACT LIKE; PARTIAL.
 KW Structural protein; Multigene family.
 FT NON TER 17 17
 SQ SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;
 Query Match 17.6%; Score 3; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 QPL 7
 Db 8 QPL 10
 RESULT 17
 ID B29K_PORGI STANDARD; PRT; 17 AA.
 AC P81784;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 29 kDa immunogenic protein (Fragment).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OC NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=VEB 3547;
 RX MEDLINE=20198497; PubMed=10731616;
 RA Norris J.M., Love D.N.;
 RT "Serum antibody responses of cats to soluble whole cell antigens of
 RT feline Porphyromonas gingivalis.";
 RL Vet. Microbiol. 73:37-49(2000).
 KW Antigen.
 FT NON TER 17 17
 SQ SEQUENCE 17 AA; 1756 MW; 383DE6AA14331AE0 CRC64;
 Query Match 17.6%; Score 3; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 15 QGD 17
 Db 14 QGD 16
 RESULT 18
 ID PSBL_SYNVU STANDARD; PRT; 17 AA.
 AC P12241;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Photosystem II reaction center L protein (PSII 5 kDa protein)
 DE (Fragment).
 GN PSBL.
 OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
 OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
 OC NCBI_TaxID=32053;
 RN [1]
 RP SEQUENCE.

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RA Ikeuchi M., Koike H., Inoue Y.;
RT "Identification of psbI and psbL gene products in cyanobacterial
RT photosystem II reaction center preparation.";
RL FEBS Lett. 251:155-160(1989).
CC -!- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME
CC B559.
CC -!- SIMILARITY: BELONGS TO THE PSBL FAMILY.
DR PIR: S05033; S05033.
DR InterPro: IPR003372; PSII_PsBL.
DR Pfam: PF02419; PsbL; I.
KW Photosynthesis; Photosystem II.
FT NON_TER 17
FT SEQUENCE 17 AA; 2018 MW; A86FD372B70B9847 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MEP 14
Db 1 MEP 3

RESULT 19
UC03_MAIZE
ID_UC03_MAIZE STANDARD; PRT; 18 AA.
AC P80609;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 146)
DE (Fragments).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
CX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.1, ITS MW IS: 29.3 kDa.
CC -!- CAUTION: THE ORDER OF THE PEPTIDES SHOWN IS UNCERTAIN.
DR Maize-2DPAGE; P80609; COLEOPTILE.
DR MaizeDB; 123924; -.
FT NON_TER 1
FT NON_CONS 9 10
FT NON_TER 18 18
FT SEQUENCE 18 AA; 1938 MW; 6F513BBEC35881C0 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQ 9
Db 5 LLQ 7

RESULT 20
AIBG_EQUAS
ID_AIBG_EQUAS STANDARD; PRT; 20 AA.
AC P39030;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-1B-glycoprotein (Alpha-1-B glycoprotein) (Postalbumin)
DE (Fragment).

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GN AIBG.
OS Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
CX NCBI_TaxID=9793;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=91330579; PubMed=1868686;
RA Patterson S.D., Bell K., Shaw D.C.;
RT "Donkey and horse alpha 1 B-glycoprotein: partial characterization
RT and new alleles.";
RL Comp. Biochem. Physiol. 98B:523-528(1991).
CC -!- FUNCTION: Unknown.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
KW Immunoglobulin domain; Glycoprotein; Plasma.
FT NON_TER 20
FT SEQUENCE 20 AA; 2197 MW; 65857DFDA68EBD9F CRC64;

Query Match 17.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 POP 6
Db 6 POP 8

RESULT 21
APAL_ERYPA
ID_APAL_ERYPA STANDARD; PRT; 20 AA.
AC P18647;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apolipoprotein A-I (Apo-AI) (Fragment).
GN APOA1
OS Erythrocytes patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Erythrocybus.
CX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RX MEDLINE=76184721; PubMed=178359;
RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
RT "Characterization of the plasma lipoproteins and apoproteins of the
RT Erythrocybus patas monkey.";
RL Biochemistry 15:1928-1933(1976).
CC -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
DR PIR; A05313; A05313.
KW Plasma; Lipid transport; HDL; Cholesterol metabolism.
FT NON_TER 20
FT SEQUENCE 20 AA; 2387 MW; 9C970997C7FC976A CRC64;

Query Match 17.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTP 4
Db 5 QTP 7

RESULT 22

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OMPW VIBAL
ID OMPW VIBAL STANDARD; PRT; 20 AA.
AC P83151;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein W (Outer membrane protein 25Va) (Omp25Va)
DE (Fragment).
GN OMPW.
OS Vibrio alginolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=663;
RN [1]_TaxID=663;
RP SEQUENCE.
RC STRAIN=NCIMB 1903T;
RA Onji M., Hirabayashi J., Suzuki S.;
RT "Characterization of major outer membrane proteins of Vibrio
alginolyticus and the stability against proteases.";
RL Microbes Environ. 0:0-0(2002).
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- SIMILARITY: BELONGS TO THE OMPW/ALKL FAMILY.
KW Outer membrane.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2096 MW; D29EE7FCA16C0D37 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QGD 17
DB |||
3 QGD 5

RESULT 23
SCB1 CANFA
ID SCB1 CANFA STANDARD; PRT; 20 AA.
AC P99507;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial
DE (EC 6.2.1.5) (Succinyl-CoA synthetase, betaA chain) (SCS-betaA) (ATP-
specific succinyl-CoA synthetase beta subunit) (fragment).
GN SUCLA2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]_TaxID=9615;
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- CATALYTIC ACTIVITY: ATP + succinate + CoA = ADP + succinyl-CoA +
phosphate.
CC -!- PATHWAY: SUBSTRATE LEVEL PHOSPHORYLATION STEP OF THE TRICARBOXYLIC
ACID CYCLE.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC -!- SIMILARITY: Belongs to the succinate/malate CoA ligase beta
subunit family.
DR HSC-2DPAGE; P99507; DOG.
DR InterPro; IPR005809; CoA_lig_beta.
DR PROSITE; PS01217; SUCCINYL-CoA_lig_3; PARTIAL.
KW Ligase; Glycolysis; Tricarboxylic acid cycle; Mitochondrion.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2248 MW; BE9AEFD54DBDAC2E CRC64;
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Query Match 17.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
DB |||
11 LLQ 13

RESULT 24
OCPI OCTMI
ID OCPI OCTMI STANDARD; PRT; 4 AA.
AC P58648;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-1/Ocp-2.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
inotropic effects on the heart. Ocp-2 is a 1000 time less
active than Ocp-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=WALDI.
KW Hormone; D-amino acid.
FT MOD_RES 2
2 D-PHENYLALANINE.
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810C00000 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GD 17
DB |||
3 GD 4

RESULT 25
RM01 YEAST
ID RM01 YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]_TaxID=4932;
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56(1991).
DR FIR; S17255; S17255.
DR SGD; L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4
4
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SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;
  Query Match 11.8%; Score 2; DB 1; Length 4;
  Best Local Similarity 100.0%; Pred. No. 1.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4
  ||
Db 3 TP 4

RESULT 26
UXXA4_CHLTR STANDARD; PRT; 5 AA.
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.,
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
DR Siena-2DPAGE; P38005; -.
FT NON_TER 5
SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;

  Query Match 11.8%; Score 2; DB 1; Length 5;
  Best Local Similarity 100.0%; Pred. No. 1.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GD 17
  ||
Db 3 GD 4

RESULT 27
ACPH_RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (BC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
DR APEH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=92222120; PubMed=1807161;
RA Krishna R.G., Chin C.C.Q., Wolf F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
RT unblocking with N-acylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199;45-50(1991).
CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
CC + peptide.
CC -!- SUBUNIT: Homotetramer.

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CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR PIR; A49792; A49792.
DR MEROPS; S09.004; -.
DR InterPro; IPR002471; Prol_endopep_ser.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 ACETYLATION.
FT NON_TER 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

  Query Match 11.8%; Score 2; DB 1; Length 6;
  Best Local Similarity 100.0%; Pred. No. 1.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QV 10
  ||
Db 4 QV 5

RESULT 28
VP19_HSV1K STANDARD; PRT; 6 AA.
ID VP19_HSV1K
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Capsid assembly and DNA maturation protein (Virion protein UL38)
DE (Capsid protein VP19C) (Fragment).
GN UL38.
OS Herpes simplex virus (type 1 / strain KOS).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxId=10306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly.";
RL J. Virol. 65;769-786(1991).
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
CC EMBEDDED. BINDS DNA.
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M57646; AAA45830.1; -.
KW Capsid assembly; Coat protein; DNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

  Query Match 11.8%; Score 2; DB 1; Length 6;
  Best Local Similarity 100.0%; Pred. No. 1.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
  ||
Db 5 PL 6

RESULT 29
ALL3_CARMA STANDARD; PRT; 7 AA.
ID ALL3_CARMA
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

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DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 3.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 SQ SEQUENCE 7 AA; 796 MW; 672879CDBC476B70 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EP 14
 Db 1 EP 2

RESULT 30
 E105_LITRU
 ID E105_LITRU STANDARD; PRT; 7 AA.
 AC P82101;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Electrin 5.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 KW Amphibian defense peptide; Amidation.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EP 14
 Db 3 EP 4

RESULT 31
 FAR1_HELTI
 ID FAR1_HELTI STANDARD; PRT; 7 AA.
 AC P41871;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE FMRFamide-like neuropeptide GDPFLRF-amide.
 OS Helisoma trivolvis (Snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Basommatophora;
 OC Lymnaeoidea; Planorbidae; Helisoma.
 OX NCBI_TaxID=27815;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
 RT trivolvis.";
 RL Peptides 15:31-36(1994).
 CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
 CC THE KIDNEY, MANTLE AND SKIN.
 CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GD 17
 Db 1 GD 2

RESULT 32
 GFRP_MOUSE
 ID GFRP_MOUSE STANDARD; PRT; 7 AA.
 AC P99025;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
 GN GCHFR OR GFRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
 RA Cowthorne M.;
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.
 CC -!- FUNCTION: MEDIATES TETRAHYDROBIOTRIN INHIBITION OF GTP
 CC CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
 CC (BY SIMILARITY).
 CC -!- SUBUNIT: Homodimer (By similarity).
 DR SWISS-2DPAGE; P99025; MOUSE.
 FT INIT MET 0
 FT NON TER 7
 SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LL 8
 Db 3 LL 4

RESULT 33
 LANC_CARUI
 ID LANC_CARUI STANDARD; PRT; 7 AA.
 AC P36960;

DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lantibiotic carnocin U149 (Fragment).
 OS Carnobacterium sp. (strain U149).
 OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
 OC Carnobacterium.
 OX NCBI_TaxID=35782;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=92321768; PubMed=1622206;
 RA Scoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
 RA Nes I.F.;
 RT "Purification and characterization of a new bacteriocin isolated from
 RT a Carnobacterium sp.";
 RL Appl. Environ. Microbiol. 58:1417-1422(1992).
 CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
 CC ACTIVE ON GRAM-POSITIVE BACTERIA.
 KW Antibiotic; Bacteriocin; Lantibiotic.
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;
 Query Match 11.8%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QP 6
 DB 5 QP 6
 RESULT 34
 MNP1 LEPOE
 ID MNP1 LEPOE STANDARD; PRT; 7 AA.
 AC P42984;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Myotropin neurotropic peptide 1 (Lad-MNP-I).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
 OC Chrysomelini; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=95380343; PubMed=7651886;
 RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
 RA Grauwels L., van Leuven F., de Loof A.;
 RT "Identification, characterization, and immunological localization of
 RT a novel myotropin neurotropic peptide in the Colorado potato beetle,
 RT Leptinotarsa decemlineata.";
 RL Peptides 16:365-374(1995).
 CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC OVIDUCT.
 KW Neurotropic; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;
 Query Match 11.8%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PL 7
 DB 5 PL 6
 RESULT 35
 PPH2 LYCES
 ID PPH2 LYCES STANDARD; PRT; 7 AA.

AC P83379;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Purple acid phosphatase isozyme LesAP2 (EC 3.1.1.3.2) (Fragment).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
 RP GLYCOSYLATION.
 RC STRAIN=cv. Moneymaker; TISSUE=Seed;
 RX MEDLINE=22361242; PubMed=12473124;
 RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
 RT "Purification and characterization of two secreted purple acid
 RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon
 RT esculentum) cell cultures.";
 RL Eur. J. Biochem. 269:6278-6286(2002).
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 CC alcohol + phosphate.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: Glycosylated.
 CC -!- MISCELLANEOUS: In L. esculentum there are at least two isozymes of
 CC purple acid phosphatase.
 KW Hydrolase; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;
 Query Match 11.8%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 GD 17
 DB 5 GD 6
 RESULT 36
 UH11 RAT
 ID UH11 RAT STANDARD; PRT; 7 AA.
 AC P56376;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Heart;
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
 RA Jungblut P.R.;
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 8.5, ITS MW IS: 42 kDa.
 FT UNSURE 2
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;
 Query Match 11.8%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 QG 16
 DB 6 QG 7

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RESULT 37
ACI_THUAL
ID ACI_THUAL STANDARD; PRT; 8 AA.
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415888;
RA Kohama Y., Matsunoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR; A31570; A31570.
SQ SEQUENCE 8 AA; 933 MW; 6AA863733051F1B7 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GD 17
Db 7 GD 8

RESULT 38
AKHG_GRYBI
ID AKHG_GRYBI STANDARD; PRT; 8 AA.
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
of a peptide with adipokinetic activity from the corpora cardiaca of
the cricket Gryllus bimaculatus.";
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR InterPro; IPR002047; AKH.
RN [1]

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DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 QV 10
Db 1 QV 2

RESULT 39
AKH_LIBAU
ID AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
concentrating hormone family isolated and sequenced from a
dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; S10596; S10596.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TP 4
Db 5 TP 6

RESULT 40
AKH_TABAT
ID AKH_TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
DE (DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]

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RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RCH FAMILY.
DR PR; A33995; A33995.
DR InterPro; IPRO02047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4
Db 5 TP 6

RESULT 41
ALL6_CVDPO
ID -ALL6_CVDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaastatin 6
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
Db 2 PL 3

RESULT 42
COW2_CONPU
ID -COW2_CONPU STANDARD; PRT; 8 AA.
AC P88785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RCH FAMILY.
DR PR; A33995; A33995.
DR InterPro; IPRO02047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4
Db 5 TP 6

RESULT 41
ALL6_CVDPO
ID -ALL6_CVDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaastatin 6
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
Db 2 PL 3

RESULT 42
COW2_CONPU
ID -COW2_CONPU STANDARD; PRT; 8 AA.
AC P88785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=99388899; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD RES 4 4 D-LEUCINE.
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LL 8
Db 4 LL 5

RESULT 43
CPD1_ENTFA
ID -CPD1_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cPDL.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cPDL.";
RL Science 226:849-850(1984).
CC -1- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOCIN PLASMID PPDL.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VM 11
Db 3 VM 4

RESULT 44
FARL_PENMO
ID -FARL_PENMO STANDARD; PRT; 8 AA.
AC P83316;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLPI (GDRNFLRP-amide).
```

OS Penaeus monodon (Pencoid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]_SEQUENCE, AND MASS SPECTROMETRY.
 RP TISSUE=Eyestalk;
 RC MEDLINE=21956277; PubMed=11959015;
 RX Sathigorngul P., Pupem J., Krungkarn C., Longyant S.,
 RA Chaivutikulangkura P., Sathigorngul W., Petsom A.;
 RA "Seven novel PMRamide-like neuropeptide sequences from the eyestalk
 of the giant tiger prawn *Penaeus monodon*.";
 RT Comp. Biochem. Physiol. 133B:325-337(2002).
 RL CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FAP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;
 Query Match 11.8%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 GD 17
 DB 1 GD 2
 RESULT 45
 HTF1_PERAM
 ID HTF1 PERAM STANDARD; PRT; 8 AA.
 AC P04548;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-I)
 DE (Pea-CAH-I) (LeD-CC-I) (Hypertrehalosaemic neuropeptide I).
 OS Periplaneta americana (American cockroach),
 OS Lepidoptera decemlineata (Colorado potato beetle), and
 Blatta orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 RN [1]_SEQUENCE.
 RP SPECIES=P.americana;
 RC MEDLINE=85046530; PubMed=6548628;
 RX Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L. Jr.;
 RA "Structures of two cockroach neuropeptides assigned by fast atom
 bombardment mass spectrometry.";
 RT Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]_SEQUENCE.
 RP SPECIES=P.americana;
 RC MEDLINE=84298179; PubMed=6591205;
 RX Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 cardioacceleratory and hyperglycemic activity from the corpora
 cardiaca of *Periplaneta americana*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]_SEQUENCE.
 RP SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RC MEDLINE=90160053; PubMed=2576128;
 RX Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiacum from the potato
 beetle and the American cockroach are identical.";

Peptides 10:1287-1289(1989).
 RL [4]_SEQUENCE.
 RP SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RC MEDLINE=90253659; PubMed=2340112;
 RX Gaede G., Rinehart K.L. Jr.;
 RA "Primary structures of hypertrehalosaemic neuropeptides isolated from
 the corpora cardiaca of the cockroaches *Leucophaea maderae*,
Gromphadorhina portentosa, *Blattella germanica* and *Blatta orientalis*
 and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
 atom bombardment mass spectrometry.";
 RT Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 RL CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A44960; A44960.
 DR PIR; A49823; A49823.
 DR PIR; S08995; S08995.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;
 Query Match 11.8%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 QV 10
 DB 1 QV 2
 RESULT 46
 HTF2_PERAM
 ID HTF2 PERAM STANDARD; PRT; 8 AA.
 AC P04549;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplanetin CC-2)
 DE (Pea-CAH-II) (LeD-CC-II) (Hypertrehalosaemic neuropeptide II).
 OS Periplaneta americana (American cockroach),
 OS Lepidoptera decemlineata (Colorado potato beetle), and
 Blatta orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 RN [1]_SEQUENCE.
 RP SPECIES=P.americana;
 RC MEDLINE=85046530; PubMed=6548628;
 RX Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L. Jr.;
 RA "Structures of two cockroach neuropeptides assigned by fast atom
 bombardment mass spectrometry.";
 RT Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]_SEQUENCE.
 RP SPECIES=P.americana;
 RC MEDLINE=84298179; PubMed=6591205;
 RX Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 cardioacceleratory and hyperglycemic activity from the corpora
 cardiaca of *Periplaneta americana*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]_SEQUENCE.
 RP SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RC MEDLINE=90160053; PubMed=2576128;
 RX Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiacum from the potato
 beetle and the American cockroach are identical.";

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RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiacum from the potato
RL beetle and the American cockroach are identical.";
RN Peptides 10:1287-1289(1989).
[4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrichosomic neuropeptides isolated from
RL the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -!- FUNCTION: HYPERTRICHOSOMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; B44960; B44960.
DR PIR; B49823; B49823.
DR PIR; S08996; S08996.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4
DB 5 TP 6

RESULT 47
LCX3 LEUMA STANDARD; PRT; 8 AA.
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin III (L.III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberiidae; Leucophaea.
OX NCBI_TaxID=6988;
[1]
RN SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RL from Leucophaea maderae: members of a new family of
RL Cephalomyotropeptides.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC -!- ACTIVITY OF COCKROACH PROTEIN (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QG 16
DB 5 TP 6

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Db 2 QG 3

RESULT 48
LMT2 LOCMI STANDARD; PRT; 8 AA.
ID LMT2 LOCMI STANDARD; PRT; 8 AA.
AC P22336;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Locustamyotropin 2 (LOM-MT-2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
[1]
RN SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin II, an
RT additional neuropeptide of Locusta migratoria. Member of the
RT cephalomyotrophic peptide family.";
RL Insect Biochem. 20:479-484(1990).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; PYROKININ.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4
DB 5 TP 6

RESULT 49
LPK LEUMA STANDARD; PRT; 8 AA.
ID LPK LEUMA STANDARD; PRT; 8 AA.
AC P13049;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucopyrokinin (LPK) (LEM-PK).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberiidae; Leucophaea.
OX NCBI_TaxID=6988;
[1]
RN SEQUENCE.
RC TISSUE=Head;
RA Nachman R.J., Holman G.M., Cook B.J.;
RT "Active fragments and analogs of the insect neuropeptide
RL leucopyrokinin: structure-function studies.";
RL Biochem. Biophys. Res. Commun. 137:936-942(1986).
[2]
RN SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of a blocked myotropic
RL neuropeptide isolated from the cockroach, Leucophaea maderae.";
RL Comp. Biochem. Physiol. 85C:219-224(1986).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS

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CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE
CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST
CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE
CC PENTAPEPTIDE FRAGMENT FTPLR.
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR: A23967; A23967.
DR IncerPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QT 3
Db 1 QT 2

RESULT 50
NPB_BOVIN
ID_NPB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 4 QP 5

RESULT 51
UC26_MAIZE
ID_UC26_MAIZE STANDARD; PRT; 8 AA.
AC P80632;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
DE (Fragment).
OC Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;

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RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernellet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.0, ITS MW IS: 57.2 kDa.
DR Maize-2DPAGE; P80632; COLEOPTILE.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EP 14
Db 2 EP 3

RESULT 52
UF06_MOUSE
ID_UF06_MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RT Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EP 14
Db 3 EP 4

RESULT 53
WP1_PERAT
ID_WP1_PERAT STANDARD; PRT; 8 AA.
AC P83195;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Wall protein-1 (PWP-1) (Fragment).
OS Perkinsus atlanticus.
OC Eukaryota; Alveolata; Perkinsa; Perkinsida; Perkinsidae; Perkinsus.
OX NCBI_TaxID=106964;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RX MEDLINE=22044350; PubMed=12049410;
RA Montes J.F., Durfort M., Llado A., Garcia-Valero J.;

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RT "Characterization and immunolocalization of a main proteinaceous
RT component of the cell wall of the protozoan parasite Perkinsus
RL atlanticus";
RL Parasitology 124:477-484(2002).
CC -!- FUNCTION: is a major protein component of the cell wall. May play
CC a key role in the organization of the cell wall and in promoting
CC the survival of this parasite.
CC -!- SUBCELLULAR LOCATION: Cell wall. Disulfide-linked to other cell
CC wall components.
CC -!- DEVELOPMENTAL STAGE: Expressed throughout all walled developmental
CC stages.
KW Cell wall.
FT NON_TER 8
SQ SEQUENCE 8 AA; 765 MW; F1787DD87B1AAB16 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ME 13
Db 1 ME 2

RESULT 54
BUK CLOPA STANDARD; PRT; 9 AA.
ID AC P81337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).
GN BUK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl
CC phosphate to butyrate (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.
CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the acetokinase family.
DR HAMAP; MF_00542; -, 1.
DR InterPro; IPR000890; Acetate kin.
DR PROSITE; PS01075; ACETATE_KINASE_1; PARTIAL.
DR PROSITE; PS01076; ACETATE_KINASE_2; PARTIAL.
KW Transferase; Kinase.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LL 8
Db 4 LL 5

RESULT 55
COW CONVE STANDARD; PRT; 9 AA.
ID AC P83047;
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Contryphan-Vn.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=117992;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=21547785; PubMed=11688995;
RA Massilia G.R., Schinina M.E., Ascenzi P., Politicelli P.;
RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
RT snail Conus ventricosus.";
RL Biochem. Biophys. Res. Commun. 288:908-913(2001).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1088.6; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Amidation; D-amino acid.
FT DISULFID 3 9
FT MOD_RES 5 5 D-TRYPTOPHAN.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GD 17
Db 1 GD 2

RESULT 56
COXE THUOB STANDARD; PRT; 9 AA.
ID AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver".
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1136 MW; 62E073C9CB0776DB CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
 ||
 Db 3 QP 4

RESULT 57
 DSIP RABIT STANDARD; PRT; 9 AA.
 ID _DSIP RABIT STANDARD; PRT; 9 AA.
 AC P01158;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Delta sleep-inducing peptide (DSIP).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77185324; PubMed=862769;
 RA Monnier M., Dudler L., Gachter R., Maier P.F., Tobler H.J.,
 RA Schoenenberger G.A.;
 RT "The delta sleep inducing peptide (DSIP). Comparative properties of
 RT the original and synthetic nonapeptide.";
 RL Experientia 33:548-552(1977).
 RN [2]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=79054421; PubMed=568769;
 RA Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;
 RT "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid
 RT analysis, sequence, synthesis and activity of the nonapeptide.";
 RL Pflugers Arch. 376:119-129(1978).
 RN [3]
 RP REVIEW.
 RX MEDLINE=87175129; PubMed=3550726;
 RA Graf M.V., Kastin A.J.;
 RT "Delta-sleep-inducing peptide (DSIP): an update.";
 RL Peptides 7:1165-1187(1986).
 CC -!- FUNCTION: WHEN INFUSED INTO THE MESODIENCEPHALIC VENTRICLE OF
 CC RECIPIENT RABBITS INDUCES SPINDLE AND DELTA EEG ACTIVITY AND
 CC REDUCED MOTOR ACTIVITIES.
 CC -!- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM DIALYSATES OF
 CC OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC
 CC STIMULATION OF THE THALAMUS.
 CC -!- DATABASE: NAME=Protein Spotlight;
 CC NOTE=Issue 8 of March 2001;
 CC WWW="http://www.expasy.org/spotlight/articles/splt008.html".
 DR PIR; A01422; QDRB.
 SQ SEQUENCE 9 AA; 849 MW; DDD365BDDAA8787D CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GD 17
 ||
 Db 4 GD 5

RESULT 58
 FAR2_CALVO STANDARD; PRT; 9 AA.
 ID FAR2 CALVO STANDARD; PRT; 9 AA.
 AC P41857;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CallifMRamide 2.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Thoracic ganglion;
 RC MEDLINE=92196111; PubMed=1549595;
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Renfield J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated callifMRamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
 CC SALIVARY GLAND OF CALLIPHORA.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR; B41978; B41978.
 KW Neuropeptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1128 MW; 29D00699CAB6CSA7 CRC64;
 AMIDATION.

Query Match 11.8%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TP 4
 ||
 Db 1 TP 2

RESULT 59
 FAR3_PENMO STANDARD; PRT; 9 AA.
 ID FAR3 PENMO STANDARD; PRT; 9 AA.
 AC P83318;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLP3 (AQPSMRLRP-amide).
 OS Penaeus monodon (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 RT of the giant tiger prawn Penaeus monodon.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;
 AMIDATION.

Query Match 11.8%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
 ||
 Db 2 QP 3

RESULT 60
 FAR4_PENMO STANDARD; PRT; 9 AA.
 ID FAR4 PENMO STANDARD; PRT; 9 AA.


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AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP4 (SQFSMRURF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupem J., Krungkarn C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 2 QP 3

RESULT 61
FAR9 ASCSU
ID FAR9 ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FMRamide-like neuropeptide Af9.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PL 7
Db 6 PL 7

RESULT 62
FARA CALVO
ID FARA_CALVO STANDARD; PRT; 9 AA.

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AC P41865;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 10.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duye H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A44787; A44787.
KW Neuropeptide; Amidation.
FT MOD RES 9
FT UNSURE 1 1
SQ SEQUENCE 9 AA; 1183 MW; 29D00699CAB40457 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TP 4
Db 1 TP 2

RESULT 63
FRF1 SARBU
ID FRF1 SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Neb-FMRFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 5 QP 6
||
Db 1 QP 2

RESULT 64
ID KNL3_BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Ch'en T.B., Orr D.P., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TP 4
||
Db 6 TP 7

RESULT 65
ID LMT3_LOCM1 STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 3 (LOM-WT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452 (1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TP 4
||
Db 7 TP 8

RESULT 67
ID OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspartocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
```

RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophyseal hormones. Two new active peptides
RL isolated from a cartilaginous fish, *Squalus acanthias*.";
RN Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (*Squalus acanthias*).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam: PF00220; hormone4; 1
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9
FT SEQUENCE 9 AA; 996 MW; 17F8376EB44404B CRC64;
SQ

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PL 7
Db 7 PL 8

RESULT 68
ID OXYT RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit).
OS Hippopotamus amphibius (Hippopotamus).
OS Balaenoptera physalus (finback whale), (Common rorqual),
OS Tachyglus aculeatus aculeatus (Australian echidna), and
OS Hydroglus collieri (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RP SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophyseal hormones: isolation of active
RL principles from rabbits and rats.";
RN Biochimie 53:1099-1104(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=H. amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RL neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [3]
RP SEQUENCE.
RC SPECIES=B. physalus;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin.";
RL Nature 201:191-192(1964).
RN [4]
RP SEQUENCE.
RC SPECIES=A. aculeatus;
RX MEDLINE=73223515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;

RT "Neurohypophyseal hormones and evolution of tetrapods.";
RL Nature New Biol. 244:124-126(1973).
RN [5]
RP SEQUENCE.
RC SPECIES=H. colliiei;
RX MEDLINE=70088110; PubMed=5366118;
RA Pickering B.T., Heller H.;
RT "Oxytocin as a neurohypophyseal hormone in the holocephalian
RT elasmobranch fish, *Hydrolagus collei*.";
RL J. Endocrinol. 45:597-606(1969).
CC -!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
CC UTERUS AND OF THE MAMMARY GLAND.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR: A91466; A91466.
DR PIR: A92774; A92774.
DR PIR: A93147; A93147.
DR PIR: A93408; A93408.
DR PIR: B90667; B90667.
DR PDB: 1XY1; 15-OCT-90.
DR PDB: 1XY2; 15-OCT-90.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Hypothalamus; Amidation; 3D-structure.
FT DISULFID 1 6
FT MOD RES 9
FT SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;
SQ

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PL 7
Db 7 PL 8

RESULT 69
ID PPH1_LYCES STANDARD; PRT; 9 AA.
AC P83380;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Purple acid phosphatase isozyme LeSAP1 (EC 3.1.3.2) (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
RP GLYCOSYLATION.
RC STRAIN=cv. Moneymaker; TISSUE=Seed;
RX MEDLINE=22361242; PubMed=12473124;
RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
RT "Purification and characterization of two secreted purple acid
RT phosphatase isozymes from phosphate-starved tomato (*Lycopersicon
RL esculentum*) cell cultures.";
RL Eur. J. Biochem. 269:6278-6286(2002).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Glycosylated.
CC -!- MISCELLANEOUS: In *L. esculentum* there are at least two isozymes of
CC purple acid phosphatase.
KW Hydrolase; Glycoprotein.
FT NON_TER 1 1
FT NON_TER 9 9
FT SEQUENCE 9 AA; 1005 MW; 3F17C04B5042CAA8 CRC64;
SQ

Query Match 11.8%; Score 2; DB 1; Length 9;

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Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 16 GD 17
DB 2 GD 3

RESULT 70
RE42 LITRU
ID RE42 LITRU STANDARD; PRT; 9 AA.
AC P82075; P82093;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 4.2/4.3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN secretion;
RA Steinborner S.I.; Wabnitz P.A.; Waugh R.J.; Bowie J.H.; Gao C.;
RA Tyler M.J.; Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
RN [2]
RP SEQUENCE.
RC TISSUE=SKIN secretion;
RA Wabnitz P.A.; Bowie J.H.; Tyler M.J.; Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
RN [1]
RP SEQUENCE.
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- PTM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-
CC terminal amidation.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 9
FT SEQUENCE 9 AA; 884 MW; 2C2D77205AA72728 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LL 8
DB 3 LL 4

RESULT 71
TALI PICJA
ID TALI PICJA STANDARD; PRT; 9 AA.
AC P17440;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transaldolase I (EC 2.2.1.2) (Fragment).
OS Pichia jadinii (Yeast) (Candida utilis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4903;
RN [1]
RP SEQUENCE.
RX MEDLINE=7110646; PubMed=556924;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LL 8
DB 3 LL 4

RESULT 72
TAL3 PICJA
ID TAL3 PICJA STANDARD; PRT; 9 AA.
AC P17441;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transaldolase III (EC 2.2.1.2) (Fragment).
OS Pichia jadinii (Yeast) (Candida utilis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4903;
RN [1]
RP SEQUENCE.
RX MEDLINE=75145197; PubMed=1092268;
RA Tsolas O.; Sun S.C.;
RT "Isolation of a peptide containing a histidyl-cysteinyl sequence
RT from the active center of transaldolase.";
RL Arch. Biochem. Biophys. 167:525-533(1975).
CC -!- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
CC -!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
CC -!- PATHWAY: Pentose phosphate pathway; nonoxidative part.
CC -!- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
DR PIR; A11497; A11497.
DR InterPro; IPR001585; Transaldolase.
DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
KW Transferase; Pentose shunt.
FT NON_TER 1
FT NON_TER 9
FT SEQUENCE 9 AA; 1008 MW; 274F31AF0EB1E058 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LL 8
DB 8 LL 9

RESULT 73
TAL3 PICJA
ID TAL3 PICJA STANDARD; PRT; 9 AA.
AC P17441;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transaldolase III (EC 2.2.1.2) (Fragment).
OS Pichia jadinii (Yeast) (Candida utilis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4903;
RN [1]
RP SEQUENCE.
RX MEDLINE=75145197; PubMed=1092268;
RA Tsolas O.; Sun S.C.;
RT "Isolation of a peptide containing a histidyl-cysteinyl sequence
RT from the active center of transaldolase.";
RL Arch. Biochem. Biophys. 167:525-533(1975).
CC -!- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
CC -!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
CC -!- PATHWAY: Pentose phosphate pathway; nonoxidative part.
CC -!- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
DR PIR; A11497; A11497.
DR InterPro; IPR001585; Transaldolase.
DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
KW Transferase; Pentose shunt.
FT NON_TER 1
FT NON_TER 9
FT SEQUENCE 9 AA; 1033 MW; 325A31A44EB1E058 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LL 8
DB 8 LL 9

RESULT 73
TAL3 PICJA
ID TAL3 PICJA STANDARD; PRT; 9 AA.
AC P17441;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transaldolase I (EC 2.2.1.2) (Fragment).
OS Pichia jadinii (Yeast) (Candida utilis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4903;
RN [1]
RP SEQUENCE.
RX MEDLINE=7110646; PubMed=556924;

```

THYF PIG
ID -THYF PIG STANDARD; PRT; 9 AA.
AC P01255;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thymic factor.
DE Thymic factor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9821;
RN [1]
RP SEQUENCE.
RX MEDLINE=78026571; PubMed=914862;
RA Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
RT "Structural study of circulating thymic factor: a peptide isolated
RT from pig serum. II. Amino acid sequence.";
RL J. Biol. Chem. 252:8045-8047(1977).
CC -!- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
CC PIR; A01523; YFPG.
DR Pyrrolidone carboxylic acid.
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 9 AA; 876 MW; D500B87866C5B33D CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QG 16
DB 5 QG 6

RESULT 74
UF02 MOUSE STANDARD; PRT; 9 AA.
AC P38670;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX TISSUE=Fibroblast;
RX MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 32 kDa.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1102 MW; 7E73EAB6D05B1AAB CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ME 13
DB 1 ME 2

RESULT 75
ULAD HUMAN STANDARD; PRT; 9 AA.
ID ULAD HUMAN
AC P31929;
DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6, ITS MW IS: 15 kDa.
DR SWISS-2DPAGE; P31929; HUMAN.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1129 MW; D02DFB41B6D33322 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QT 3
DB 5 QT 6

Search completed: November 25, 2003, 18:17:22
Job time : 9.22872 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 40.9628 Seconds
(without alignments)
107.095 Million cell updates/sec

Title: US-09-641-801-2
Perfect score: 17
Sequence: 1 LQFPQLQVWMPQGD 17

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archesp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	23.5	12	11	Q8CG32
2	4	23.5	18	4	Q16167
3	4	23.5	18	5	Q9TWM9
4	4	23.5	19	4	Q8IWT8
5	4	23.5	20	2	Q46499
6	4	23.5	20	6	Q9T856
7	4	23.5	20	10	Q9S8Y7
8	3	17.6	7	12	Q9YQ10
9	3	17.6	8	4	Q15893
10	3	17.6	8	5	Q94623
11	3	17.6	8	11	Q8K3Z7
12	3	17.6	8	11	Q9SP40
13	3	17.6	9	2	Q47556
14	3	17.6	9	13	Q8AYL5
15	3	17.6	9	13	Q8AUM7
16	3	17.6	9	15	Q85723

Q9r7J8	helicobacte	10	2	Q9R7J8
P83154	anabaena sp	10	2	P83154
Q9h3r9	homo sapien	10	4	Q9H3R9
Q9uJ48	homo sapien	10	4	Q9UJ48
Q9qVx7	mus sp. mep	10	11	Q9QVX7
Q9Jl15	mus musculus	10	11	Q9JL15
Q39957	hepatitis g	10	12	Q39957
O82625	infectious	10	12	O82625
Q75595	human immun	10	15	Q75595
Q8X4e5	escherichia	10	16	Q8X4E5
Q48933	mycobacteri	11	2	Q48933
Q9r7u8	pseudomonas	11	2	Q9R7U8
O4237	anabaena sp	11	2	O4237
O56972	versinia pe	11	2	O56972
Q9un18	homo sapien	11	4	Q9UNL8
Q8tda8	homo sapien	11	4	Q8TDA8
Q9ucr1	homo sapien	11	4	Q9UCR1
Q81vG8	homo sapien	11	4	Q81VG8
P83168	struthio ca	11	13	P83168
Q8adi8	human immun	11	15	Q8ADI8
Q9spc5	pisum sativ	12	10	Q9SPT5
P82328	mus musculu	12	10	P82328
Q8eqv3	mus musculu	12	11	Q8EQV3
Q8QDY5	human immun	12	15	Q8QDY5
Q8Qe47	human immun	12	15	Q8QE47
O8QDY4	human immun	12	15	O8QDY4
O8Qe41	human immun	12	15	O8QE41
Q8Qe45	human immun	12	15	Q8QE45
Q8Qe43	human immun	12	15	Q8QE43
Q8QDY6	human immun	12	15	Q8QDY6
Q9uee2	homo sapien	13	4	Q9UEE2
Q14182	homo sapien	13	4	Q14182
Q9ub66	homo sapien	13	4	Q9UB66
Q9um46	homo sapien	13	4	Q9UM46
Q16007	homo sapien	13	4	Q16007
Q81zr0	homo sapien	13	4	Q81ZR0
Q9u7d6	neospora ca	13	5	Q9U7D6
O97122	toxoplasma	13	5	O97122
Q9r224	campylobact	14	2	Q9R2Z4
Q9r517	escherichia	14	2	Q9R517
Q9r225	campylobact	14	2	Q9R2Z5
O8rk22	pseudomonas	14	2	O8RK22
Q9X715	campylobact	14	2	Q9XW79
Q9w779	campylobact	14	2	Q9W779
O8GMC4	salmonella	14	2	O8GMC4
Q9r7w0	trypanosoma	14	5	Q9R7W0
Q9zrs3	arabidopsis	14	10	Q9ZRS3
Q8v1h7	hepatitis b	14	12	Q8V1H7
O9py99	murine hepa	14	12	O9PY99
O88400	simian t-ly	14	15	O88400
Q9r3a0	micrococcu	15	2	Q9R3A0
Q9x637	klebsiella	15	2	Q9X637
Q9x635	escherichia	15	2	Q9X635
Q9umt6	homo sapien	15	4	Q9UMT6
P78482	homo sapien	15	4	P78482
Q96rx1	homo sapien	15	4	Q96RX1
Q9uc60	homo sapien	15	4	Q9UC60
Q9trp1	sus scrofa	15	6	Q9TRP1
Q9stng1	mus sp. bet	15	7	Q9STNQ1
Q9s8v7	tritium ae	15	7	Q9S8V7
Q40562	nicotiana t	15	10	Q40562
Q988d4	cynara card	15	10	Q988D4
Q40563	nicotiana t	15	10	Q40563
Q9gvk9	mus sp. mep	15	11	Q9GVK9
Q69353	herpes simp	15	12	Q69353
O9pxh0	human t-lym	15	15	O9PXH0
Q47603	escherichia	16	2	Q47603
Q9r4i3	mycobacteri	16	2	Q9R4I3
Q48417	klebsiella	16	2	Q48417
Q8gfr1	citrobacter	16	2	Q8GFR1
Q9nnz2	homo sapien	16	4	Q9NNZ2
Q9uc44	homo sapien	16	4	Q9UC44
Q9uch1	homo sapien	16	4	Q9UCH1

90 Q9TWK1 mytilus edu
 91 Q9Cwk0 mytilus edu
 92 Q9Tr99 canis fam1
 93 Q9Trr1 oryctolagus
 94 Q9T2R0 solanum tub
 95 Q9ctj7 mus musculus
 96 Q9r2d2 mus musculus
 97 Q9pru6 gallus gall
 98 Q9kddg bacillus ha
 99 Q9vme2 pseudomonas
 100 Q9ucr7 homo sapien

ALIGNMENTS

RESULT 1
 Q8CG32 ID Q8CG32 PRELIMINARY; PRT; 12 AA.
 AC Q8CG32;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE L-histidine decarboxylase (Fragment).
 GN HDC.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96198284; PubMed=8928792;
 RA Hocker M., Zhang Z., Fenstermacher D.A., Tagerud S., Chulak M.,
 RA Joseph D., Wang T.C.;
 RT "Rat histidine decarboxylase promoter is regulated by gastrin through
 RT a protein kinase C pathway";
 RL Am. J. Physiol. 270:G619-G633(1996).
 DR EMBL; S83368; AAN86715.1; -.
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1515 MW; 8783853D28FB5B05 CRC64;

Query Match 23.5%; Score 4; DB 11; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MWEP 14
 Db 1 MWEP 4
 RESULT 2
 Q16167 ID Q16167 PRELIMINARY; PRT; 18 AA.
 AC Q16167;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Serum albumin (Fragment).
 GN SERUM ALBUMIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94294404; PubMed=8022807;
 RA Madison J., Galliano M., Watkins S., Minchiotti L., Porta F.,
 RA Rossi A., Putnam F.W.;
 RT "Genetic variants of human serum albumin in Italy: point mutants and a
 RT caboxyl-terminal variant";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:6476-6480(1994).
 DR EMBL; S70799; AAB31177.1; -.
 FT NON_TER 1

SQ SEQUENCE 18 AA; 2089 MW; 2CCF6C5B0B08690B CRC64;
 Query Match 23.5%; Score 4; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 LLQV 10
 Db 12 LLQV 15
 RESULT 3
 Q9TWM9 ID Q9TWM9 PRELIMINARY; PRT; 18 AA.
 AC Q9TWM9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE NKTAG antigen (Fragment).
 OS Tetrahymena pyriformis.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
 OC Tetrahymenina; Tetrahymena.
 OX NCBI_TaxID=5908;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94323706; PubMed=7519359;
 RA Leary J.H.3rd, Evans D.L., Jaso-Friedmann L.;
 RT "Partial amino acid sequence of a novel protozoan parasite antigen
 RT that inhibits non-specific cytotoxic cell activity";
 RL Scand. J. Immunol. 40:158-164(1994).
 SQ SEQUENCE 18 AA; 2082 MW; 13BCB737B1FF92A3 CRC64;

Query Match 23.5%; Score 4; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 14 PQGD 17
 Db 9 PQGD 12

RESULT 4
 Q81WT8 ID Q81WT8 PRELIMINARY; PRT; 19 AA.
 AC Q81WT8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Aspecific BCL2 ARE-binding protein 2 (Fragment).
 GN ASBAP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Donini M., Schiavone N., Lapucci A., Papucci L., Witort E.,
 RA Capaccioli S.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY140907; AAN25598.1; -.
 FT NON_TER 1
 SQ SEQUENCE 19 AA; 2324 MW; 9352F38D59FC642D CRC64;

Query Match 23.5%; Score 4; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 LLQV 10
 Db 14 LLQV 17

```
RESULT 5
Q46499
ID Q46499 PRELIMINARY; PRT; 20 AA.
AC Q46499;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE Periplasmic (Fragment).
OS Desulfovibrio desulfuricans.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=876;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=M6;
RA Lim S.K., Lee S.J., Kim B.H.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
FR EMBL; U49192; AAA91808.1; -.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 1996 MW; E93207D26C22999B CRC64;

Query Match 23.5%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 POPL 7
DB 10 POPL 13

RESULT 6
Q9TR56
ID Q9TR56 PRELIMINARY; PRT; 20 AA.
AC Q9TR56;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE TAUROCHENOXYCHOLIC acid 6 alpha-hydroxylase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]_
RP SEQUENCE.
RX MEDLINE=95377322; PubMed=7649186;
RA Araya Z., Hellman U., Hansson R.;
RT "Characterisation of taurochenodeoxycholic acid 6 alpha-hydroxylase
RT from pig liver microsomes."
RL Eur. J. Biochem. 231:855-861(1995).
SQ SEQUENCE 20 AA; 1893 MW; F126282696D54D8D CRC64;

Query Match 23.5%; Score 4; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
DB 11 LLQV 14

RESULT 7
Q9S8Y7
ID Q9S8Y7 PRELIMINARY; PRT; 20 AA.
AC Q9S8Y7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 2S storage albumin large subunit (Fragment).
OS Raphanus sativus (Radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Raphanus.

Query Match 23.5%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OX NCBI_TaxID=3726;
RN [1]_
RP SEQUENCE.
RX MEDLINE=92348373; PubMed=1639777;
RA Terras F.R., Schoofs H.M., De Boile M.F., van Leuven F., Rees S.B.,
RA Vanderleyden J., Cammue B.P., Broekaert W.F.;
RT "Analysis of two novel classes of plant antifungal proteins from
RT radish (Raphanus sativus L.) seeds."
RL J. Biol. Chem. 267:15301-15309(1992).
SQ SEQUENCE 20 AA; 2276 MW; DCB4B3960A1960B7 CRC64;

Query Match 23.5%; Score 4; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
DB 9 PLLQ 12

RESULT 8
Q9YQ10
ID Q9YQ10 PRELIMINARY; PRT; 7 AA.
AC Q9YQ10;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical fusion protein.
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11149;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=9909045; PubMed=9882359;
RA Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Piana-Duran J.,
RA Enjuanes L.;
RT "Replication and packaging of transmissible gastroenteritis
RT coronavirus-derived synthetic minigenomes."
RL J. Virol. 73:1535-1545(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95159435; PubMed=7856095;
RA Eleouet J., Rasschaert D., Lambert P., Levy L., Verde P., Laude H.;
RT "Complete sequence (20 kilobases) of the polyprotein-encoding gene 1
RT of transmissible gastroenteritis virus."
RL Virology 206:817-822(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88078100; PubMed=2825819;
RA Rasschaert D., Gelfi J., Laude H.;
RT "Enteric coronavirus TGEV: partial sequence of the genomic RNA its
RT organization and expression."
RL Biochimie 69:591-600(1987).
RL EMBL; AJ011482; CAA09625.1; -.
SQ SEQUENCE 7 AA; 927 MW; 69D6D7273B5726F0 CRC64;

Query Match 17.6%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
DB 4 LLQ 6

RESULT 9
Q15893
ID Q15893 PRELIMINARY; PRT; 8 AA.
AC Q15893;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
```



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DE (Clone XP587A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32073; AAA73883.1; -.
FT NON TER 1
FT NON TER 8
SQ SEQUENCE 8 AA; 874 MW; DAA1B6D7376456C5 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOT 3
Db 5 LOT 7

RESULT 10
Q94623 PRELIMINARY; PRT; 8 AA.
ID Q94623
AC Q94623;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE MSUP-2 protein (Fragment).
DE USP.
GN Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Spingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epidermis;
RX MEDLINE=97165493; PubMed=9013254;
RA Jindra M., Huang J.Y., Malone F., Ashahina M., Riddiford L.M.;
RT "Identification and mRNA developmental profiles of two ultraspiracle
RT isoforms in the epidermis and wings of Manduca sexta.";
RL Insect Mol. Biol. 6:41-53(1997).
DR EMBL; U57921; AAB64235.1; -.
FT NON TER 8
FT NON TER 8
SQ SEQUENCE 8 AA; 892 MW; F165BB0415A76B16 CRC64;

Query Match 17.6%; Score 3; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MEP 14
Db 1 MEP 3

RESULT 11
Q8K327 PRELIMINARY; PRT; 8 AA.
ID Q8K327
AC Q8K327;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE C-mer proto-oncogene (Fragment).
GN MER.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22148657; PubMed=12153576;
RA Wong C.C.S., Lee W.M.;
RA "The proximal cis-acting elements Sp1, Sp3 and E2F regulate mouse mer
RT gene transcription in Sertoli cells.";
RL Eur. J. Biochem. 269:3789-3800(2002).
DR EMBL; AF517125; AAM77639.1; -.
FT NON TER 8
FT NON TER 8
SQ SEQUENCE 8 AA; 869 MW; FE2727376DD732C6 CRC64;

Query Match 17.6%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLL 8
Db 5 PLL 7

RESULT 12
Q99P40 PRELIMINARY; PRT; 8 AA.
ID Q99P40
AC Q99P40;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Repressor of GATA (Fragment).
DE ROG.
GN ROG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57B6;
RA Miao S., Ho I.;
RT "ROG is a NF-AT target gene that partly rescues the phenotype of NF-
RT Atc2/NF-Atc3 deficient Th cells.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335542; AAG59843.1; -.
FT NON TER 8
FT NON TER 8
SQ SEQUENCE 8 AA; 943 MW; FE3411B771B6C766 CRC64;

Query Match 17.6%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTP 4
Db 3 QTP 5

RESULT 13
Q47556 PRELIMINARY; PRT; 9 AA.
ID Q47556
AC Q47556;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 09, Last annotation update)
DE Aspartate transcarbamoylase regulatory chain (Fragment).
GN PYRI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82275057; PubMed=7051000;
RA Pauza C.D., Karels M.J., Navre M., Schachman H.K.;

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RT "Genes encoding Escherichia coli aspartate transcarbamoylase: The
 RT pyrB-pyri operon."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982).
 RN [2]
 RP SEQUENCE OF 1-5 FROM N.A.
 RX MEDLINE=83195078; PubMed=6302686;
 RA Hoover T.A., Roof W.D., Foltermann K.F., O'Donovan G.A., Bencini D.A.,
 RA Wild J.R.;
 RT "Nucleotide sequence of the structural gene (pyrB) that encodes the
 RT catalytic polypeptide of aspartate transcarbamoylase of Escherichia
 RT coli."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).
 DR EMBL; J01670; AAA24475.1; --
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1085 MW; 99EFD723344AA1F1 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LQV 10
 DB 7 LQV 9

RESULT 14
 ID Q8AVL5 PRELIMINARY; PRT; 9 AA.
 AC Q8AVL5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cytochrome P450 aromatase (Fragment).
 GN CYP19A
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 ON NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
 RT "Promoter characteristics of two CYP19 genes differentially expressed
 RT in the brain and ovary of teleost fish."
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
 DR EMBL; AF324897; AAN32618.1; --
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1060 MW; C49E76D7272B040D CRC64;

Query Match 17.6%; Score 3; DB 13; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
 DB 5 LLQ 7

RESULT 15
 ID Q8AUM7 PRELIMINARY; PRT; 9 AA.
 AC Q8AUM7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cytochrome P450 aromatase (Fragment).
 GN CYP19A
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 ON NCBI_TaxID=7957;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
 RT "Promoter characteristics of two CYP19 genes differentially expressed
 RT in the brain and ovary of teleost fish."
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
 DR EMBL; AF324895; AAN32616.1; --
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;

Query Match 17.6%; Score 3; DB 13; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
 DB 5 LLQ 7

RESULT 16
 ID Q85723 PRELIMINARY; PRT; 9 AA.
 AC Q85723;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE V-sis and p28-sis genes (Fragment).
 OS Simian sarcoma virus.
 OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
 ON NCBI_TaxID=11817;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84106822; PubMed=6319011;
 RA Devare S.G., Shatzman A., Robbins K.C., Rosenberg M., Aaronson S.A.;
 RT "Expression of the PDGF-related transforming protein of simian sarcoma
 RT virus in E. coli."
 RL Cell 36:43-49(1984).
 DR EMBL; K01473; AAA46816.1; --
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1048 MW; 9C53A866C361A731 CRC64;

Query Match 17.6%; Score 3; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QGD 17
 DB 6 QGD 8

RESULT 17
 ID Q9R7J8 PRELIMINARY; PRT; 10 AA.
 AC Q9R7J8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Vacuolating cytotoxin (Fragment).
 GN VACA.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteraceae; Helicobacter.
 ON NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Kobe 500;
 RA Shirasaka D.;
 RT "Helicobacter pylori vacA gene, strain Kobe 500, partial cds."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017599; BAA33412.1; --
 FT NON_TER 1
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1018 MW; 414390C76879CDD7 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16
 |||
 Db 7 PQG 9
 |||

RESULT 18

P83154
 ID P83154 PRELIMINARY; PRT; 10 AA.
 AC P83154;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Phycobilisome rod-core linker polypeptide cpcG3 (Fragment).
 OS Anabaena sp. (strain L31).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TaxID=29412;
 RN [1]
 RP SEQUENCE.
 RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
 RL Submitted (OCT-2001) to the SWISS-PROT data bank.
 CC -!- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
 CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
 CC -!- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
 CC AND THE LOCATION OF THE DISK-SHAPED PHYCOBILIPROTEIN UNITS WITHIN
 CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN
 CC ORDER TO MEDIANE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
 CC -!- SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCOIDAL STRUCTURE THAT IS
 CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT
 CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
 CC THE CORE.
 CC -!- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE.
 CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
 KW Phycobilisome; Photosynthesis; Thylakoid; Membrane.
 FT NON_TER 10
 FT TER 10
 SQ SEQUENCE 10 AA; 1144 MW; 2F9B62B5B172737 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
 |||
 Db 3 PLL 5
 |||

RESULT 19

Q9H3R9
 ID Q9H3R9 PRELIMINARY; PRT; 10 AA.
 AC Q9H3R9;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Deoxyribonuclease II (Fragment).
 GN DNASE2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yasuda T.;
 RL "The 5'-flanking region of human deoxyribonuclease II gene."; Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB031422; BAB20386.1; -.
 FT NON_TER 10
 FT TER 10
 SQ SEQUENCE 10 AA; 1067 MW; 3D5514DDD7272737 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
 |||
 Db 3 PLL 5
 |||

RESULT 20

Q9UJ48
 ID Q9UJ48 PRELIMINARY; PRT; 10 AA.
 AC Q9UJ48;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE latrophilin-2 (Fragment).
 GN LPHH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA White G.R.M., Varley J.M., Heighway J.;
 RL "Isolation and characterisation of a human homologue of the
 RL latrophilin gene from a region of 1p31.1 implicated in breast
 RL cancer.";
 RN Oncogene 17:3513-3519 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA White G.R.M., Varley J.M., Heighway J.;
 RL "Genomic structure and expression profile of LPHH1, a 7TM gene
 RL variably expressed in breast cancer cell lines.";
 RL Biochim. Biophys. Acta 1491:75-92 (2000).
 DR EMBL; AJ244514; CAB60206.1; -.
 FT NON_TER 1
 FT TER 1
 SQ SEQUENCE 10 AA; 1112 MW; 06CC4C2720544724 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
 |||
 Db 7 LLQ 9
 |||

RESULT 21

Q9QVK7
 ID Q9QVK7 PRELIMINARY; PRT; 10 AA.
 AC Q9QVK7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE MEPRIN-METALLOENDOPEPTIDASE (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=91363409; PubMed=1888759;
 RA Flannery A.V., Macadam G.C., Beynon R.J.;
 RL "Immunological characterisation of different meprin species in mice."; Biochim. Biophys. Acta 1079:119-122 (1991).
 FT NON_TER 1
 FT TER 1
 SQ SEQUENCE 10 AA; 1138 MW; FC01BFB5BAA866D1 CRC64;

Query Match 17.6%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QGD 17
Db 4 QGD 6

RESULT 22
ID Q9JUL5 PRELIMINARY; PRT; 10 AA.
AC Q9JUL5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Melanocortin type 1 receptor MCLR (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=20090876; PubMed=10623832;
RA Adachi S., Morii E., Kim D.-k, Ogiwara H., Jippo T., Ito A., Lee Y.M.,
RA Kitamura Y.;
RT "Involvement of mi-transcription factor in expression of alpha-
RT melanocyte-stimulating hormone receptor in cultured mast cells of
RT mice.";
RL J. Immunol. 164:855-860(2000).
RL EMBL; AF176016; AAF37323.1; -.
KW Receptor.
FT NON_TER
SQ SEQUENCE 10 AA; 1148 MW; 95B58A26C76B06C1 CRC64;

Query Match 17.6%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
Db 5 EPQ 7

RESULT 23
ID O39957 PRELIMINARY; PRT; 10 AA.
AC O39957;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
OS Hepatitis GB virus C.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=39839;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Edinburgh haemophilic;
RX MEDLINE=97368412; PubMed=9225026;
RA Smith D.B., Cuceanu N., Davidson F., Jarvis L.M., Mokili J.L.,
RA Hamid S., Ludlam C.A., Simmonds P.;
RT "Discrimination of hepatitis G virus/GBV-C geographical variants by
RT analysis of the 5' non-coding region.";
RL J. Gen. Virol. 78:1533-1542(1997).
RL EMBL; AF003175; AAC57986.1; -.
FT NON_TER
SQ SEQUENCE 10 AA; 1067 MW; CC88FE2727273772 CRC64;

Query Match 17.6%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8

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Db 4 PLL 6

RESULT 24
ID Q82625 PRELIMINARY; PRT; 10 AA.
AC Q82625;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Small ORF.
OS Infectious bursal disease virus (Gumboro virus).
OC Viruses; dsRNA viruses; Birnaviridae; Avibirnavirus.
OX NCBI_TaxID=10995;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=86259073; PubMed=3014441;
RA Hudson P.J., McKern N.M., Power B.E., Azad A.A.;
RT "Genomic structure of the large RNA segment of infectious bursal
RT disease virus.";
RL Nucleic Acids Res. 14:5001-5012(1986).
RN [2]_
RP SEQUENCE FROM N.A.
RX MEDLINE=90016880; PubMed=2552417;
RA Spies U.;
RT "Nucleotide sequence of infectious bursal disease virus genome segment
RT A delineates two major open reading frames.";
RL Nucleic Acids Res. 17:7982-7982(1989).
RN [3]_
RP SEQUENCE FROM N.A.
RX MEDLINE=90278420; PubMed=2161902;
RA Bayliss C.D., Spies U., Shaw K., Peters R.W., Papageorgiou A.,
RA Muller H., Boursnell M.E.;
RT "A comparison of the sequences of segment A of four infectious bursal
RT disease virus strains and identification of a variable region in VP2.";
RL J. Gen. Virol. 71:1303-1312(1990).
DR EMBL; D00869; BAA00743.1; -.
DR EMBL; A33255; CAA02133.1; -.
SQ SEQUENCE 10 AA; 1316 MW; 58B57D16D7272727 CRC64;

Query Match 17.6%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LIQ 9
Db 5 LIQ 7

RESULT 25
ID Q75595 PRELIMINARY; PRT; 10 AA.
AC Q75595;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=T12B;
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
RT "The TAT and C2-V3 Envelope Genes in the Molecular Epidemiology of
RT Human Immunodeficiency Virus-1.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJF databases.
DR EMBL; U57303; AAB17863.1; -.
FT NON_TER
SQ SEQUENCE 10 AA; 1182 MW; 22252E34176AB2D7 CRC64;

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Query Match      17.6%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 MEP 14
      |||
Db      1 MEP 3

RESULT 26
Q8X4E5 PRELIMINARY; PRT; 10 AA.
AC Q8X4E5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein z5903.
GN Z5903.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
DR EMBL; AE005662; AAG59489.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 10 AA; 1161 MW; 98AC9BD2D6D7205A CRC64;

Query Match      17.6%; Score 3; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LQV 10
      |||
Db      5 LQV 7

RESULT 27
Q48933 PRELIMINARY; PRT; 11 AA.
AC Q48933; P77701; Q48932;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Alkyl hydroperoxide reductase C (Fragment).
GN AHPc.
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OC NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC35728, and ATCC35727;
RA Zhang Y., Deretic V.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC35735;
RX MEDLINE=96256622; PubMed=8655566;
RA Dhandayuthapani S., Zhang Y., Deretic V.;
RT "Oxidative stress response and its role in sensitivity to isoniazid in
RT mycobacteria: characterization and inducibility of ahpC by peroxides in
RT Mycobacterium smegmatis and lack of expression in M. aurum and M.
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tuberculosis.".
RL J. Bacteriol. 178:3641-3649 (1996).
DR EMBL; U58031; AAB00320.1; -.
DR EMBL; U57979; AAA99830.1; -.
DR EMBL; U57978; AAA99829.1; -.
DR EMBL; U57762; AAB00317.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1231 MW; 455099E3A87041A7 CRC64;

Query Match      17.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLL 8
      |||
Db      2 PLL 4

RESULT 28
Q9R7U8 PRELIMINARY; PRT; 11 AA.
AC Q9R7U8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNR protein (A regulatory protein for the expression of the Nir and
DE nor genes) (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OC NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAO1;
RX MEDLINE=95226457; PubMed=7711073;
RA Arai H., Igarashi Y., Kodama T.;
RT "The structural genes for nitric oxide reductase from Pseudomonas
RT aeruginosa.";
RL Biochim. Biophys. Acta 1261:279-284 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PAO1;
RX MEDLINE=95394152; PubMed=7664887;
RA Arai H., Igarashi Y., Kodama T.;
RT "Expression of the nir and nor genes for denitrification of
RT Pseudomonas aeruginosa requires a novel CRP/FNR-related
RT transcriptional regulator, DNR, in addition to ANR.";
RL FEBS Lett. 371:73-76 (1995).
DR EMBL; D50019; BAA08746.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1543 MW; DF363CAE141B5736 CRC64;

Query Match      17.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LIQ 9
      |||
Db      2 LIQ 4

RESULT 29
Q44237 PRELIMINARY; PRT; 11 AA.
AC Q44237;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glutamine synthetase (Fragment).
GN GLNA.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OC NCBI_TaxID=103690;
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RN  SEQUENCE FROM N.A.
RP  STRAIN=PCC 7120;
RA  Warner L.E., Ligon P.J., Stahel A.W., Curtis S.E.;
RT  "The apcf gene of Anabaena sp. strain PCC 7120 is regulated by
RL  nitrogen and the apcf and glnA promoters overlap.";
RLL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
[2]
RN  SEQUENCE FROM N.A.
RP  STRAIN=PCC 7120;
RA  Scappino L.A.;
RL  Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR  EMBL; U21853; AAA65652.1; -.
FT  NON_TER 11
SQ  SEQUENCE 11 AA; 1316 MW; 2000580E32CB06C7 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQ 5
DB 3 TPQ 5

RESULT 30
Q56972
ID Q56972 PRELIMINARY; PRT; 11 AA.
AC Q56972;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Lcrkb protein (Fragment).
GN LCRKB.
OS Yersinia pestis.
OG Plasmid Lcr.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]_TaxID=632;
RP SEQUENCE FROM N.A.
RC STRAIN=358;
RX MEDLINE=92250432; PubMed=1577700;
RA Rimpilaenen M., Forsberg A., Wolf-Watz H.;
RT "A novel protein LcrQ, involved in the low-calcium response of
RL Yersinia pseudotuberculosis, shows extensive homology to YopH.";
RLL J. Bacteriol. 174:3355-3363 (1992).
DR EMBL; X78303; CAA55113.1; -.
KW Plasmid.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1377 MW; 0478BFECA1A04B54 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MME 13
DB 1 MME 3

RESULT 31
Q9UNL8
ID Q9UNL8 PRELIMINARY; PRT; 11 AA.
AC Q9UNL8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE APC2 protein (Fragment).
GN APC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[1]
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Carr I.M., Markham A.F., Colleta P.L., Wai L., Askham J., Morrison E.,
RA Meredith D.M.;
RT "APC2 partial gene sequence.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF110338; AAD29275.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1326 MW; 75881D7BB441EAB4 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3
DB 9 LQT 11

RESULT 32
Q8TDA8
ID Q8TDA8 PRELIMINARY; PRT; 11 AA.
AC Q8TDA8;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Glutathione synthetase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Cho Y.-W., Lee Y.-Y., Lim C.-J.;
RT "Cloning and characterization of glutathione synthetase gene from
RL human placenta DNA.";
RLL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF485789; AAL91591.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1235 MW; 1CE28D1E35B86374 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
DB 8 LLQ 10

RESULT 33
Q9UCR1
ID Q9UCR1 PRELIMINARY; PRT; 11 AA.
AC Q9UCR1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffmann E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RL autotaxin, a novel motility-stimulating protein.";
RLL J. Biol. Chem. 267:2524-2529 (1992).
FT NON_TER 1

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FT  NON TER      11      11
SQ  SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;

Query Match      17.6%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 QPL 7
Db  3 QPL 5

RESULT 34
Q81VG8
ID  Q81VG8      PRELIMINARY;      PRT;      11 AA.
AC  Q81VG8;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Low density lipoprotein receptor related protein 1 (Fragment).
GN  LRP.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Blood;
RA  Schulz S., Schagdarsurengin U., Greiser P., Birkenmeier G.,
RA  Muller-Werdan U., Hagemann M., Riemann D., Werdan K., Glaser C.;
RT  "The LDL receptor-related protein (LRP1/A2MR) and coronary
RT  atherosclerosis - novel genomic variants and functional
RT  consequences.";
RL  Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; Y18524; CAD57169.1; -.
KW  Receptor; Lipoprotein.
FT  NON TER      11      11
SQ  SEQUENCE 11 AA; 1221 MW; 373D041E27273777 CRC64;

Query Match      17.6%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 PLL 8
Db  5 PLL 7

RESULT 35
P83168
ID  P83168      PRELIMINARY;      PRT;      11 AA.
AC  P83168;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Alpha-2-antiplasmin (Alpha-2-plasmin inhibitor) (Alpha-2-Pi) (Alpha-2-
DE  AP) (Fragment).
OS  Struthio camelus (Ostrich).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
OC  Struthio.
OX  NCBI_TaxID=8801;
RN  [1]
RP  SEQUENCE, AND FUNCTION.
RC  TISSUE=Plasma;
RX  MEDLINE=21328857; PubMed=11435135;
RA  Thomas A.R., Naude R.J., Oelofsen W., Naganuma T., Muramoto K.;
RT  "Purification and partial characterisation of alpha(2)-antiplasmin and
RT  plasmin(ogen) from ostrich plasma.";
RL  Comp. Biochem. Physiol. 129B:809-820(2001).
CC  -!- FUNCTION: THE MAJOR TARGETS OF THIS INHIBITOR ARE PLASMIN AND
CC  TRYPSIN, BUT IT ALSO INACTIVATES CHYMOTRYPSIN.
CC  -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

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KW  Serpin; Serine protease inhibitor.
FT  NON TER      11      11
SQ  SEQUENCE 11 AA; 1261 MW; 9B08C06B32C73B5A CRC64;

Query Match      17.6%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8 LQV 10
Db  1 LQV 3

RESULT 36
Q8ADI8
ID  Q8ADI8      PRELIMINARY;      PRT;      11 AA.
AC  Q8ADI8;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Truncated vif protein.
GN  VIF.
OS  Human immunodeficiency virus 1.
OC  Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX  NCBI_TaxID=11676;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=98UG57135;
RX  MEDLINE=22375625; PubMed=12487816;
RA  Harris M.E., Serwadda D., Sewankambo N., Wabwire F., Kim B.,
RA  Kigozi G., Kiwanuka N., Phillips J.B., Meehen M., Lutalo T.,
RA  Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L.,
RA  McCutchan F.E.;
RT  "Among 46 Near Full Length HIV Type 1 Genome Sequences from Rakai
RT  District, Uganda, Subtype D and AD Recombinants Predominate.";
RL  AIDS Res. Hum. Retroviruses 18:1281-1290(2002).
DR  EMBL; AF484508; AAN73711.1; -.
SQ  SEQUENCE 11 AA; 1492 MW; 75C18E6F82D6C364 CRC64;

Query Match      17.6%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 QVM 11
Db  6 QVM 8

RESULT 37
Q9SPT5
ID  Q9SPT5      PRELIMINARY;      PRT;      12 AA.
AC  Q9SPT5;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Topoisomerase II (Fragment).
OS  Pisum sativum (Garden pea).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX  NCBI_TaxID=3888;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=20023730; PubMed=10561074;
RA  Reddy M.K., Nair S., Tewari K.K., Mudgil Y., Yadav B.S., Sopory S.K.;
RT  "Cloning and characterization of a cDNA encoding topoisomerase II in
RT  pea and analysis of its expression in relation to cell
RT  proliferation.";
RL  Plant Mol. Biol. 41:125-137(1999).
DR  EMBL; AF144649; AAD30165.1; -.
KW  Isomerase.
FT  NON TER      12      12
SQ  SEQUENCE 12 AA; 1346 MW; 2A1F261B98B6D737 CRC64;

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Query Match		17.6%;	Score 3;	DB 10;	Length 12;
Best Local Similarity		100.0%;	Pred. No. 7.4e+03;	Indels	0;
Matches		3;	Conservative	0;	Mismatches 0; Gaps 0;
QY	1 LQT 3				
Db	6 LQT 8				
RESULT 38					
P82328					
ID	P82328	PRELIMINARY;	PRT;	12 AA.	
AC	P82328;				
DT	01-JUN-2000 (TrEMBLrel. 14, Created)				
DT	01-JUN-2000 (TrEMBLrel. 14, Last sequence update)				
DT	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)				
DE	Unknown protein from 2D-page of thylakoid lumen (SPOT110) (Fragment).				
OS	Pisum sativum (Garden pea).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.				
OX	NCBI_TaxID=3888;				
RN	[1]				
RP	SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.				
RC	STRAIN=cv. DE GRACE; TISSUE=LEAF;				
RX	MEDLINE=20181728; PubMed=10715320;				
RA	Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,				
RA	Adamska I., van Wijk K.J.;				
RT	"Proteomics of the chloroplast: systematic identification and				
RT	targeting analysis of luminal and peripheral thylakoid proteins.";				
RL	Plant Cell 12:319-341(2000).				
CC	-!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.				
CC	-!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.				
CC	-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN				
CC	PROTEIN IS: 6.0, ITS MW IS: 21.3 KDA.				
KW	Chloroplast; Thylakoid membrane.				
FT	NON TER 12 12				
SQ	SEQUENCE 12 AA; 1264 MW; 96691CBC663B1B01 CRC64;				
Query Match					
Best Local Similarity		17.6%;	Score 3;	DB 10;	Length 12;
Matches		3;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	6 PLL 8				
Db	10 PLL 12				
RESULT 39					
Q9EQV3					
ID	Q9EQV3	PRELIMINARY;	PRT;	12 AA.	
AC	Q9EQV3;				
DT	01-MAR-2001 (TrEMBLrel. 16, Created)				
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)				
DE	Alpha-sarcoglycan (Fragment).				
GN	SGCA.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=21099368; PubMed=11179961;				
RA	Wakabayashi-Takai E., Noguchi S., Ozawa E.;				
RT	"Identification of myogenesis-dependent transcriptional enhancers in				
RT	promoter region of mouse gamma-sarcoglycan gene.";				
RL	Eur. J. Biochem. 268:948-957(2001).				
DR	EMBL; AB044625; BAB18770.1; -.				
FT	NON TER 12 12				
SQ	SEQUENCE 12 AA; 1257 MW; D382726D594361B2 CRC64;				
Query Match					
Best Local Similarity		17.6%;	Score 3;	DB 11;	Length 12;
Matches		3;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	6 PLL 8				
Db	9 PLL 11				
RESULT 40					
Q8QDY5					
ID	Q8QDY5	PRELIMINARY;	PRT;	12 AA.	
AC	Q8QDY5;				
DT	01-JUN-2002 (TrEMBLrel. 21, Created)				
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)				
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)				
DE	Vif protein (Fragment).				
GN	VIF.				
OS	Human immunodeficiency virus 1.				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11676;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=98BY10443;				
RA	Masharsky A.E., Eremin V.F., Kozlov A.P.;				
RT	"Molecular cloning and analysis of full-length human immunodeficiency				
RT	virus type 1 genomes of prevalent strains among IDUs in countries of				
RT	the FSU.";				
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF413998; AAL78467.1; -.				
FT	NON TER 12 12				
SQ	SEQUENCE 12 AA; 1620 MW; 2A05C18B6F82D6C3 CRC64;				
Query Match					
Best Local Similarity		17.6%;	Score 3;	DB 15;	Length 12;
Matches		3;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	9 QVM 11				
Db	6 QVM 8				
RESULT 41					
Q8QE47					
ID	Q8QE47	PRELIMINARY;	PRT;	12 AA.	
AC	Q8QE47;				
DT	01-JUN-2002 (TrEMBLrel. 21, Created)				
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)				
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)				
DE	Vif protein (Fragment).				
GN	VIF.				
OS	Human immunodeficiency virus 1.				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11676;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=98UA0116;				
RA	Masharsky A.E., Eremin V.F., Kozlov A.P.;				
RT	"Molecular cloning and analysis of full-length human immunodeficiency				
RT	virus type 1 genomes of prevalent strains among IDUs in countries of				
RT	the FSU.";				
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF413969; AAL78396.1; -.				
FT	NON_TER 12 12				
SQ	SEQUENCE 12 AA; 1648 MW; 28D5C18B6F82D6C3 CRC64;				
Query Match					
Best Local Similarity		17.6%;	Score 3;	DB 15;	Length 12;
Matches		3;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	9 QVM 11				


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Db          6 QVM 8

RESULT 42
Q8QDY4      PRELIMINARY;      PRT;      12 AA.
AC Q8QDY4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Fragment).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98BY10443;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
RT virus type 1 genomes of prevalent strains among IDUs in countries of
RT the FSU.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413999; AAL78469.1; -.
FT NON TER      12      12
SQ SEQUENCE      12 AA; 1620 MW; 2A05C18E6F82D6C3 CRC64;

Query Match      17.6%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 QVM 11
Db          6 QVM 8

RESULT 43
Q8QE41      PRELIMINARY;      PRT;      12 AA.
AC Q8QE41;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Fragment).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98UA0116;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
RT virus type 1 genomes of prevalent strains among IDUs in countries of
RT the FSU.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413972; AAL78402.1; -.
FT NON TER      12      12
SQ SEQUENCE      12 AA; 1620 MW; 2A05C18E6F82D6C3 CRC64;

Query Match      17.6%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 QVM 11
Db          6 QVM 8

RESULT 44
Q8QE45      PRELIMINARY;      PRT;      12 AA.
AC Q8QE45;

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DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Fragment).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98UA0116;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
RT virus type 1 genomes of prevalent strains among IDUs in countries of
RT the FSU.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413970; AAL78398.1; -.
FT NON TER      12      12
SQ SEQUENCE      12 AA; 1620 MW; 2A05C18E6F82D6C3 CRC64;

Query Match      17.6%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 QVM 11
Db          6 QVM 8

RESULT 45
Q8QE43      PRELIMINARY;      PRT;      12 AA.
AC Q8QE43;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Fragment).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98UA0116;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
RT virus type 1 genomes of prevalent strains among IDUs in countries of
RT the FSU.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413971; AAL78400.1; -.
FT NON TER      12      12
SQ SEQUENCE      12 AA; 1620 MW; 2A05C18E6F82D6C3 CRC64;

Query Match      17.6%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 QVM 11
Db          6 QVM 8

RESULT 46
Q8QDY6      PRELIMINARY;      PRT;      12 AA.
AC Q8QDY6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Fragment).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

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OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98BY10443;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
RT virus type 1 genomes of prevalent strains among IDUs in countries of
RT the FSU.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF4113997; AAL78465.1; -.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1620 MW; 2A05C18E6F82D6C3 CRC64;

Query Match 17.6%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QVM 11
DB 6 QVM 8

RESULT 47
Q9UEE2 PRELIMINARY; PRT; 13 AA.
AC Q9UEE2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE ERGB transcription factor (Fragment).
GN FL11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Obata K., Hiraga H., Nojima T., Yoshida M.C., Abe S.;
RT "Molecular analysis on the breakpoint region of a t(11:22)
RT translocation in Ewing's sarcoma.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB012625; BAA32806.1; -.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1541 MW; 2C677798CB566AB7 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 POP 6
DB 4 POP 6

RESULT 48
Q14182 PRELIMINARY; PRT; 13 AA.
AC Q14182;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE Deoxynucleotidyltransferase (Fragment).
GN DNTT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87213162; PubMed=3579900;
RA Koiwai O., Kaneda T., Morishita R.;
RT "Analysis of human terminal deoxynucleotidyl transferase cDNA

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RT expressible in mammalian cells.";
RL Biochem. Biophys. Res. Commun. 144:185-190 (1987).
DR EMBL; M26144; AAA74588.1; -.
KW Transferase. 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1442 MW; 25B7D365F34FC408 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
DB 8 QPL 10

RESULT 49
Q9UPB6 PRELIMINARY; PRT; 13 AA.
AC Q9UPB6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Multiple inositol polyphosphate phosphatase (Fragment).
GN MIPP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99189241; PubMed=10087200;
RA Chi H., Tiller G.E., Dasouki M.J., Romano P.R., Wang J., O'Keefe R.J.,
RA Fuzas J.E., Rosier R.N., Reynolds P.R.;
RT "Multiple inositol polyphosphate phosphatase: evolution as a distinct
RT group within the histidine phosphatase family and chromosomal
RT localization of the human and mouse genes to chromosomes 10q23 and
RT 19.";
RL Genomics 56:324-336 (1999).
DR EMBL; AF046915; AAD02438.1; -.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1325 MW; C7DF7B7BF157D772 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LQV 10
DB 4 LQV 6

RESULT 50
Q9UM46 PRELIMINARY; PRT; 13 AA.
AC Q9UM46;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hereditary haemochromatosis protein (Fragment).
GN HLA-H.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Hashimoto K., Hirai M., Kurosawa Y.;
RT "Identification of a mouse homolog for the human hereditary
RT haemochromatosis candidate gene.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

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DR EMBL; U80914; AAD00449.1; --
 FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1531 MW; 4352B39C9503BB13 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LQV 10
 Db 11 LQV 13

RESULT 51

Q16007 PRELIMINARY; PRT; 13 AA.

ID Q16007; AC Q16007; DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Lysosomal acid beta-galactosidase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91369478; PubMed=1909871;

RA Morreau H., Bonten E., Zhou X.Y., d'Azzo A.;

RT "Organization of the gene encoding human lysosomal beta-

galactosidase".

RL DNA Cell Biol. 10:495-504(1991).

DR EMBL; S59584; AAB19814.1; --

FT NON_TER 13 13

SQ SEQUENCE 13 AA; 1482 MW; D70DAEE928194412 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
 Db 10 PLL 12

RESULT 52

Q81ZRO

ID Q81ZRO PRELIMINARY; PRT; 13 AA.

AC Q81ZRO; DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Truncated axonemal dynein heavy chain 8 isoform 4 (Fragment).

GN DNAB8.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RX MEDLINE=22233532; PubMed=12297094;

RA Samant S.A., Ogunkua O., Hui L., Fossella J., Pilder S.H.;

RT "The t complex distorter 2 candidate gene, Dnahc8, encodes at least

two testis-specific axonemal dynein heavy chains that differ

extensively at their amino and carboxyl termini.";

RL Dev. Biol. 250:24-43(2002).

DR EMBL; AF527623; AAN34634.1; --

FT NON_TER 1 1

SQ SEQUENCE 13 AA; 1604 MW; 4569A2F01AA92727 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
 Db 8 LLQ 10

RESULT 53

Q9U7D6

ID Q9U7D6 PRELIMINARY; PRT; 13 AA.

AC Q9U7D6; DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE Ycf24 protein (Fragment).

GN YCF24.

OS Neospora caninum.

OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;

OC Neospora.

OX NCBI_TaxID=29176;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Nci;

RX MEDLINE=20074141; PubMed=10608442;

RA Lang-Unnasch N., Aiello D.P.;

RT "Sequence evidence for an altered genetic code in the Neospora caninum

plastid.";

RL Int. J. Parasitol. 29:1557-1562(1999).

DR EMBL; AF138960; AAF14260.1; --

FT NON_TER 1 1

SQ SEQUENCE 13 AA; 1532 MW; CC8DB4011FDCD40D CRC64;

Query Match 17.6%; Score 3; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
 Db 1 PLL 3

RESULT 54

O97122

ID O97122 PRELIMINARY; PRT; 13 AA.

AC O97122; DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)

DE Ycf24 protein (Fragment).

GN YCF24.

OS Toxoplasma gondii.

OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;

OC Toxoplasma.

OX NCBI_TaxID=5811;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RH;

RA Aiello D.P., Lang-Unnasch N.;

RT "Analysis of the rpoB gene product of Toxoplasma gondii.";

RL Submitted (SEP-1998) to the EMBL/GenBank/DDAJ databases.

DR EMBL; AF095904; AAD17841.1; --

FT NON_TER 1 1

SQ SEQUENCE 13 AA; 1532 MW; CC8DB4011FDCD40D CRC64;

Query Match 17.6%; Score 3; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
 Db 1 PLL 3

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RESULT 55
Q9R2Z4 ID Q9R2Z4 PRELIMINARY; PRT; 14 AA.
AC Q9R2Z4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Flagellin A (Fragment).
GN FLAA.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RA Studer E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,
RA Candrian U.;
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter
RT coli PCR products amplified directly from environmental samples.";
RL Food Sci. Technol. 31:337-345(1998).
DR EMBL; AJ133577; CAB39387.1; -
DR EMBL; AJ133577; CAB39387.1; -
DR EMBL; AJ133572; CAB39382.1; -
DR EMBL; AJ133573; CAB39383.1; -
FT NON TER 1
FT SEQUENCE 14 AA; 1599 MW; C7C4BEB7A1739156 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred.No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQ 9
Db 12 LLQ 14

RESULT 56
Q9R5I7 ID Q9R5I7 PRELIMINARY; PRT; 14 AA.
AC Q9R5I7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Fimbrial antigen F165 subunit 1 (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE.
RX MEDLINE=92381496; PubMed=1355108;
RA Harel J., Forget C., Saint-Amand J., Daigle F., Dubreuil D.,
RA Jacques M., Fairbrother J.;
RT "Molecular cloning of a determinant coding for fimbrial antigen
RT F165(1), a Prs-like fimbrial antigen from porcine septicaemic
RT Escherichia coli.";
RL J.Gen. Microbiol. 138:1495-1502(1992).
SQ SEQUENCE 14 AA; 1431 MW; 3B5981F6811863D8 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred.No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPQ 5
Db 4 TPQ 6

RESULT 57

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Q9R2Z5 ID Q9R2Z5 PRELIMINARY; PRT; 14 AA.
AC Q9R2Z5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Flagellin A (Fragment).
GN FLAA.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RA Studer E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,
RA Candrian U.;
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter
RT coli PCR products amplified directly from environmental samples.";
RL Food Sci. Technol. 31:337-345(1998).
DR EMBL; AJ133567; CAB55353.1; -
DR EMBL; AJ133568; CAB39378.1; -
DR EMBL; AJ133569; CAB39379.1; -
DR EMBL; AJ133570; CAB39380.1; -
DR EMBL; AJ133571; CAB39381.1; -
DR EMBL; AJ133574; CAB39384.1; -
DR EMBL; AJ133575; CAB39385.1; -
DR EMBL; AJ133576; CAB39386.1; -
FT NON TER 1
FT SEQUENCE 14 AA; 1611 MW; C7C0EFB7A1739156 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred.No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQ 9
Db 12 LLQ 14

RESULT 58
Q8RK22 ID Q8RK22 PRELIMINARY; PRT; 14 AA.
AC Q8RK22;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Transposase (Fragment).
GN TNPA.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TC29-5; TRANSPOSON=Tn5041B;
RA Khodoli G.Y., Gorlenko Z.M., Mindlin S.Z., Nikiforov V.G.;
RT "Distribution of distinct microvariants of Tn5041 in environmental
RT bacteria.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ422232; CAD19590.1; -
FT NON TER 14
FT SEQUENCE 14 AA; 1535 MW; 866834EPB82164C1 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred.No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLL 8

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Db          10 PLL 12

RESULT 59
Q9X715
ID Q9X715 PRELIMINARY; PRT; 14 AA.
AC Q9X715;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Flagellin A (Fragment).
GN FLAA.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RA Studer E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,
RA Candrian U.;
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter
RT coli PCR products amplified directly from environmental samples.";
RL Food Sci. Technol. 31:337-345(1998).
DR EMBL; AJ133578; CAB39368.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1595 MW; C7C0F96DA1739156 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
Db 12 LLQ 14

RESULT 60
Q9WW79
ID Q9WW79 PRELIMINARY; PRT; 14 AA.
AC Q9WW79;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Flagellin A (Fragment).
GN FLAA.
OS Campylobacter coli.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=195;
RN [1]
RP SEQUENCE FROM N.A.
RA Studer E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,
RA Candrian U.;
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter
RT coli PCR products amplified directly from environmental samples.";
RL Food Sci. Technol. 31:337-345(1998).
DR EMBL; AJ133579; CAB39377.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1611 MW; C7C0EB7A1739156 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
Db 12 LLQ 14

RESULT 61
Q8GMC4
ID Q8GMC4 PRELIMINARY; PRT; 14 AA.
AC Q8GMC4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rpos (Fragment).
GN RPOS.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RA Kotevich M.L., Li B., Levy D.D., LeClerc J.E., Shifflet A.W.,
RA Cebula T.A.;
RT "Evolution of multi-gene segments in the mutS-rpos intergenic region
RT of Salmonella enterica serovar Typhimurium LT2.";
RL Microbiology 148:2531-2540(2002).
DR EMBL; AY050714; AAL24442.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1632 MW; 032FD6D26DD06C54 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3
Db 1 LQT 3

RESULT 62
Q9TWW0
ID Q9TWW0 PRELIMINARY; PRT; 14 AA.
AC Q9TWW0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Histone C (fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE.
RX MEDLINE=93064852; PubMed=1437281;
RA Bender K., Betschart B., Schaller J., Kampfer U., Hecker H.;
RT "Sequence differences between histones of procyclic Trypanosoma brucei
RT brucei and higher eukaryotes.";
RL Parasitology 105:97-104(1992).
SQ SEQUENCE 14 AA; 1480 MW; 460FF4E8876C4EC7 CRC64;

Query Match 17.6%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3
Db 1 LQT 3

RESULT 63
Q9ZRS3
ID Q9ZRS3 PRELIMINARY; PRT; 14 AA.
AC Q9ZRS3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)

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DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Knotted-like homeobox protein (Fragment).
GN KNAF1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. C24;
RA Raap M., Heyer A.G.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131822; CAA10513.1; --
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1722 MW; 9B3ADC59F1EB8D4A CRC64;

Query Match 17.6%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPQ 5
Db 11 TPQ 13

RESULT 64
Q8V1H7 PRELIMINARY; PRT; 14 AA.
AC Q8V1H7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Truncated HBAg.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FH10;
RA Wen Y.M., Liu F., Ma Z.M.;
RT "Structural and functional analysis of hepatitis B virus genomes in
RT fulminant hepatitis B patients.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461362; AAL66336.1; --
SQ SEQUENCE 14 AA; 1427 MW; 2F487846CB391E28 CRC64;

Query Match 17.6%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLL 8
Db 11 PLL 13

RESULT 65
Q9PY99 PRELIMINARY; PRT; 14 AA.
AC Q9PY99;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE NON-structural protein (Truncated NON-structural protein).
OS Murine hepatitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11138;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MHV-2;

```

```

RA Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.;
RT "Pathogenesis and sequence analysis of mouse hepatitis virus type 2:
RT an experimental model system of acute meningitis and hepatitis in
RT mice.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PENN 97-1;
RA Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.;
RT "Pathogenesis and sequence analysis of mouse hepatitis virus type 2;
RT an experimental model system of acute meningitis and hepatitis in
RT mice.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF201929; AAP19387.1; --
DR EMBL; AF208066; AAF69340.1; --
SQ SEQUENCE 14 AA; 1534 MW; C2FD164C12169242 CRC64;

Query Match 17.6%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LQV 10
Db 12 LQV 14

RESULT 66
Q88400 PRELIMINARY; PRT; 14 AA.
AC Q88400;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tax protein (Fragment).
DE TAX.
GN Simian T-lymphotropic virus 1.
OS Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=33747;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94082462; PubMed=8259665;
RA Sakseena N.K., Hervé V., Durand J.P., LeGuanno B., Diop O.M.,
RA Digoutte J.P., Mathiot C., Muller M.C., Love J.L., Benz P.M.,
RA Erensoy S., Barre-Sinoussi F., Poiesz B.J.;
RT "Seroepidemiologic, molecular, and phylogenetic analyses of simian T-
RT cell leukemia viruses (STLV-I) from various naturally infected monkey
RT species from central and western Africa.";
RL Virology 198;297-310(1993).
DR EMBL; L20363; AAA47870.1; --
DR InterPro; IPR004120; Tax.
DR Pfam; PF02959; Tax; 1.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1394 MW; 8BA7726C9C6D387A CRC64;

Query Match 17.6%; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QGD 17
Db 5 QGD 7

RESULT 67
Q9R5A0 PRELIMINARY; PRT; 15 AA.
AC Q9R5A0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE DNA topoisomerase I (Fragment).
OS Micrococcus luteus (Micrococcus lysodeikticus).

```

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcineae; Micrococcaceae; Micrococcus.
 OX NCBI_TaxID=1270;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=93249439; PubMed=8387285;
 RA Anderluzzi D., Pedrini A.M.;
 RT "Structural similarities between M. luteus and E. coli DNA
 RT topoisomerase I.";
 RL Biochem. Biophys. Res. Commun. 192:657-664(1993).
 SQ SEQUENCE 15 AA; 1602 MW; 2B5457836F151383 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTP 4
 Db |||
 6 QTP 8

RESULT 68

Q9X637
 ID Q9X637 PRELIMINARY; PRT; 15 AA.
 AC Q9X637;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE MERT (Fragment).
 GN MERT.

OS Klebsiella oxytoca.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.

OX NCBI_TaxID=571;

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=509H;
 RX MEDLINE=97208220; PubMed=9055422;

RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative
 RT bacteria isolated from the fecal flora of primates.";
 RL Appl. Environ. Microbiol. 63:1066-1076(1997).
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=509H;
 RX MEDLINE=98027386; PubMed=9361435;

RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
 RT "Association of mercury resistance with antibiotic resistance in the
 RT gram-negative fecal bacteria of primates.";
 RL Appl. Environ. Microbiol. 63:4494-4503(1997).
 RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=509H;
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;

RT "15-bp tandem repeats occur at a sharp transition in gc content in the
 RT mer operon.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF131272; AAD37141.1; -.

DR InterPro; IPR003457; Transprt_Mert.

DR Pfam; PF02411; Mert; 1.

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1492 MW; 65BF0C9827A585D CRC64;

Query Match

Best Local Similarity 17.6%; Score 3; DB 2; Length 15;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
 Db |||
 3 EPQ 5

RESULT 69

Q9UMT6

ID Q9UMT6 PRELIMINARY; PRT; 15 AA.

AC Q9UMT6;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE VEGF related factor (Fragment).
 GN VRF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Grimmond S., Lagercrantz J., Drinkwater C., Silins G., Townson S.,
 RA Pollock P., Gotley D., Carson E., Rakar S., Nordenskjold M., Ward L.,
 RA Hayward N., Weber G.;
 RT "Cloning and characterization of a novel human gene related to
 RT vascular endothelial growth factor.";
 RL Genome Res. 6:122-129(1996).
 DR EMBL; U43370; AAA91464.1; -.
 FT NON_TER 15 15

Q9X635

ID Q9X635 PRELIMINARY; PRT; 15 AA.

AC Q9X635;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE MERT (Fragment).
 GN MERT.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=390;

RX MEDLINE=97208220; PubMed=9055422;

RA Liebert C.A., Wireman J., Smith T., Summers A.O.;

RT "Phylogeny of mercury resistance (mer) operons of gram-negative

RT bacteria isolated from the fecal flora of primates.";

RL Appl. Environ. Microbiol. 63:1066-1076(1997).
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=390;

RX MEDLINE=98027386; PubMed=9361435;

RA Wireman J., Liebert C.A., Smith T., Summers A.O.;

RT "Association of mercury resistance with antibiotic resistance in the

RT gram-negative fecal bacteria of primates.";

RL Appl. Environ. Microbiol. 63:4494-4503(1997).
 RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=390;

RA Wireman J., Liebert C.A., Smith T., Summers A.O.;

RT "15-bp tandem repeats occur at a sharp transition in gc content in the

RT mer operon.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF131271; AAD37139.1; -.

DR InterPro; IPR003457; Transprt_Mert.

DR Pfam; PF02411; Mert; 1.

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1492 MW; 65BF0C9827A585D CRC64;

Query Match

Best Local Similarity 17.6%; Score 3; DB 2; Length 15;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15

Db |||

3 EPQ 5

RESULT 70

Q9UMT6

ID Q9UMT6 PRELIMINARY; PRT; 15 AA.

AC Q9UMT6;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE VEGF related factor (Fragment).
 GN VRF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Grimmond S., Lagercrantz J., Drinkwater C., Silins G., Townson S.,
 RA Pollock P., Gotley D., Carson E., Rakar S., Nordenskjold M., Ward L.,
 RA Hayward N., Weber G.;
 RT "Cloning and characterization of a novel human gene related to
 RT vascular endothelial growth factor.";
 RL Genome Res. 6:122-129(1996).
 DR EMBL; U43370; AAA91464.1; -.
 FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1708 MW; 5D0AE30FE481A71E CRC64;

Query Match 17.6%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
|
|
|
Db 3 PLL 5

RESULT 71

ID P78482 PRELIMINARY; PRT; 15 AA.

AC P78482;

DT 01-MAY-1997 (TReMBLrel. 03, Created)

DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE APOB protein (Fragment).

GN APOB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88018019; PubMed=3659919;

RA Chen S.-H., Habib G., Yang C.-Y., Gu Z.-W., Lee B.R., Weng S.-A.,
RA Silberman S.R., Cai S.-J., Deslypere J.P., Rosseanu M.,
RA Gatto A.M., Jr., Li W.-H., Chan L.;
RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-
RT specific in-frame stop codon.";
RL Science 238:363-366 (1987).

DR EMBL; M18036; AARS1754.1; -.

FT NON_TER 1

SQ SEQUENCE 15 AA; 1842 MW; 9172790C16559AE8 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3
|
|
|
Db 10 LQT 12

RESULT 72

ID Q96RX1 PRELIMINARY; PRT; 15 AA.

AC Q96RX1;

DT 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE Leucocyte differentiation antigen CD84 (Fragment).

GN CD84.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20208572; PubMed=10746783;

RA Palou E., Pirotto F., Sole J., Freed J.H., Peral B., Vilardell C.,
RA Vilella R., Vives J., Gaya A.;
RT "Genomic characterization of CD84 reveals the existence of five
RT isoforms differing in their cytoplasmic domains.";
RL Tissue Antigens 55:118-127 (2000).

DR EMBL; AF114490; AAK68906.1; -.

FT NON_TER 15

SQ SEQUENCE 15 AA; 1820 MW; 1F23F01D9B227D19 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3
|
|
|
Db 13 LQT 15

RESULT 73

ID Q9UC60 PRELIMINARY; PRT; 15 AA.

AC Q9UC60;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)

DE N-acetylmuramyl-L-alanine amidase (EC 3.5.1.28) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=95392215; PubMed=7663175;

RA De Pauw P., Neyt C., Vanderwinkel E., Wattiez R., Falmagne P.;
RT "Characterization of human serum N-acetylmuramyl-L-alanine amidase
RT purified by affinity chromatography.";
RL Protein Expr. Purif. 6:371-378 (1995).

SQ SEQUENCE 15 AA; 1600 MW; 9016B00FFF9F9E780A CRC64;

Query Match 17.6%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
|
|
|
Db 3 PLL 5

RESULT 74

ID Q9TRP1 PRELIMINARY; PRT; 15 AA.

AC Q9TRP1;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)

DE LOW Mr zona pellucida binding protein (Fragment).

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE.

RX MEDLINE=92378826; PubMed=1510840;

RA Parry R.V., Barker P.J., Jones R.;
RT "Characterization of low Mr zona pellucida binding proteins from boar
RT spermatozoa and seminal plasma.";
RL Mol. Reprod. Dev. 33:108-115 (1992).

SQ SEQUENCE 15 AA; 1736 MW; 668FA50BB6120B7C CRC64;

Query Match 17.6%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
|
|
|
Db 11 LLQ 13

RESULT 75

ID Q9TNQ1 PRELIMINARY; PRT; 15 AA.

AC Q9TNQ1;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta 2M- class I-binding PEPTIDE-MAJOR histocompatibility complex
DE H-2KB-specific molecule POORLY associated with beta 2-microglobulin
DE (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=94240094; PubMed=8183884;
RA Joyce S., Kuzushima K., Kepecs G., Angeletti R.H., Nathenson S.G.;
RT "Characterization of an incompletely assembled major
RT histocompatibility class I molecule (H-2KB) associated with unusually
RT long peptides: implications for antigen processing and presentation.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149(1994).
KW MHC.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1754 MW; 2CEACDA0F1180DC7 CRC64;

Query Match 17.6%; Score 3; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
Db 4 LLQ 6

Search completed: November 25, 2003, 18:25:11
Job time : 44.0128 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 55.0691 Seconds
(without alignments)
48.999 Million cell updates/sec

Title: US-09-641-801-2

Perfect score: 17

Sequence: 1 LQTQPLQLQVMPEQGD 17

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	17	100.0	17	22	Colostrin peptid
3	17	100.0	17	22	Colostrin peptid
4	17	100.0	17	22	Ewe colostrin pe
5	17	100.0	17	22	Colostrin consti
6	17	100.0	17	23	Colostrin consti
7	17	100.0	17	23	Neural cell regula
8	17	100.0	18	22	Ewe colostrin pe
9	11	64.7	11	22	Colostrin peptid

10	11	64.7	12	22	AAE07195	Modified colostrin
11	6	35.3	8	13	AAE21055	Gamma-carboxylase,
12	6	35.3	18	22	ABG55849	Human liver peptid
13	6	35.3	18	22	ABB40529	Peptide #8035 enco
14	6	35.3	18	22	ABB24849	Protein #6848 enco
15	6	35.3	18	22	AAE61355	Human brain expres
16	6	35.3	18	22	AAE74093	Human bone marrow
17	6	35.3	18	22	AAE20225	Peptide #6659 enco
18	6	35.3	18	22	AAE34255	Peptide #8292 enco
19	6	35.3	18	23	ABG43991	Human peptide enco
20	5	29.4	7	18	AAE17515	Protein kinase C r
21	5	29.4	10	22	AAE87925	Saccharomycs cere
22	5	29.4	13	21	AAE44382	Human secreted pro
23	5	29.4	14	22	AAE98787	Human peptide #206
24	5	29.4	14	22	AAE98788	Human peptide #206
25	4	23.5	4	24	AAE33717	GNA33 mAb 25 recog
26	4	23.5	5	22	AAU07164	Substituted phenan
27	4	23.5	6	16	AAE83532	Zif268 zinc finger
28	4	23.5	6	20	AAE21560	Target hexapeptide
29	4	23.5	6	20	AAE84430	HIV-1 nucleic acid
30	4	23.5	6	24	AAE33713	N. meningitidis se
31	4	23.5	7	10	AAE90659	New antihypertensi
32	4	23.5	7	14	AAE38240	Alzheimer paired h
33	4	23.5	7	14	AAE37559	Phosphorylated tau
34	4	23.5	7	18	AAE27488	Tyrosinase cytopla
35	4	23.5	7	18	AAE17516	Protein kinase C r
36	4	23.5	7	22	AAE79271	Peptide which bind
37	4	23.5	7	22	AAE45859	H11 binding site c
38	4	23.5	7	22	AAE45914	H11 binding site c
39	4	23.5	7	22	AAE45919	H11 binding site c
40	4	23.5	7	22	AAE45924	H11 binding site c
41	4	23.5	7	22	AAE45929	H11 binding site c
42	4	23.5	7	24	AAE33721	N. meningitidis se
43	4	23.5	8	10	AAE90673	New antihypertensi
44	4	23.5	8	11	AAE03875	Hypertensive peptid
45	4	23.5	8	17	AAE93206	New contraceptive
46	4	23.5	8	22	AAE23045	HIV peptide SEQ ID
47	4	23.5	8	22	AAE23046	HIV peptide SEQ ID
48	4	23.5	8	22	AAE23047	HIV peptide SEQ ID
49	4	23.5	8	23	ABG91967	Human antibody fra
50	4	23.5	8	23	ABG91998	Human antibody fra
51	4	23.5	8	23	ABG78276	Human Fv molecule
52	4	23.5	8	23	ABG78307	Human Fv molecule
53	4	23.5	8	23	AAO17346	Alpha-isomaltosylg
54	4	23.5	8	23	ABE05026	Bacillus globispor
55	4	23.5	9	10	AAE90672	New antihypertensi
56	4	23.5	9	16	AAE84629	Wheat acetyl-Coenz
57	4	23.5	9	18	AAE17493	Protein kinase C-t
58	4	23.5	9	19	AAE60385	Tumour homing pept
59	4	23.5	9	19	AAE52801	Signal region from
60	4	23.5	9	19	AAE52802	Signal region from
61	4	23.5	9	20	AAE47643	Immunogenic peptid
62	4	23.5	9	20	AAE93711	Human breast cance
63	4	23.5	9	21	AAE21802	Human breast tumou
64	4	23.5	9	21	AAE95224	Anti-platelet glyc
65	4	23.5	9	21	AAE67365	Melanosomal protei
66	4	23.5	9	22	AAE06380	Human breast tumou
67	4	23.5	9	23	ABE15201	Immunogenic HIV pe
68	4	23.5	9	23	ABG91962	Human antibody fra
69	4	23.5	9	23	ABG91975	Human antibody fra
70	4	23.5	9	23	ABG94766	Replikin sequence
71	4	23.5	9	23	ABG78271	Human Fv molecule
72	4	23.5	9	23	ABG78284	Human Fv molecule
73	4	23.5	9	23	ABE62412	Human immunopeptid
74	4	23.5	9	23	ABE01401	158P1D7 related HL
75	4	23.5	9	23	ABE01433	158P1D7 related HL
76	4	23.5	9	23	ABE01978	158P1D7 related HL
77	4	23.5	9	23	AAU71127	Human MHC class I
78	4	23.5	9	23	AAU71209	Human MHC class I
79	4	23.5	9	23	AAU71435	Human MHC molecule
80	4	23.5	9	23	AAU71541	Human MHC class I
81	4	23.5	9	23	AAU71625	Human MHC class I
82	4	23.5	9	24	ABE04957	Human cancer-relat

83 Human cancer-relat
84 Human cancer-relat
85 Replikin peptide s
86 Human tyrosinase e
87 New antihypertensi
88 Human melanoma ass
89 Angiotensin conver
90 Plasmid pBS24Ubalp
91 Hepatitis GB virus
92 Human Leukocyte An
93 Human Leukocyte An
94 Mycoplasma genital
95 Saccharomyces cere
96 158P1D7 related HL
97 158P1D7 related HL
98 158P1D7 related HL
99 158P1D7 related HL
100 158P1D7 related HL

ALIGNMENTS

RESULT 1
AAB72247
ID AAB72247 standard; peptide; 17 AA.
XX AC AAB72247;
XX AC
DT 14-MAY-2001 (first entry)
XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 2.
XX
XX Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
XX Synthetic.
XX
XX WO200111937-A2.
PN
XX 22-FEB-2001.
PD
XX 17-AUG-2000; 2000WO-US22818.
XX
XX 17-AUG-1999; 99US-0149311.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PA (REG-) REGEN THERAPEUTICS PLC.
XX
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
PI WPI; 2001-202804/20.
XX
XX
XX Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator .
XX
XX Claim 1; Page 34; 50pp; English.

Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
a proline rich polypeptide aggregate contained in colostrum. The
peptides have immune response modulatory activity, and are capable of
inducing cytokines. Colostrinin and its derived peptides are useful for
inducing cytokine production, for modulating an immunological response
and for inducing blood cell proliferation. The peptides are useful in the
treatment of disorders of the central nervous system, neurological
disorders, mental disorders, dementia, neurodegenerative diseases,
Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
disorders of the immune system, bacterial and viral infections and
acquired immunological deficiencies.

XX Sequence 17 AA;
SQ
Query Match 100.0%; Score 17; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQTPQPLQVMMPEQGD 17
Db 1 LQTPQPLQVMMPEQGD 17
RESULT 2
AAB72501
ID AAB72501 standard; Peptide; 17 AA.
XX AC AAB72501;
XX DT 09-MAY-2001 (first entry)
XX DE Colostrinin peptide #2.
XX KW Dermatological; oxidative stress regulator; colostrinin.
XX OS Unidentified.
XX PN WO200112650-A2.
XX PD 22-FEB-2001.
XX PF 17-AUG-2000; 2000WO-US22665.
XX PR 17-AUG-1999; 99US-0149310.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Stanton GJ, Hughes TK, Boldogh I;
XX WPI; 2001-218342/22.
XX
XX Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -
XX
XX Claim 6; Page 25; 48pp; English.
XX
XX The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.
XX
XX Sequence 17 AA;
SQ
Query Match 100.0%; Score 17; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQTPQPLQVMMPEQGD 17
Db 1 LQTPQPLQVMMPEQGD 17
RESULT 3
AAB72533
ID AAB72533 standard; Peptide; 17 AA.
XX AC AAB72533;
XX DT 09-MAY-2001 (first entry)
XX

DE Colostrinin peptide #2.
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX Unidentified.
 OS
 XX WO200112651-A2.
 PN
 XX 22-FEB-2001.
 PD
 XX 17-AUG-2000; 2000WO-US22774.
 PF
 XX 17-AUG-1999; 99US-0149633.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Boldogh I;
 PI
 XX WPI; 2001-226545/23.
 DR
 XX Use of colostrinin, its constituent peptide or analog as a neural cell
 CC regulator, for promoting neural cell differentiation and treating
 CC damaged neural cells in a patient -
 CC
 CC Claim 6; Page 21; 35pp; English.
 PS
 XX The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 CC
 XX Sequence 17 AA;
 SQ
 Query Match 100.0%; Score 17; DB 22; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.2e-11;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQTPQPLLQVMMEPQGD 17
 DB 1 LQTPQPLLQVMMEPQGD 17
 DE
 AAB59310
 ID AAB59310 standard; Peptide; 17 AA.
 XX
 AC AAB59310;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Ewe colostrinin peptide fragment A-1.
 XX
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 OS Ovis sp.
 XX
 PN WO200075173-A2.
 XX
 PD 14-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-GB02128.
 XX
 PR 02-JUN-1999; 99GB-0012852.
 XX
 XX (REG-) REGEN THERAPEUTICS PLC.
 PA
 XX Georgiades JA;
 PI
 XX WPI; 2001-071058/08.
 DR
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 PS Claim 7; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 17; DB 22; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.2e-11;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQTPQPLLQVMMEPQGD 17
 DB 1 LQTPQPLLQVMMEPQGD 17
 DE
 AAE20229
 ID AAE20229 standard; peptide; 17 AA.
 XX
 AC AAE20229;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Colostrinin constituent peptide #2.
 XX
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnary.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 17 /note= "Optionally C-terminal amide"
 FT
 XX WO200213850-A1.
 PN
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22776.
 PF
 XX 17-AUG-2000; 2000WO-US22776.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Stanton GJ, Hughes TK, Boldogh I;
 PI
 XX WPI; 2002-269151/31.
 DR
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 XX
 PS Claim 6; Page 25; 51pp; English.
 XX
 CC The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 17; DB 23; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMPEQGD 17
|||||
Db 1 LQTPQPLLQVMPEQGD 17
|||||

RESULT 6
AAM51037
ID AAM51037 standard; Peptide; 17 AA.
AC AAM51037;
DT 30-MAY-2002 (first entry)
XX Colostrinin constituent peptide.
XX Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; human.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 17 /note= "optional C-terminal amidation"
FT
FT
XX WO200213849-A1.
XX 21-FEB-2002.
XX 17-AUG-2000; 2000WO-US22775.
XX 17-AUG-2000; 2000WO-US22775.
XX (TEXA) UNIV TEXAS SYSTEM.
PA (REGG-) REGEN THERAPEUTICS PLC.
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX WPI; 2002-269150/31.
XX
XX Modulation of blood cell proliferation in a patient involves use of
PT blood cell regulator selected from colostrinin, its constituent peptide
PT and/or analogue -
XX
XX Claim 1; Page 34; 54pp; English.
XX
XX The present sequence is that of a colostrinin constituent peptide
CC that is preferred for use as an immunological regulator and as a
CC blood cell regulator in claimed methods of the invention. Methods
CC are claimed for: inducing a cytokine in a cell by contact with an
CC immunological regulator, where the cell is present in a cell
CC culture, a tissue, an organ or an organism, and the cell is
CC mammalian, including human; modulating an immune response in a cell
CC by contact with the immunological regulator under conditions
CC effective to induce a cytokine; modulating an immune response in a

CC patient by administering an immunological regulator under conditions
CC effective to induce a cytokine, where the immunological regulator
CC is administered topically or as part of a dietary supplement, and
CC where the immune response is specific or non specific, an interferon
CC response or an antibody response; modulating blood cell proliferation
CC by contacting blood cells with a blood cell regulator, where the
CC blood cells are present in a cell culture or an organism, are
CC mammalian or human, and where the blood cells are increased in
CC number or differentiated; and a method for modulating blood cell
CC proliferation in a patent. A claimed cytokine-inducing composition
CC comprises a pharmaceutical carrier and an active agent such as the
CC present peptide. Cytokines induced by this peptide in human
CC leucocyte cultures include interferon-gamma, tumour necrosis
CC factor-alpha, interleukin-4, interleukin-6, interleukin-10 and
CC interleukin-12. It was one of the best overall inducers in almost
CC all cytokine and blood cell proliferation experiments conducted.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 17; DB 23; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMPEQGD 17
|||||
Db 1 LQTPQPLLQVMPEQGD 17
|||||

RESULT 7
AAO14578
ID AAO14578 standard; peptide; 17 AA.
AC AAO14578;
DT 27-MAY-2002 (first entry)
XX Neural cell regulatory colostrinin peptide 2.
XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
KW neural cell treatment.
XX Unidentified.
XX
XX Key Location/Qualifiers
FH Modified-site 17 /note= "Optional C-terminal amide"
FT
FT
XX WO200213851-A1.
XX 21-FEB-2002.
XX 17-AUG-2000; 2000WO-US22777.
XX 17-AUG-2000; 2000WO-US22777.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Boldogh I, Stanton JG, Hughes TK;
XX WPI; 2002-269152/31.
XX
XX Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog -
XX
XX Claim 7; Page 21; 37pp; English.
XX
XX The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the

CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 17; DB 23; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.2e-11;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQLQVMMPEPQGD 17
 |||||
 Db 1 LQTPQLQVMMPEPQGD 17
 |||||

RESULT 8

AAE07185
 ID AAB59341 standard; Peptide; 18 AA.

XX AC AAB59341;

DT 21-MAR-2001 (first entry)

XX Ewe colostrinin peptide fragment derived sequence #1.

DE Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX Ovis sp.

XX WO200075173-A2.

PN 14-DEC-2000.

XX 02-JUN-2000; 2000WO-GB02128.

XX 02-JUN-1999; 99GB-0012852.

XX (REG-) REGEN THERAPEUTICS PLC.

PA Georgiades JA;

XX WPI; 2001-071058/08.

XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system

PT and immune system, viral and bacterial infections, and diseases

PT characterized by amyloid plaques -

XX Claim 8; Page 27; 63pp; English.

XX The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 17; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.4e-11;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQLQVMMPEPQGD 17
 |||||
 Db 2 LQTPQLQVMMPEPQGD 18
 |||||

RESULT 9

AAE07195
 ID AAE07195 standard; peptide; 12 AA.

AAE07185

ID AAE07185 standard; peptide; 11 AA.

XX AC AAE07185;

XX 06-NOV-2001 (first entry)

XX Colostrinin peptide 1.

DE Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral.

XX Unidentified.

XX WO200155199-A1.

PD 02-AUG-2001.

XX 26-JAN-2001; 2001WO-GB00329.

XX 26-JAN-2000; 2000GB-0001825.

XX (REG-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -

XX Claim 1; Page 15; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is colostrinin peptide 1 related to the invention.

XX SQ Sequence 11 AA;

Query Match 64.7%; Score 11; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.3e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPQLQVMMPEPQ 15
 |||||
 Db 1 QPQLQVMMPEPQ 11
 |||||

RESULT 10

AAE07195

```

XX AAE07195;
XX AC
XX 06-NOV-2001 (first entry)
XX DE
XX Modified colostrinin cyclic peptide #1.
XX DE
XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
XX KW Central nervous system disorder; neurodegenerative disorder; weight loss;
XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
XX KW acquired immunological deficiency; neurological disorder; dementia;
XX KW antiviral; cyclic.
XX OS Synthetic.
XX FH
XX Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "N-terminal acetyl; this residue forms a cyclic
XX FT linkage with Gln found at the C-terminal end"
XX FT
XX PN WO200155199-A1.
XX XX
XX 02-AUG-2001.
XX XX
XX 26-JAN-2001; 2001WO-GB00329.
XX PF
XX 26-JAN-2000; 2000GB-0001825.
XX PR
XX (REG- ) REGEN THERAPEUTICS PLC.
XX PA
XX Georgiades JA;
XX PI
XX WPI; 2001-488775/53.
XX DR
XX
XX Peptide useful as an inter alia in the treatment of e.g. disorders of
XX PT the immune system and the central nervous system comprises ten
XX PT amino-terminal amino acid sequence derived from peptides present in
XX PT colostrinin -
XX XX
XX Example 2; Page 8; 40pp; English.
XX
XX The invention relates to colostrinin peptide fragments which are useful,
XX CC inter alia, in the treatment of chronic disorders of the immune system
XX CC and the central nervous system. Colostrinin peptides are used as a
XX CC medicament in the treatment of neurological disorders e.g., dementia,
XX CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
XX CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
XX CC neurosis, in acquired immunological deficiencies, chronic bacterial and
XX CC viral infections and diseases characterised by the presence of beta-
XX CC amyloid plaques and as a dietary supplement for babies, small children,
XX CC adults and senile persons, who have been subjected to chemotherapy or
XX CC have suffered from cachexia or weight loss due to the chronic disease.
XX CC Colostrinin peptides are also used as food additives and as an auxiliary
XX CC withdrawal treatment for drug addicts, after a period of detoxification
XX CC and in persons dependent on stimulants. Colostrinin peptides are used to
XX CC prepare antibodies and to treat emotional disturbances, e.g. emotional
XX CC disturbances of psychiatric patients in a state of depression. These
XX CC colostrinin peptides improves the development of immune system in a new
XX CC born child and to correct the immunological deficiencies in a child.
XX CC The present sequence is modified colostrinin cyclic peptide #1 related to
XX CC the invention.
XX XX
XX Sequence 12 AA;
XX SQ
XX Query Match 64.7%; Score 11; DB 22; Length 12;
XX Best Local Similarity 100.0%; Pred.No. 5.8e-05;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 5 QPLLQVMMEPQ 15
XX Db 2 QPLLQVMMEPQ 12

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RESULT 11
AAR21055
ID AAR21055 standard; Peptide; 8 AA.
XX
XX AAR21055;
XX AC
XX 25-MAR-2003 (updated)
XX DT 01-JUN-1992 (first entry)
XX DE Gamma-carboxylase, N-terminus.
XX KW Degenerate; Vitamin K dependent proteins; PCR.
XX OS Homo sapiens.
XX PN WO9201795-A.
XX PD 06-FEB-1992.
XX PF 22-JUL-1991; 91WO-US05177.
XX PR 14-MAR-1991; 91US-0669735.
XX PR 23-JUL-1990; 90US-0557220.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Berkner KL;
XX WPI; 1992-064951/08.
XX Gamma-carboxylase protein compens. - used in recombinant prodn.
XX PT of active vitamin-K dependent proteins
XX PS Claim 6; Table 9; 91pp; English.
XX CC Nucleotide sequences encoding gamma-carboxylase were obtd. using PCR,
XX CC and oligonucleotides designed from amino acid sequences determined
XX CC by oligosequencing of partially purified material. SEQ ID No 19
XX CC (peptide 5) is one of seven alternative sequences for the N-terminus
XX CC of gamma carboxylase, due to the degeneracy of the genetic code.
XX CC Obtaining the full DNA and protein sequence of gamma-carboxylase
XX CC will allow proteins such as Factor VII, Factor IX, prothrombin,
XX CC (activated) protein C, protein S, protein Z, or osteocalcin to be
XX CC easily produced by recombinant techniques.
XX CC See also AAR21049-56, AAR23010.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 8 AA;
XX Query Match 35.3%; Score 6; DB 13; Length 8;
XX Best Local Similarity 100.0%; Pred.No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3 TPQPILL 8
XX Db 1 TPQPILL 6
XX
XX RESULT 12
XX ABG55849
XX ID ABG55849 standard; Peptide; 18 AA.
XX AC ABG55849;
XX XX
XX 25-FEB-2003 (first entry)
XX DE Human liver peptide, SEQ ID No 34497.
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX KW hypercholesterolaemia; coronary heart disease.
XX OS Homo sapiens.

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XX WO200157273-A2.
 PN
 XX
 PD 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US00664.
 PF
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488998/53.
 PI
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analysing gene expression in human adult liver -
 PT
 XX Claim 27; SEQ ID No 34497; 658pp; English.
 PS
 XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult
 CC liver. (I) may be used for predicting, measuring and displaying gene
 CC expression in samples derived from human adult liver. The genes
 CC identified may be involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
 CC is associated with coronary heart disease. ABG47348-ABG59930 represent
 CC human liver single exon encoded peptides of the invention.
 CC Note: The sequence information for this patent does not appear in the
 CC printed specification but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 18 AA;
 Query Match 35.3%; Score 6; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 QPLLQV 10
 Db |||||
 3 QPLLQV 8
 RESULT 13
 ABB40529
 ID ABB40529 standard; Peptide; 18 AA.
 XX
 AC ABB40529;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Peptide #8035 encoded by human foetal liver single exon probe.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 EN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US00669.
 XX
 PF 04-FEB-2000; 2000US-0180312.
 XX

PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.
 PI
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analysing gene expression in human fetal liver -
 PT
 XX Claim 27; SEQ ID NO 33164; 639pp + sequence listing; English.
 PS
 XX The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a peptide encoded by a single exon
 CC nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 18 AA;
 Query Match 35.3%; Score 6; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 QPLLQV 10
 Db |||||
 3 QPLLQV 8
 RESULT 14
 ABB24849
 ID ABB24849 standard; Protein; 18 AA.
 XX
 AC ABB24849;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Protein #6848 encoded by probe for measuring heart cell gene expression.
 XX
 KW Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease.
 XX
 OS Homo sapiens.
 XX
 EN WO200157274-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US00666.
 PF
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX

DR WPI; 2001-488899/53.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts -
 XX
 PS Claim 15; SEQ ID No 26619; 530pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 18 AA;
 Query Match 35.3%; Score 6; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPLLQV 10
 Db |||||
 3 QPLLQV 8
 RESULT 15
 AAM61355
 ID AAM61355 standard; Protein; 18 AA.
 AC
 XX
 AC AAM61355;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33460.
 XX
 XX Human; brain expressed exon; gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW epilepsy; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157275-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000667.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2001-483446/52.
 XX
 PF Single exon nucleic acid probes for analyzing gene expression in human
 XX brains -
 XX
 PS Example 4; SEQ ID NO: 33460; 650pp + Sequence Listing; English.
 XX
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.
 XX
 SQ Sequence 18 AA;
 Query Match 35.3%; Score 6; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPLLQV 10
 Db |||||
 3 QPLLQV 8
 RESULT 16
 AAM74093
 ID AAM74093 standard; Protein; 18 AA.
 AC
 XX
 AC AAM74093;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34399.
 XX
 XX Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX
 OS Homo sapiens.
 XX
 PN WO200157276-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000668.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2001-488900/53.
 XX
 PF Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human bone marrow -
 XX
 PS Example 4; SEQ ID NO: 34399; 659pp + Sequence Listing; English.
 XX
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.
 XX
 SQ Sequence 18 AA;
 Query Match 35.3%; Score 6; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPLLQV 10
 Db |||||
 3 QPLLQV 8

```

Db      3 QPLLQV 8

RESULT 17
AAM20225
ID      AAM20225 standard; Protein; 18 AA.
XX
XX      AC      AAM20225;
XX
XX      DT      12-OCT-2001 (first entry)
XX
XX      DE      Peptide #6659 encoded by probe for measuring cervical gene expression.
XX      KW      Probe; human; microarray; gene expression; cervical epithelial cell;
XX      KW      cervical cancer.
XX      OS      Homo sapiens.
XX
XX      FN      WO200157278-A2.
XX
XX      PD      09-AUG-2001.
XX
XX      PF      30-JAN-2001; 2001WO-US00670.
XX
XX      PR      04-FEB-2000; 2000US-0180312.
XX      PR      26-MAY-2000; 2000US-0207456.
XX      PR      30-JUN-2000; 2000US-0608408.
XX      PR      03-AUG-2000; 2000US-0632366.
XX      PR      21-SEP-2000; 2000US-0234687.
XX      PR      27-SEP-2000; 2000US-0236359.
XX      PR      04-OCT-2000; 2000GB-0024263.
XX
XX      PA      (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX      PI      Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX      DR      WPI; 2001-488901/53.
XX
XX      PT      Human genome-derived single exon nucleic acid probes useful for
XX      PT      analyzing gene expression in human cervical epithelial cells -
XX
XX      PS      Claim 27; SEQ ID No 25051; 487pp; English.
XX
XX      CC      The present invention relates to human single exon nucleic acid probes
XX      CC      (SNP: see AAI10068-AA128459). The present sequence is a peptide encoded
XX      CC      by one such probe. The SENPs are derived from human HeLa cells. The SENPs
XX      CC      can be used to produce a single exon microarray, which can be used for
XX      CC      measuring human gene expression in a sample derived from human cervical
XX      CC      epithelial cells. By measuring gene expression, the probes are therefore
XX      CC      useful in grading and/or staging of diseases of the cervix, notably
XX      CC      cervical cancer.
XX      CC      Note: The sequence data for this patent did not form part of the printed
XX      CC      specification, but was obtained in electronic format directly from WIPO
XX      CC      at ftp.wipo.int/pub/published_pct_sequences.
XX
XX      SQ      Sequence 18 AA;
XX
XX      Query Match      35.3%; Score 6; DB 22; Length 18;
XX      Best Local Similarity 100.0%; Pred. No. 12;
XX      Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      Qy      5 QPLLQV 10
XX      Db      3 QPLLQV 8

RESULT 18
AAM34255
ID      AAM34255 standard; Protein; 18 AA.
XX
XX      AC      AAM34255;
XX
XX      DT      17-OCT-2001 (first entry)
XX
XX      DE      Peptide #8292 encoded by probe for measuring placental gene expression.
XX      KW      Probe; microarray; human; placenta; antenatal diagnosis;
XX      KW      genetic disorder.
XX      OS      Homo sapiens.
XX
XX      FN      WO200157272-A2.
XX
XX      PD      09-AUG-2001.
XX
XX      PF      30-JAN-2001; 2001WO-US00663.
XX
XX      PR      04-FEB-2000; 2000US-0180312.
XX      PR      26-MAY-2000; 2000US-0207456.
XX      PR      30-JUN-2000; 2000US-0608408.
XX      PR      03-AUG-2000; 2000US-0632366.
XX      PR      21-SEP-2000; 2000US-0234687.
XX      PR      27-SEP-2000; 2000US-0236359.
XX      PR      04-OCT-2000; 2000GB-0024263.
XX
XX      PA      (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX      PI      Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX      DR      WPI; 2001-488901/53.
XX
XX      PT      Human genome-derived single exon nucleic acid probes useful for
XX      PT      analyzing gene expression in human placenta -
XX
XX      PS      Claim 27; SEQ ID No 34524; 654pp; English.
XX
XX      CC      The present invention relates to single exon nucleic acid probes (SENP:
XX      CC      see AAI31315-AA157546). The present sequence is a peptide encoded by one
XX      CC      such probe. The probes are useful for producing a microarray for
XX      CC      predicting, measuring and displaying gene expression in samples derived
XX      CC      from human placenta. The probes are useful for antenatal diagnosis of
XX      CC      human genetic disorders.
XX
XX      SQ      Sequence 18 AA;
XX
XX      Query Match      35.3%; Score 6; DB 22; Length 18;
XX      Best Local Similarity 100.0%; Pred. No. 12;
XX      Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      Qy      5 QPLLQV 10
XX      Db      3 QPLLQV 8

RESULT 19
ABG43991
ID      ABG43991 standard; Peptide; 18 AA.
XX
XX      AC      ABG43991;
XX
XX      DT      19-AUG-2002 (first entry)
XX
XX      DE      Human peptide encoded by genome-derived single exon probe SEQ ID 33656.
XX
XX      KW      Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX      KW      chronic obstructive pulmonary disease; interstitial lung disease;
XX      KW      familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX      KW      tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX      KW      Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX      KW      pulmonary histiocytosis; lymphangioleiomyomatosis; Karagenen syndrome;
XX      KW      pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX      KW      primary ciliary dyskinesia; pulmonary hypertension;
XX      KW      hyaline membrane disease.
XX      OS      Homo sapiens.
XX

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PN WO200186003-A2.
 XX 15-NOV-2001.
 XX 30-JAN-2001; 2001WO-US000665.
 XX 04-FEB-2000; 2000US-180312P.
 XX 26-MAY-2000; 2000US-207456P.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2002-114183/15.
 XX
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples -
 XX
 XX Claim 27; SEQ ID No 33656; 634bp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridise at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemorrhoidosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a peptide/protein
 CC encoded by a single exon probe of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 18 AA;
 SQ
 Query Match 35.3%; Score 6; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPLIQV 10

Db 3 QELQV 8
 |||||
 RESULT 20
 AAW17515
 ID AAW17515 standard; Peptide; 7 AA.
 XX
 AC AAW17515;
 XX
 DT 31-OCT-1997 (first entry)
 XX
 DE Protein kinase C related kinase 1 peptide PRK1-3 (465-471).
 XX
 KW Signal transduction; cell signalling; modulator; immunomodulator;
 KW protein kinase C related kinase 1; receptor for activated kinase C;
 KW RACK; PRK1; cognate; graft rejection; autoimmune disease;
 KW allergy; asthma; therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO9714038-A1.
 XX
 XX 17-APR-1997.
 XX
 XX 10-OCT-1996; 96WO-US16195.
 XX
 XX 18-JUN-1996; 96US-0665647.
 PR 10-OCT-1995; 95US-0541964.
 PR 31-JAN-1996; 96US-0594447.
 XX
 XX (TERR-) TERRAPIN TECHNOLOGIES INC.
 PA
 XX Kauvar LM, Mochly-Rosen D, Napolitano EW, Ron D;
 PI Vasquez NJ, Voronova A;
 XX
 XX WPI; 1997-236030/21.
 DR
 XX Identifying a modulator of intracellular signal transduction - by
 PT determining the interaction of a signal generating peptide with the
 PT test substance, allows modulation of the immune system
 XX
 XX Example 4; Page 34; 74pp; English.
 PS
 XX This sequence is a peptide, designated PRK1-3, that corresponds
 CC to amino acid residues 465-471 of protein kinase C related kinase
 CC 1 (PRK1). It was tested as a signal generating peptide in a
 CC claimed method for identifying modulators of intracellular signal
 CC transduction. This method assesses the ability of candidate
 CC modulators to affect the interaction between a signal-generating
 CC protein (see AAW15778-79, AAW15781, AAW15784-85, AAW17452-78), and a
 CC cognate binding protein involved in modulating the signal
 CC transduction function. Identified substances are useful as
 CC immunomodulators (claimed). They reduce T-cell activity, reduce
 CC the rate of graft rejection, reduce the severity of an autoimmune
 CC disorder, ameliorate allergy and/or asthma, or diminish a cytokine
 CC response (claimed).
 XX
 SQ Sequence 7 AA;
 Query Match 29.4%; Score 5; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 MEPQG 16
 |||||
 Db 1 MEPQG 5
 RESULT 21
 AAG87925
 ID AAG87925 standard; Peptide; 10 AA.
 XX

```

AC AAG87925;
XX
XX DT 11-SEP-2001 (first entry)
XX DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2874.
XX
XX DE Saccharomyces cerevisiae; complementary peptide; peptide identification;
XX KW drug discovery; drug design.
XX
XX OS Saccharomyces cerevisiae.
XX
XX PN W0200142276-A1.
XX
XX PD 14-JUN-2001.
XX
XX PF 13-DEC-2000; 2000WO-GB04773.
XX
XX PR 13-DEC-1999; 99GB-0029471.
XX
XX PA (PROT-) PROTEOM LTD.
XX
XX PI Roberts GW, Heal JR;
XX
XX XX WPI: 2001-367863/38.
XX
XX PT Identifying complementary peptides by analysis of protein and
XX PT nucleotide sequence databases, useful in drug design -
XX
XX PS Example 5; Page 426; 488pp; English.
XX
XX CC The invention relates to the identification of complementary peptides
XX CC by analysis of protein and nucleotide sequence databases from higher
XX CC eukaryotic genomes, excluding human and plants. The specific
XX CC complementary peptides interact with their relevant target proteins
XX CC encoded in the eukaryote genome. The peptides may be used as reagents
XX CC and drugs for drug discovery and as lead ligands for drug design and
XX CC development. The present sequence is a complementary peptide from
XX CC Saccharomyces cerevisiae.
XX
XX SQ Sequence 10 AA;

Query Match 29.4%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred.No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQPL 7
DB 3 TPQPL 7

RESULT 22
AAB44382
ID AAB44382 standard; Protein; 13 AA.
XX
XX AC AAB44382;
XX
XX DT 14-FEB-2001 (first entry)
XX
XX DE Human secreted protein encoded by gene 49 clone HPWAV82.
XX
XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
XX KW vulvular; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX KW neurological disease; infection; human; secreted protein.
XX
XX OS Homo sapiens.
XX
XX PN W0200058358-A1.
XX
XX PD 05-OCT-2000.
XX
XX PF 23-MAR-2000; 2000WO-US07725.

```

PR 27-DEC-2000; 2000US-0173419.
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shimkets RA, Leach M;
 PI
 XX WPI; 2001-465210/50.
 XX
 DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 PT
 XX Disclosure; Page 4120; 4143pp; English.
 XX
 CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms.
 XX
 SQ Sequence 14 AA;

 Query Match 29.4%; Score 5; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 PQPLL 8
 Db |||||
 7 PQPLL 11

 RESULT 24
 AAM98788
 ID AAM98788 standard; Peptide; 14 AA.
 AC AAM98788;
 XX
 DT 24-JAN-2002 (first entry)
 DE Human peptide #2063 encoded by a SNP oligonucleotide.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200147944-A2.
 PN
 XX 05-JUL-2001.
 PD
 XX 28-DEC-2000; 2000WO-US35498.
 PF
 XX 28-DEC-1999; 99US-0173419.
 PR
 PT 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;
 PI
 XX WPI; 2001-465210/50.
 XX
 DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 PT
 XX Disclosure; Page 4120; 4143pp; English.
 XX
 CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms.
 XX
 SQ Sequence 14 AA;

 Query Match 29.4%; Score 5; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 PQPLL 8
 Db |||||
 8 PQPLL 12

 RESULT 25
 AAE33717
 ID AAE33717 standard; peptide; 4 AA.
 XX
 AC AAE33717;
 XX
 DT 16-APR-2003 (first entry)
 DE GNA33 mAb 25 recognition VR2 peptide.
 XX
 KW Genome derived antigen 33; GNA33; Neisseria meningitidis serogroup B;
 KW MenB; immune response; infection; vaccine; antibacterial.
 XX
 XX Unidentified.
 OS
 XX WO200283711-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 11-APR-2002; 2002WO-US11501.
 PF
 XX 17-APR-2001; 2001US-284554P.
 PR
 XX 03-OCT-2001; 2001US-326838P.
 XX
 PA (CHIR) CHIRON CORP.
 PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
 XX
 PI Granoff D, Moe G, Rappuoli R;
 XX
 XX WPI; 2003-120415/11.
 DR
 XX New GNA33 peptides that elicit production of antibodies exhibiting
 PT complement-mediated bactericidal activity against a Neisseria
 PT meningitidis serogroup B (MenB), useful for diagnosing or preventing

AC AAY21560;
 XX
 DT 04-AUG-1999 (first entry)
 XX
 DE Target hexapeptide used in skin lightening composition.
 XX
 KW Skin lightening; targeting molecule.
 XX
 OS Unidentified.
 XX
 PN WO9912518-A1.
 XX
 PD 18-MAR-1999.
 XX
 PF 19-JUN-1998; 98WO-EP04012.
 XX
 PR 09-SEP-1997; 97GB-0019195.
 XX
 PA (UNIL) UNILEVER NV.
 PA (UNIL) UNILEVER PLC.
 XX
 PI Raghupathi S, Ramaiah A, Raman G, Wagh SS;
 XX
 DR WPI; 1999-357348/30.
 XX
 PT New cosmetic composition for lightening skin comprising peptide with
 PT isoelectric point of 2-5.5
 XX
 PS Claim 8; Page 9; 14pp; English.
 XX
 CC The invention provides a cosmetic composition for lightening the skin
 CC that comprises 0.1-10 wt.% of a peptide with an isoelectric point of
 CC 2-5.5. The peptide in the composition is attached to a hydrophobic amino
 CC acid residue or a targeting molecule or vehicle. The present sequence is
 CC a hexapeptide that can act as the targeting molecule. The composition is
 CC useful for lightening the skin. The skin lightening effected by the
 CC composition is reversible and has no known side effects and is active
 CC during both the day and night unlike the prior art.
 XX
 SQ Sequence 6 AA;
 Query Match 23.5%; Score 4; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 QPLL 8
 Db ||||
 2 QPLL 5
 RESULT 29
 AAW84430
 ID AAW84430 standard; Peptide; 6 AA.
 XX
 AC AAW84430;
 XX
 DT 22-MAR-1999 (first entry)
 XX
 DE HIV-1 nucleic acid binding protein zinc finger 2 peptide.
 XX
 KW zinc finger; nucleotide-binding protein; cell proliferative disorder;
 KW gene therapy; cancer; psoriasis; pemphigus vulgaris; Behcet's syndrome;
 KW lipid histiocytosis; human immune deficiency virus; HIV; viral infection;
 KW transgenic plant.
 XX
 OS Synthetic.
 XX
 PN WO9854311-A1.
 XX
 PD 03-DEC-1998.
 XX
 PF 27-MAY-1998; 98WO-US10801.
 XX

PR 27-MAY-1997; 97US-0863813.
 XX (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Gottesfeld JM, Wright PE;
 XX
 DR WPI; 1999-059831/05.
 XX
 PT New zinc finger nucleotide-binding protein variant that modulates
 PT selected nucleotide sequence - used for treatment of proliferative
 PT and viral diseases by gene therapy, and can be made selective for
 PT any target sequence
 XX
 PS Example 10; Fig 9; 158pp; English.
 XX
 CC AAW84422-41 represent the peptides obtained from randomised finger 2
 CC sequences of zinc finger nucleotide-binding proteins that bind to HIV-1
 CC target sequences. The peptides were produced in the course of the
 CC invention. The specification describes zinc finger nucleotide-binding
 CC protein variants with at least two zinc finger modules that bind to a
 CC cellular nucleotide sequence and modulate its function. Zinc finger
 CC proteins, and compositions containing them, are used to increase or
 CC reduce transcription of a gene linked to the cellular nucleotide
 CC sequence. The proteins are used specifically for treating or preventing
 CC cell proliferative disorders (in humans, animals or plants, including
 CC those induced by viruses), particularly where expressed from nucleic
 CC acid by gene therapy (including ex vivo methods). Typical diseases that
 CC can be treated are many forms of cancer, psoriasis, pemphigus vulgaris,
 CC Bechet's syndrome and lipid histiocytosis, also treatment of human
 CC immune deficiency virus (HIV) and other viral infections, and production
 CC of transgenic plants resistant to bacterial and viral diseases. The
 CC present oligonucleotide is used in the course of the invention.
 XX
 SQ Sequence 6 AA;
 Query Match 23.5%; Score 4; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PQPL 7
 Db ||||
 1 PQPL 4
 RESULT 30
 AAE33713
 ID AAE33713 standard; peptide; 6 AA.
 XX
 AC AAE33713;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE N. meningitidis serogroup B Pl.2 serosubtype Por A loop4 peptide #3.
 XX
 KW Genome derived antigen 33; GNA33; Neisseria meningitidis serogroup B;
 KW MenB; immune response; infection; vaccine; antibacterial.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO200283711-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 11-APR-2002; 2002WO-US11501.
 XX
 PR 17-APR-2001; 2001US-284554P.
 PR 03-OCT-2001; 2001US-326838P.
 XX
 PA (CHIR) CHIRON CORP.
 PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
 XX
 PI Granoff D, Moe G, Rappuoli R;
 XX

```

DR WPI; 2003-120415/11.
XX
PT New GNA33 peptides that elicit production of antibodies exhibiting
PT complement-mediated bactericidal activity against a Neisseria
PT meningitidis serogroup B (MenB), useful for diagnosing or preventing
XX (as vaccine) MenB infection -
XX
PS Example 3; Page 46; 70pp; English.
XX
CC The invention relates to novel genome derived antigen 33 (GNA33) peptides
CC which are capable of eliciting the production of antibodies that exhibit
CC complement-mediated bactericidal activity and/or opsonic activity against
CC a surface-exposed epitope on loop 4 of PorA of Neisseria meningitidis
CC serogroup B (MenB) Pl.2 serosubtype. GNA33 sequences are useful for
CC eliciting an immune response against MenB bacterium in a mammalian
CC subject. They are useful for detecting MenB antibodies in a biological
CC sample. GNA33 sequences are useful to prevent or diagnose MenB bacterium
CC infection. Sequences of the invention are used as vaccines. The present
CC sequence is N. meningitidis serogroup B Pl.2 serosubtype Por A loop4
XX peptide.
XX
SQ Sequence 6 AA;
XX
Query Match 23.5%; Score 4; DB 24; Length 6;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QTPQ 5
DB 1 QTPQ 4
XX
RESULT 31
AAP90659
ID AAP90659 standard; protein; 7 AA.
XX
AC AAP90659;
XX
DT 10-MAR-2003 (updated)
DT 26-MAY-1990 (first entry)
XX
DE New antihypertensive peptide.
XX
KW Antihypertensive peptide; angiotensin-converting enzyme;
KW ACE.
XX
OS Synthetic.
XX
PN JP01083096-A.
XX
PD 28-MAR-1989.
XX
PF 25-SEP-1987; 87JP-0241646.
XX
PR 25-SEP-1987; 87JP-0241646.
XX
PA (AJIN ) AJINOMOTO KK.
XX
DR WPI; 1989-136272/18.
XX
DE New antihypertensive peptide(s) -
PT used to inhibit angiotensin-converting enzyme
XX
PS Disclosure; Page -; 20pp; Japanese.
XX
CC The peptide and its salts inhibit angiotensin-converting
CC enzyme (ACE) and are useful as antihypertensives. They may be
CC administered orally, parenterally or rectally in the form of tablets,
CC capsules, granules, powder, syrup, suspension, suppositories,
CC ointment, cream, gel, plaster, inhalation compn. or
CC injection at a dose of 0.001-1000, pref. 0.01-10, mg, 1-3 times per day.
CC (Updated on 10-MAR-2003 to add missing OS field.)
XX
SQ Sequence 7 AA;
XX
Query Match 23.5%; Score 4; DB 14; Length 7;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQTP 4
XX
SQ Sequence 7 AA;
XX
Query Match 23.5%; Score 4; DB 10; Length 7;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PQPL 7
DB 1 PQPL 4
XX
RESULT 32
AAR38240
ID AAR38240 standard; peptide; 7 AA.
XX
AC AAR38240;
XX
DT 25-MAR-2003 (updated)
DT 08-OCT-1993 (first entry)
XX
DE Alzheimer paired helical filament tau protein epitope 47-53.
XX
KW Alzheimer tau protein; phosphorylation-dependent; PHF;
KW neuronal microtubule; mitogen activated protein kinase; MAP kinase.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 4..5
FT /label= Phosphorylation_motif
XX
PN WO9311231-A1.
XX
PD 10-JUN-1993.
XX
PF 07-DEC-1992; 92WO-EP028229.
XX
PR 06-DEC-1991; 91EP-0120974.
PR 16-NOV-1992; 92EP-0119551.
XX
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow E;
PI Steiner B;
XX
DR WPI; 1993-197050/24.
XX
PT Tau protein epitope(s), specific antibodies and protein kinase(s)
PT - used in the prevention, diagnosis and treatment of Alzheimer's
PT disease
XX
PS Claim 5; Page 89; 148pp; English.
XX
CC This is one of 26 preferred epitopes which occur in a phosphorylated
CC state in tau protein from Alzheimer paired helical filaments. The
CC epitopes all include phosphorylatable serine residues in Ser-Pro
CC motifs, Ile-Gly-Ser motifs or Cys-Gly-Ser motifs and/or
CC phosphorylatable threonine residues in Thr-Pro motifs. The pattern
CC of tau protein phosphorylation differs between Alzheimer's and
CC non-Alzheimer's individuals. Knowledge of the phosphorylated
CC epitopes and antibodies which recognise them may be useful in
CC diagnosis, treatment and prevention of Alzheimer's Disease. The
CC protein kinases present in mammalian brain which phosphorylate the
CC different epitopes are also claimed but no sequences are given.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 7 AA;
XX
Query Match 23.5%; Score 4; DB 14; Length 7;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQTP 4

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Db      |||||
        2 LQTP 5

RESULT 33
AAR37559
ID AAR37559 standard; peptide; 7 AA.
XX
AC AAR37559;
XX
XX 25-MAR-2003 (updated)
DT 07-OCT-1993 (first entry)
XX
XX Phosphorylated tau protein epitope.
DE
XX Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
KW treatment; formation; inhibition; inhibitor.
KW
XX Homo sapiens.
OS
XX EP544942-A1.
PN
XX 09-JUN-1993.
PD
XX 06-DEC-1991; 91EP-0120974.
PF
XX 06-DEC-1991; 91EP-0120974.
PR
XX (PLAC ) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.
PA
XX Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow EM, Steiner B;
PI WPI; 1993-183841/23.
XX
XX Phosphorylated tau protein epitope associated with Alzheimer's
PT disease - is used as protein kinase inhibitor for treatment and
PT diagnosis
XX
XX Claim 4; Page 16; 34pp; English.
PS
XX The sequence is that of an epitope of tau protein which specifically
CC occurs in a phosphorylated state in tau protein from Alzheimer's
CC paired helical fragments. It may be used as part of a method for the
CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may
CC also be used in an in vitro model for the study of the generation of
CC the Alzheimer state of proteins and the testing of substances which
CC prevent the conversion of normal to Alzheimer tau protein. The
CC epitope occurs at residues 47-53 of human tau protein.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 7 AA;
SQ

Query Match 23.5%; Score 4; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
Db |||||
   2 LQTP 5

RESULT 34
AAW27488
ID AAW27488 standard; peptide; 7 AA.
XX
AC AAW27488;
XX
XX 14-APR-1998 (first entry)
DT
DE Tyrosinase cytoplasmic domain derived peptide SEQ ID NO:3.
XX
XX Tyrosinase cytoplasmic domain; trypsin; epidermal melanocyte;
KW phosphorylation; pigmentation; modulator; protein kinase C-beta;

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```

KW hyperpigmentation; hypopigmentation; hair; skin; fur; wool.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9735998-A1.
PN
XX 02-OCT-1997.
PD
XX 27-MAR-1997; 97WO-US04752.
PF
XX 28-MAR-1996; 96US-0623364.
PR
XX (UYBO-) UNIV BOSTON.
PA
XX Gilchrist BA, Park H;
PI WPI; 1997-489658/45.
XX
XX Modulating activation of tyrosinase in epidermal melanocytes - by
PT regulating phosphorylation of specific serine or threonine residues
PT in cytoplasmic domain, useful to reduce or increase skin
PT pigmentation
XX
XX Example 5; Page 23; 40pp; English.
PS
XX A method has been developed of modulating, specifically preventing, the
CC activation of tyrosinase in vertebrate epidermal melanocytes. The method
CC comprises modulating, specifically inhibiting, the protein kinase C beta
CC (PKC beta) mediated phosphorylation of a Ser or Thr residue in the
CC tyrosinase's cytoplasmic domain. The present sequence represents a
CC tyrosinase cytoplasmic domain derived peptide. The method can be used
CC to therapeutically or cosmetically alter, particularly reduce, skin,
CC hair, wool or fur pigmentation, e.g. to treat hyperpigmentation or
CC hypopigmentation. Pigmentation can be reduced without surgery, or the
CC use of harsh chemicals.
XX
XX Sequence 7 AA;
SQ

Query Match 23.5%; Score 4; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLL 8
Db |||||
   1 QPLL 4

RESULT 35
AAW17516
ID AAW17516 standard; Peptide; 7 AA.
XX
AC AAW17516;
XX
XX 31-OCT-1997 (first entry)
DT
DE Protein kinase C related kinase 2 peptide PRK2-3 (467-473).
XX
XX Signal transduction; cell signalling; modulator; immunomodulator;
KW protein kinase C related kinase 2; receptor for activated kinase C;
KW RACK; PRK2; cognate; graft rejection; autoimmune disease;
KW allergy; asthma; therapy.
XX
XX Homo sapiens.
OS
XX WO9714038-A1.
PN
XX 17-APR-1997.
PD
XX 10-OCT-1996; 96WO-US16195.
PF
XX 18-JUN-1996; 96US-0665647.
PR 10-OCT-1995; 95US-0541964.
PR

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PR 31-JAN-1996; 96US-0594447.
XX (TERR-) TERRAPIN TECHNOLOGIES INC.
XX
PI Kauvar LM, Mochly-Rosen D, Napolitano EW, Ron D;
PI Vasquez NJ, Voronova A;
XX
DR WPI; 1997-236030/21.
XX
XX Identifying a modulator of intracellular signal transduction - by
PT determining the interaction of a signal generating peptide with the
PT test substance, allows modulation of the immune system
XX
PS Example 4; Page 34; 74pp; English.
XX
CC This sequence is a peptide, designated PRK2-3, that corresponds
CC to amino acid residues 467-473 of protein kinase C related kinase
CC 2 (PRK2). It was tested as a signal generating peptide in a
CC claimed method for identifying modulators of intracellular signal
CC transduction. This method assesses the ability of candidate
CC modulators to affect the interaction between a signal-generating
CC protein (see AAM15778-79, AAM15781, AAM15784-85, AAM17452-78), and a
CC cognate binding protein involved in modulating the signal
CC transduction function. Identified substances are useful as
CC immunomodulators (claimed). They reduce T-cell activity, reduce
CC the rate of graft rejection, reduce the severity of an autoimmune
CC disorder, ameliorate allergy and/or asthma, or diminish a cytokine
CC response (claimed).
XX
SQ Sequence 7 AA;
Query Match 23.5%; Score 4; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQG 16
DB 2 EPQG 5

RESULT 36
AAG79271
ID AAG79271 standard; peptide; 7 AA.
XX
AC AAG79271;
XX
XX 03-JAN-2002 (first entry)
XX
DE Peptide which binds specifically to the kinase domain receptor.
XX
KW Kinase domain receptor; KDR; vascular endothelial growth factor; VEGF;
KW VEGF antibody; angiogenesis; cancer; diabetic retinopathy; psoriasis;
KW hemangioblastoma; Kaposi's sarcoma.
XX
OS Synthetic.
XX
XX WO200172829-A2.
XX
XX 04-OCT-2001.
XX
XX 29-MAR-2001; 2001WO-IB00577.
XX
XX 31-MAR-2000; 2000US-193396P.
XX
XX (INSP ) INST PASTEUR.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX (UTPA-) UNIV PARIS 13 NORD.
XX
XX Tournaire R, Demangel C, Derbin C, Perret G, Mazie J, Plouet J;
XX Vassy R;
XX
XX WPI; 2001-616471/71.
XX
PT Novel peptides inhibiting binding of vascular endothelial growth factor
PT (VEGF) to kinase domain receptor, or inhibiting binding of anti-VEGF
PT antibody to VEGF, useful for treating diabetic retinopathy and
PT psoriasis -
XX
PS Claim 6; Page 19; 55pp; English.
XX
CC AAG79260-73 represent peptides which affect vascular endothelial growth
CC factor (VEGF) binding to antibodies or the kinase domain receptor (KDR).
CC Peptides AAG79260-66 were selected by their ability to bind to an
CC anti-VEGF antibody, and peptides AAG79267-73 were selected for their
CC ability to bind to CHO cells expressing a KDR which binds VEGF. The
CC peptides inhibit the binding of VEGF to KDR, and inhibit binding of
CC anti-VEGF antibody to VEGF. The peptides are useful for inhibiting
CC angiogenesis and for treating diseases including cancer, diabetic
CC retinopathy, psoriasis, hemangioblastoma, and Kaposi's sarcoma.
XX
SQ Sequence 7 AA;
Query Match 23.5%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
DB 4 LQTP 7

RESULT 37
AAM45859
ID AAM45859 standard; Peptide; 7 AA.
XX
AC AAM45859;
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #2130.
DE
DE Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated
XX antigen-binding fragments of an antibody that binds specifically to the
XX complex -
XX
XX Example 4; Page 108; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPPC) associated with tumours that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPPCs specific to target cancer (TC). Also described is an isolated

```

CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;
 SQ Query Match 23.5%; Score 4; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
 ||||
 Db 4 PQPL 7

RESULT 38
 AAM45914
 ID AAM45914 standard; Peptide; 7 AA.

AC AAM45914;

XX 25-OCT-2001 (first entry)

XX H11 binding site consensus conforming peptide (CCP) #2195.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

OS Homo sapiens.
 OS Synthetic.

PN CA2290722-A1.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -

XX Example 4; Page 108; 154pp; English.

XX The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response

CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;

SQ Query Match 23.5%; Score 4; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
 ||||
 Db 4 PQPL 7

RESULT 39
 AAM45919
 ID AAM45919 standard; Peptide; 7 AA.

XX AAM45919;

XX 25-OCT-2001 (first entry)

XX H11 binding site consensus conforming peptide (CCP) #2190.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

OS Homo sapiens.
 OS Synthetic.

PN CA2290722-A1.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -

XX Example 4; Page 108; 154pp; English.

XX The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including

CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;
SQ Query Match 23.5%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQL 7
Db |||||
4 PQL 7

RESULT 40
AAM45924
ID AAM45924 standard; Peptide; 7 AA.

XX AAM45924;
AC
XX 25-OCT-2001 (first entry)
DE H11 binding site consensus conforming peptide (CCP) #2195.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW endodermoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.
OS Synthetic.
OS
XX CA2290722-Al.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KB;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -

XX Example 4; Page 108; 154pp; English.

XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, endodermoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;
SQ Query Match 23.5%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQL 7
Db |||||
4 PQL 7

RESULT 41
AAM45929
ID AAM45929 standard; Peptide; 7 AA.

XX AAM45929;
AC
XX 25-OCT-2001 (first entry)
DE H11 binding site consensus conforming peptide (CCP) #2200.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW endodermoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.
OS Synthetic.
OS
XX CA2290722-Al.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KB;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -

XX Example 4; Page 108; 154pp; English.

XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, endodermoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 23.5%; Score 4; DB 22; Length 7;

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Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PQPL 7
Db 4 PQPL 7

RESULT 42
AAE33721
ID AAE33721 standard; peptide; 7 AA.
XX
AC AAE33721;
XX
DT 16-APR-2003 (first entry)
XX
DE N. meningitidis serogroup B Pl.2 serosubtype VR2 loop 4 peptide #2.
XX
KW Genome derived antigen 33; GNA33; Neisseria meningitidis serogroup B;
KW MenB; immune response; infection; vaccine; antibacterial.
XX
OS Neisseria meningitidis.
XX
PN WO200283711-A2.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US11501.
XX
PR 17-APR-2001; 2001US-284554P.
PR 03-OCT-2001; 2001US-326838P.
XX
XX (CHIR ) CHIRON CORP.
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
XX
PI Granoff D, Moe G, Rappuoli R;
XX
DR WPI; 2003-120415/11.
XX
XX
XX New GNA33 peptides that elicit production of antibodies exhibiting
PT complement-mediated bactericidal activity against a Neisseria
PT meningitidis serogroup B (MenB), useful for diagnosing or preventing
PT (as vaccine) MenB infection -
XX
PS Example 4; Page 48; 70pp; English.
XX
CC The invention relates to novel genome derived antigen 33 (GNA33) peptides
CC which are capable of eliciting the production of antibodies that exhibit
CC complement-mediated bactericidal activity and/or opsonic activity against
CC a surface-exposed epitope on loop 4 of PorA of Neisseria meningitidis
CC serogroup B (MenB) Pl.2 serosubtype. GNA33 sequences are useful for
CC eliciting an immune response against MenB bacterium in a mammalian
CC subject. They are useful for detecting MenB antibodies in a biological
CC sample. GNA33 sequences are useful to prevent or diagnose MenB bacterium
CC infection. Sequences of the invention are used as vaccines. The present
CC sequence is N. meningitidis serogroup B Pl.2 serosubtype VR2 loop 4
CC peptide.
XX
SQ Sequence 7 AA;

Query Match 23.5%; Score 4; DB 24; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPQ 5
Db 4 QTPQ 7

RESULT 43
AAP90673
ID AAP90673 standard; protein; 8 AA.
XX

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AC AAP90673;
XX
DT 10-MAR-2003 (updated)
DT 26-MAY-1990 (first entry)
XX
XX New antihypertensive peptide.
DE
XX Antihypertensive peptide; angiotensin-converting enzyme;
KW ACE.
KW
XX Synthetic.
OS
XX JP01083096-A.
PN
XX 28-MAR-1989.
PD
XX 25-SEP-1987; 87JP-0241646.
PF
XX 25-SEP-1987; 87JP-0241646.
PR
XX (AJIN ) AJINOMOTO KK.
PA
XX WPI; 1989-136272/18.
DR
XX New antihypertensive peptide(s) -
PT used to inhibit angiotensin-converting enzyme
PT
XX Disclosure; Page -; 20pp; Japanese.
XX
CC The peptide and its salts inhibit angiotensin-converting
CC enzyme (ACE) and are useful as antihypertensives. They may be
CC administered orally, parenterally or rectally in the form of tablets,
CC capsules, granules, powder, syrup, suspension, suppositories,
CC ointment, cream, gel, plaster, inhalation compsn. or
CC injection at a dose of 0.001-1000, pref. 0.01-10, mg, 1-3 times per day.
CC (Updated on 10-MAR-2003 to add missing OS field.)
XX
SQ Sequence 8 AA;

Query Match 23.5%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PQPL 7
Db 2 PQPL 5

RESULT 44
AAR03875
ID AAR03875 standard; Protein; 8 AA.
XX
AC AAR03875;
XX
XX 17-FEB-1993 (first entry)
DT
XX Hypotensive peptide (14).
DE
XX Hypotensor; salt.
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
XX Modified-site 1 /note= "pyroGlutamic acid"
FT
XX JP02062828-A.
PN
XX 02-MAR-1990.
PD
XX 26-AUG-1988; 88JP-0211696.
PF
XX 26-AUG-1988; 88JP-0211696.
PR

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XX (AJIN ) AJINOMOTO KK.
XX WPI; 1990-111933/15.
XX
XX New peptide used as active ingredient of hypotensive agent -
XX which may be prep'd. e.g. as tablets, capsules, powder, syrup,
XX injection prepn. etc.
XX
XX Claim; Page ?; 9pp; Japanese.
XX
XX The peptides given in AAR03862-76 and their salts can be used as
XX components of hypotensive agents.
XX The hypotensor may be in the form of tablets, capsules, powder,
XX syrup or injection prepn. contg. 0.001-1000 mg, esp. 0.01-10 mg of
XX the peptide.
XX
XX Sequence 8 AA;
SQ
Query Match 23.5%; Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PQPL 7
Db 2 PQPL 5
RESULT 45
AAR93206
ID AAR93206 standard; peptide; 8 AA.
XX
XX AAR93206;
AC
XX
XX 04-OCT-1996 (first entry)
DT
XX
XX New contraceptive peptide #2 derived from Zona Pellucida ZP3 protein.
DE
XX
XX Zona pellucida; ZP3; vaccine; humoral response; contraception; epitope;
KW pathogenic T cell response; ovary; assay; autoimmune; antibody;
KW passive immunisation.
XX
XX Synthetic.
OS
XX
XX WO9606113-A1.
PN
XX
XX 29-FEB-1996.
PD
XX
XX 18-AUG-1995; 95WO-EP03311.
PF
XX
XX 22-AUG-1994; 94EP-0202392.
PR
XX
XX (ALKU ) AKZO NOBEL NV.
PA
XX
XX Bunschoten EJ, Grootenhuis AJ, Van DUIN M;
PI
XX
XX WPI; 1996-151331/15.
DR
XX
XX Immuno-contraceptive peptide(s) derived from Zona Pellucida protein
PT ZP3 - used to prepare contraceptive vaccine and in assays to measure
PT autoimmune antibodies
XX
XX Claim 4; Page 31; 43pp; English.
XX
XX Peptides AAR93205-9 are examples of peptides derived from the sequence
XX of the Zona Pellucida protein ZP3 which contain the amino acid sequences
XX AAR93210 or AAR93214-5. The peptides are esp. based on amino acids 23-30
XX of the ZP3 protein. The novel peptides can be used in vaccines to induce
XX a humoral response against the ZP3 protein e.g. for contraception, esp.
XX as they do not raise a pathogenic T cell response since they do not
XX contain T cell epitopes. The novel peptides thus avoid potential ovarian
XX damage caused by some peptides used as vaccines. The peptides are also
XX useful in assays for detecting autoimmune antibodies or for generating

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CC antibodies for passive immunisation.
XX
XX Sequence 8 AA;
SQ
Query Match 23.5%; Score 4; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PQPL 7
Db 1 PQPL 4
RESULT 46
AAM23045
ID AAM23045 standard; Peptide; 8 AA.
XX
XX AAM23045;
AC
XX
XX 22-OCT-2001 (first entry)
DT
XX
XX HIV peptide SEQ ID NO 930.
DE
XX
XX Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
KW human immunodeficiency virus; vaccine.
KW
XX
XX Human immunodeficiency virus.
OS
XX
XX Synthetic.
OS
XX
XX WO200155177-A2.
PN
XX
XX 02-AUG-2001.
PD
XX
XX 29-JAN-2001; 2001WO-DK00059.
PF
XX
XX 28-JAN-2000; 2000EP-0610017.
PR
XX
XX 31-JAN-2000; 2000US-0179333.
XX
XX (STAT-) STATENS SERUM INST.
PA
XX
XX Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;
PI
XX
XX WPI; 2001-476184/51.
DR
XX
XX The generation of cytotoxic T cell lymphocytes epitopes for use in
XX anti-HIV vaccines -
PT
XX
XX Example 4; Page 70; 383pp; English.
XX
XX The invention relates to identification of cytotoxic T cell lymphocyte
XX (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL
XX are a major protective mechanism against viral diseases. Antibodies may
XX neutralise extracellular human immunodeficiency virus (HIV) and limit or
XX prevent infection of cells in the host, but CTL will limit viral
XX production by killing the cell. The CTL epitopes are useful in medicine,
XX in the manufacture of vaccines or diagnostic agents.
XX
XX Sequence 8 AA;
SQ
Query Match 23.5%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 PQGD 17
Db 1 PQGD 4
RESULT 47
AAM23046
ID AAM23046 standard; Peptide; 8 AA.
XX
XX AAM23046;
AC

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XX DT 22-OCT-2001 (first entry)
XX DE HIV peptide SEQ ID NO 931.
XX KW Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
XX KW human immunodeficiency virus; vaccine.
XX OS Human immunodeficiency virus.
XX OS Synthetic.
XX PN WO200155177-A2.
XX PD 02-AUG-2001.
XX PF 29-JAN-2001; 2001WO-DK00059.
XX PR 28-JAN-2000; 2000EP-0610017.
XX PR 31-JAN-2000; 2000US-0179333.
XX PA (STAT-) STATENS SERUM INST.
XX PI Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;
XX DR WPI; 2001-476184/51.
XX PT The generation of cytotoxic T cell lymphocytes epitopes for use in
XX PT anti-HIV vaccines -
XX PS Example 4; Page 70; 383pp; English.
XX CC The invention relates to identification of cytotoxic T cell lymphocyte
XX CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL
XX CC are a major protective mechanism against viral diseases. Antibodies may
XX CC neutralise extracellular human immunodeficiency virus (HIV) and limit or
XX CC prevent infection of cells in the host, but CTL will limit viral
XX CC production by killing the cell. The CTL epitopes are useful in medicine,
XX CC in the manufacture of vaccines or diagnostic agents.
XX SQ Sequence 8 AA;
XX Query Match 23.5%; Score 4; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 14 PQGD 17
XX Db 1 PQGD 4
XX RESULT 48
XX AAM23047
XX ID AAM23047 standard; Peptide; 8 AA.
XX AC AAM23047;
XX XX 22-OCT-2001 (first entry)
XX DT HIV peptide SEQ ID NO 932.
XX DE Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
XX KW human immunodeficiency virus; vaccine.
XX OS Human immunodeficiency virus.
XX OS Synthetic.
XX PN WO200155177-A2.
XX XX 02-AUG-2001.
XX PD 29-JAN-2001; 2001WO-DK00059.
XX PF 28-JAN-2000; 2000EP-0610017.
XX PR 31-JAN-2000; 2000US-0179333.
XX PA (STAT-) STATENS SERUM INST.
XX PI Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;
XX DR WPI; 2001-476184/51.
XX PT The generation of cytotoxic T cell lymphocytes epitopes for use in
XX PT anti-HIV vaccines -
XX PS Example 4; Page 70; 383pp; English.
XX CC The invention relates to identification of cytotoxic T cell lymphocyte
XX CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL
XX CC are a major protective mechanism against viral diseases. Antibodies may
XX CC neutralise extracellular human immunodeficiency virus (HIV) and limit or
XX CC prevent infection of cells in the host, but CTL will limit viral
XX CC production by killing the cell. The CTL epitopes are useful in medicine,
XX CC in the manufacture of vaccines or diagnostic agents.
XX SQ Sequence 8 AA;
XX Query Match 23.5%; Score 4; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 14 PQGD 17
XX Db 1 PQGD 4
XX RESULT 48
XX AAM23047
XX ID AAM23047 standard; Peptide; 8 AA.
XX AC AAM23047;
XX XX 22-OCT-2001 (first entry)
XX DT HIV peptide SEQ ID NO 932.
XX DE Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
XX KW human immunodeficiency virus; vaccine.
XX OS Human immunodeficiency virus.
XX OS Synthetic.
XX PN WO200155177-A2.
XX XX 02-AUG-2001.
XX PD 29-JAN-2001; 2001WO-DK00059.
XX PF 28-JAN-2000; 2000EP-0610017.
XX PR 31-JAN-2000; 2000US-0179333.
XX PA (STAT-) STATENS SERUM INST.
XX PI Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;
XX DR WPI; 2001-476184/51.
XX PT The generation of cytotoxic T cell lymphocytes epitopes for use in
XX PT anti-HIV vaccines -
XX PS Example 4; Page 70; 383pp; English.
XX CC The invention relates to identification of cytotoxic T cell lymphocyte
XX CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL
XX CC are a major protective mechanism against viral diseases. Antibodies may
XX CC neutralise extracellular human immunodeficiency virus (HIV) and limit or
XX CC prevent infection of cells in the host, but CTL will limit viral
XX CC production by killing the cell. The CTL epitopes are useful in medicine,
XX CC in the manufacture of vaccines or diagnostic agents.
XX SQ Sequence 8 AA;
XX Query Match 23.5%; Score 4; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 14 PQGD 17
XX Db 1 PQGD 4
XX RESULT 49
XX ABG91967
XX ID ABG91967 standard; Peptide; 8 AA.
XX AC ABG91967;
XX XX 04-DEC-2002 (first entry)
XX DT Human antibody fragment #151.
XX DE Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
XX KW metastasis; hypervariable region; autoimmune disease; thrombosis;
XX KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
XX KW myocardial infarction; retinopathic disease; abnormal platelet function;
XX KW sulphated tyrosine-dependent protein-protein interaction.
XX OS Homo sapiens.
XX PN WO200253700-A2.
XX XX 11-JUL-2002.
XX PD 31-DEC-2001; 2001WO-US49442.
XX PF 29-DEC-2000; 2000US-258948P.
XX PR 29-DEC-2000; 2000US-0751181.
XX XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX PA Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
XX PI Santhorn E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX DR WPI; 2002-674776/72.
XX XX Novel isolated epitope present on cancer cells and important in
XX PT physiological phenomena such as cell rolling, metastasis and
XX PT inflammation, for treating autoimmune, inflammatory or cardiovascular
XX PT diseases, and cancer -
XX XX Disclosure; Page 294; 310pp; English.

```

CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody.
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,
 CC platelet-platelet and/or cell-platelet adhesion or aggregation, for
 CC increasing mortality of tumour or leukaemia cells, for increasing the
 CC susceptibility of diseased cells to damage by anti-disease, anti-cancer
 CC or anti-leukaemia agents, or for decreasing the number of tumour or
 CC leukaemia cells in a patient, or in the manufacture of a medicament for
 CC the above mentioned purposes. The epitopes are useful for diagnosing and
 CC treating diseases such as cancer, leukaemia, autoimmune diseases,
 CC inflammatory diseases, cardiovascular diseases such as myocardial
 CC infarction, retinopathic diseases and other diseases mediated by abnormal
 CC platelet function and diseases caused by sulphated tyrosine-dependent
 CC protein-protein interactions. This sequence represents a human antibody
 CC fragment of the invention.

XX Sequence 8 AA;

Query Match 23.5%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
 ||||
 Db 4 LQTP 7

RESULT 50

ABG91998
 ID ABG91998 standard; Peptide; 8 AA.

XX AC ABG91998;

XX DT 04-DEC-2002 (first entry)

XX DE Human antibody fragment #182.

XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.

XX OS Homo sapiens.

XX PN WO200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US49442.

XX PR 29-DEC-2000; 2000US-258948P.

XX PR 29-DEC-2000; 2000US-0751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX DR WPI; 2002-674776/72.

XX PT Novel isolated epitope present on cancer cells and important in

PT physiological phenomena such as cell rolling, metastasis and

PT inflammation, for treating autoimmune, inflammatory or cardiovascular

XX diseases, and cancer -

PS Disclosure; Page 302; 310pp; English.

XX CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,
 CC platelet-platelet and/or cell-platelet adhesion or aggregation, for
 CC increasing mortality of tumour or leukaemia cells, for increasing the
 CC susceptibility of diseased cells to damage by anti-disease, anti-cancer
 CC or anti-leukaemia agents, or for decreasing the number of tumour or
 CC leukaemia cells in a patient, or in the manufacture of a medicament for
 CC the above mentioned purposes. The epitopes are useful for diagnosing and
 CC treating diseases such as cancer, leukaemia, autoimmune diseases,
 CC inflammatory diseases, cardiovascular diseases such as myocardial
 CC infarction, retinopathic diseases and other diseases mediated by abnormal
 CC platelet function and diseases caused by sulphated tyrosine-dependent
 CC protein-protein interactions. This sequence represents a human antibody
 CC fragment of the invention.

XX Sequence 8 AA;

Query Match 23.5%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
 ||||
 Db 4 LQTP 7

RESULT 51

ABG78276
 ID ABG78276 standard; Peptide; 8 AA.

XX AC ABG78276;

XX DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #151.

XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; biasoma; seminoma; melanoma; acute myeloid leukaemia.

XX OS Homo sapiens.

XX PN WO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US49440.

XX PR 29-DEC-2000; 2000US-0751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;

XX DR WPI; 2002-619166/66.

XX PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favour of other
 XX cells -

XX PS Claim 34; Page 218; 232pp; English.

XX CC The invention relates to a peptide or polypeptide comprising an Fv

CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention.

XX Sequence 8 AA;

Query Match 23.5%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
 DB 4 LQTP 7

RESULT 52
 ABG78307
 ID ABG78307 standard; Peptide; 8 AA.
 XX AC ABG78307;

15-NOV-2002 (first entry)

Human Fv molecule hypervariable region related peptide #182.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX Homo sapiens.

WO200259264-A2.

01-AUG-2002.

31-DEC-2001; 2001WO-US49440.

29-DEC-2000; 2000US-0751181.

(BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Feretz T;

WPI; 2002-619166/66.

Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 or fragment, or construct of fragment with enhanced binding
 characteristics so as to selectively bind target cell in favour of other
 cells -

Claim 34; Page 226; 232pp; English.

CC The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer

CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention.

SQ Sequence 8 AA;

Query Match 23.5%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
 DB 4 LQTP 7

RESULT 53
 AAO17346
 ID AAO17346 standard; peptide; 8 AA.
 XX AC AAO17346;

08-JUL-2002 (first entry)

Alpha-isomaltosylglucosaccharide synthase related peptide #17.

XX Alpha-isomaltosylglucosaccharide synthase; enzyme; sweetener; food;
 KW drink; cosmetics; pharmaceutical; cyclic tetrasaccharide.

OS Bacillus globisporus.

WO200210361-A1.

07-FEB-2002.

25-JUL-2001; 2001WO-JP06412.

01-AUG-2000; 2000JP-0233364.

02-AUG-2000; 2000JP-0234937.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Kubota M, Tsusaki K, Higashiyama T, Fukuda S, Miyake T;

WPI; 2002-315302/35.

Alpha-Isomaltosylglucosaccharide synthase capable of transferring
 Alpha-glucosyl from saccharide, useful in producing cyclic
 tetrasaccharides and related carbohydrates industrially for application
 in compositions e.g. as drugs -

Disclosure; Page 204; 209pp; Japanese.

CC The present invention relates to an alpha-isomaltosylglucosaccharide
 CC synthase which is capable of transferring alpha-glucosyl from a
 CC saccharide to form a specific saccharide which carries an alpha-1,6
 CC glucosyl linkage at its non-reducing end and an alpha-1,4 glucosyl
 CC linkage at ends other than the non-reducing end and has a degree of
 CC glucose polymerization of at most 3, but without substantially elevating
 CC the reducing ability. The synthase is useful in producing cyclic
 CC tetrasaccharides and related carbohydrates industrially for application
 CC in compositions e.g. as sweeteners, low calorie food materials, taste
 CC improvers, flavour improvers, quality improvers, water-separation
 CC inhibitors, stabilizers, excipients, binding agents and pulverisation
 CC bases, especially in foods, drinks, cosmetics and pharmaceuticals. The
 CC present sequence is a peptide described in the exemplification of the
 CC invention.

SQ Sequence 8 AA;

Query Match 23.5%; Score 4; DB 23; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17
|||||

Db 5 PQGD 8
|||||

RESULT 54
ABB05026
ID ABB05026 standard; peptide; 8 AA.
XX
AC ABB05026;
XX
DT 22-MAR-2002 (first entry)
XX
DE Bacillus globisporus peptide SEQ ID NO:7.
XX
KW Bacillus globisporus; alpha-isomaltosyltransferase; saccharide;
KW cyclic tetrasaccharide; alpha-isomaltosyl transfer; food; drink;
KW glucose polymerisation; cosmetic; pharmaceutical; sweetening agent.
XX
OS Sporosarcina globisporus.
XX
PN WO200190338-A1.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-JF04276.
XX
PR 22-MAY-2000; 2000JP-0149484.
XX
PT 28-JUL-2000; 2000JP-0229557.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Kubota M, Nishimoto T, Aga H, Fukuda S, Miyake T;
XX
DR WPI; 2002-089929/12.
XX
PT Microorganism-produced alpha-isomaltosyltransferase capable of forming
PT cyclic tetrasaccharide of specific structure and its derivatives, for
PT use in food, pharmaceutical and cosmetic industries -
XX
PS Disclosure; Page 156; 158pp; Japanese.
XX
CC The present invention describes an alpha-isomaltosyltransferase, capable
CC of producing a cyclic tetrasaccharide with a (1,6)-alpha-D-
CC glucopyranosyl-(1,3)-alpha-D-glucopyranosyl-(1,6)-alpha-D-glucopyranosyl
CC structure via a reaction involving alpha-isomaltosyl transfer from a
CC saccharide having specific linkages and degree of glucose polymerisation.
CC The alpha-isomaltosyltransferase can be used to produce a cyclic
CC tetrasaccharide of specific structure and its derivatives for
CC formulation into compositions for foods and drinks, cosmetics and
CC pharmaceuticals, both of which can be applied in sweetening agents, low
CC tooth-decaying and low calorie food materials, flavour improvers,
CC quality improvers, water retainers, aroma retainers, stabiliser,
CC excipients, adhesives or powdering base. The cheap, industrially-
CC producible, easily handleable, substantially non-reducing or lowly
CC reducing saccharides can prevent starch from aging, protein from
CC denaturation and fat from deterioration as well as colouring, and are
CC no hygroscopic, with acid and heat stability, which can undergo
CC aminocarbonyl reaction. The present sequence represents a peptide
CC isolated from Bacillus globisporus (also called Sporosarcina globisporus)
CC which is used in the exemplification of the present invention.
XX
XX Sequence 8 AA;
SQ
Query Match 23.5%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17
|||||

Db 5 PQGD 8
|||||

RESULT 55
AAP90672
ID AAP90672 standard; protein; 9 AA.
XX
AC AAP90672;
XX
DT 10-MAR-2003 (updated)
DT 26-MAY-1990 (first entry)
XX
DE New antihypertensive peptide.
XX
KW Antihypertensive peptide; angiotensin-converting enzyme;
KW ACE.
XX
OS Synthetic.
XX
PN JP01083096-A.
XX
PD 28-MAR-1989.
XX
PF 25-SEP-1987; 87JP-0241646.
XX
PR 25-SEP-1987; 87JP-0241646.
XX
PA (AJIN) AJINOMOTO KK.
XX
DR WPI; 1989-136272/18.
XX
PT New antihypertensive peptide(s) -
PT used to inhibit angiotensin-converting enzyme
XX
PS Disclosure; Page -; 20pp; Japanese.
XX
CC The peptide and its salts inhibit angiotensin-converting
CC enzyme (ACE) and are useful as antihypertensives. They may be
CC administered orally, parenterally or rectally in the form of tablets,
CC capsules, granules, powder, syrup, suspension, suppositories,
CC ointment, cream, gel, plaster, inhalation compsn. or
CC injection at a dose of 0.001-1000 pref. 0.01-10, mg, 1-3 times per day.
CC (Updated on 10-MAR-2003 to add missing OS field.)
XX
XX Sequence 9 AA;
SQ
Query Match 23.5%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
|||||

Db 3 PQPL 6
|||||

RESULT 56
AAR84629
ID AAR84629 standard; Peptide; 9 AA.
XX
AC AAR84629;
XX
DT 02-JUN-1996 (first entry)
XX
DE Wheat acetyl-Coenzyme-A-carboxylase peptide sequence.
XX
KW Acetyl Coenzyme A carboxylase; ACCase; plasmid pK11;
KW transgenic plant; modified oil content;
KW polyhydroxyalkanoate polymer; herbicide resistance;
KW monocot crop improvement.
XX
OS Triticum aestivum.
XX
PN WO9529246-A1.

XX PD 02-NOV-1995.
 XX PF 21-APR-1994; 94WO-GB00846.
 XX PR 21-APR-1994; 94WO-GB00846.
 XX PA (ZENE) ZENECA LTD.
 XX PI Bright SWJ, Elborough KM, Fentem PA, Slabas AR;
 XX DR WPI; 1995-382994/49.
 XX PT DNA encoding acetyl Coenzyme A carboxylase - used for developing
 PT plants with controlled expression of Accase, e.g. for controlling
 PT fatty acid synthesis.
 XX PS Disclosure; Fig 3; 61pp; English.
 XX CC Wheat acetyl Coenzyme A carboxylase (ACCase) was partially
 CC purified from wheat germ and a dominant 220 KDa band was identified
 CC as ACCase by column chromatography and SDS-PAGE. After
 CC purification in the gel, the protein was hydrolysed using
 CC Endoproteinase LysC, and resulting peptides were purified by
 CC electrophoresis and loaded onto an ABI 477A pulse liquid
 CC protein sequencer. Sequence data of 4 peptides (this peptide and
 CC peptides AAR84625, AAR84627 and AAR84631) were compared with plasmid
 CC pK111-deduced amino acid sequences (AAR84630, AAR84626, AAR84628 and
 CC AAR84632) so as to authenticate pK111 (see AAR04948) as wheat ACCase
 CC partial cDNA. More specifically, this peptide corresponds to
 CC amino acids 319-327 of the pK111 deduced AA sequence AAR84619
 CC (i.e. AAR84630). Partial cDNA clone pK111 (NCIF 40553) can be
 CC used to create a sense/antisense expression cassette to
 CC transform rape and other oilseed plants (canola, soybean,
 CC sunflower) to downregulate production of the ACCase enzyme.
 CC The transgenic plants have a lower or a modified oil content.
 CC Down-regulation of oil synthesis can be used to divert the
 CC substrate, acetyl Coenzyme A, into synthesis of alternative
 CC storage materials (starch, protein or novel polymers e.g.
 CC polyhydroxyalkanoates). Full-length ACCase clones can be used
 CC to create transgenic plants over-expressing ACCase, and
 CC therefore with increased oil content. ACCase over-expression in
 CC monocot plants such as wheat, barley, maize and rice, which are
 CC normally sensitive to herbicides, results in
 CC aryloxyphenoxy-propionate and alkylketone herbicide resistance in
 CC the transgenic plants (dicots are normally resistant to these
 CC herbicides).
 XX SQ Sequence 9 AA;
 Query Match 23.5%; Score 4; DB 16; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 13 EPQG 16
 Db 4 EPQG 7
 RESULT 57
 AAW17493
 ID AAW17493 standard; Peptide; 9 AA.
 XX AC AAW17493;
 XX DT 31-OCT-1997 (first entry)
 XX DE Protein kinase C-theta peptide theta V3-2 (337-345).
 XX KW Signal transduction; cell signalling; modulator; immunomodulator;
 KW protein kinase C; receptor for activated kinase C; RACK;
 KW PKC-theta; cognate; graft rejection; autoimmune disease;
 KW allergy; asthma; therapy.

XX OS Homo sapiens.
 XX PN WO9714038-A1.
 XX PD 17-APR-1997.
 XX PF 10-OCT-1996; 96WO-US16195.
 XX PR 18-JUN-1996; 96US-0665647.
 PR 10-OCT-1995; 95US-0541964.
 PR 31-JAN-1996; 96US-0594447.
 XX (TERR-) TERRAPIN TECHNOLOGIES INC.
 XX PA Kauvar LM, Mochly-Rosen D, Napolitano EW, Ron D;
 XX PI Vasquez NJ, Voronova A;
 PI WPI; 1997-236030/21.
 DR DR
 XX XX
 PT Identifying a modulator of intracellular signal transduction - by
 PT determining the interaction of a signal generating peptide with the
 PT test substance, allows modulation of the immune system
 XX PS Example 4; Page 33; 74pp; English.
 XX CC This sequence is a peptide, designated theta V3-2, that corresponds
 CC to amino acid residues 337-345 in the V3 region of protein kinase C
 CC (PKC)-theta. It was tested as a signal generating peptide in a
 CC claimed method for identifying modulators of intracellular signal
 CC transduction. This method assesses the ability of candidate
 CC modulators to affect the interaction between a signal-generating
 CC protein, such as a PKC isozyme peptide (see AAW15781, AAW15781,
 CC AAW15784-85, AAW17452-78), and a cognate binding protein involved in
 CC modulating the signal transduction function. Identified substances
 CC are useful as immunomodulators (claimed). They reduce T-cell
 CC activity, reduce the rate of graft rejection, reduce the severity
 CC of an autoimmune disorder, ameliorate allergy and/or asthma, or
 CC diminish a cytokine response (claimed).
 XX SQ Sequence 9 AA;
 Query Match 23.5%; Score 4; DB 18; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 13 EPQG 16
 Db 4 EPQG 7
 RESULT 58
 AAW60385
 ID AAW60385 standard; peptide; 9 AA.
 XX AC AAW60385;
 XX DT 24-AUG-1998 (first entry)
 XX DE Tumour homing peptide of the invention.
 XX KW Tumour homing peptide; in vivo panning;
 KW alpha-V-containing integrin binding motif; tumour.
 XX OS Synthetic.
 XX PN WO9810795-A2.
 XX PD 19-MAR-1998.
 XX PF 10-SEP-1997; 97WO-US16086.
 XX PR 10-SEP-1996; 96US-0710067.

XX PA (BURN-) BURNHAM INST.
 XX PI Pasqualini R, Ruoslahti E;
 XX DR WPI; 1998-207151/18.
 XX PT Tumour homing molecules and their conjugates - useful for, e.g.
 XX PT directing linked moiety to tumour containing angiogenic vasculature
 XX PT Example 3; Page 74; 105pp; English.
 XX PS
 XX CC AAW60303-89 represent peptides recovered from human breast cancer.
 CC The peptides are tumour homing peptides, and are identified by in
 CC vivo panning. The in vivo panning comprises administering a library
 CC of diverse peptides to a subject having a tumour, collecting a sample of
 CC the tumour, identifying a peptide that homes to the tumour, collecting a
 CC sample of normal tissue corresponding to the tumour, and determining
 CC that the peptide that homes to the tumour is not present in the normal
 CC tissue. The tumour homing peptides can be linked to a moiety (e.g.
 CC doxorubicin), and used to direct the moiety to a tumour.
 XX CC
 XX SQ Sequence 9 AA;
 Query Match 23.5%; Score 4; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 LLQV 10
 Db 4 LLQV 7
 RESULT 59
 AAW52801
 ID AAW52801 standard; peptide; 9 AA.
 AC AAW52801;
 XX 07-JUL-1998 (first entry)
 XX Signal region from human gp75 (brown locus protein).
 DE Sorting signal region; intracellular transport; endosome;
 XX endoplasmic reticulum; genetic immunisation.
 OS Homo sapiens.
 XX WO9804720-A1.
 XX 05-FEB-1998.
 XX 18-JUL-1997; 97WO-US12675.
 XX 26-JUL-1996; 96US-0022710.
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 PI Bartido SM, Houghton A, Yu Y;
 XX WPI; 1998-130707/12.
 XX Nucleic acid for genetic immunisation including subcellular
 PT localisation signal - provides better loading of major
 PT histocompatibility complex molecules and increased immune response
 Claim 4; Page 22; 31pp; English.
 XX Peptides AAW52801-05 represent sorting signal regions for various
 CC proteins. AAW52801-04 direct intracellular transport to the endosomes,
 CC while AAW52805 directs intracellular transport to the endoplasmic
 CC reticulum. The specification describes a nucleic acid construct for
 CC genetic immunisation which comprises sequence encoding an antigenic
 CC protein or peptide, and sequence encoding a second protein or peptide
 CC that acts as a sorting signal to direct intracellular transport of the
 CC antigen to the endosome or endoplasmic reticulum. The constructs or
 CC vaccines including them are used to induce an immune response against the
 CC antigen.

CC protein or peptide, and sequence encoding a second protein or peptide
 CC that acts as a sorting signal to direct intracellular transport of the
 CC antigen to the endosome or endoplasmic reticulum. The constructs or
 CC vaccines including them are used to induce an immune response against the
 CC antigen.
 XX SQ Sequence 9 AA;
 Query Match 23.5%; Score 4; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 QPLL 8
 Db 4 QPLL 7
 RESULT 60
 AAW52802
 ID AAW52802 standard; peptide; 9 AA.
 AC AAW52802;
 XX 07-JUL-1998 (first entry)
 XX Signal region from human tyrosinase (albino locus protein).
 DE Sorting signal region; intracellular transport; endosome;
 XX endoplasmic reticulum; genetic immunisation.
 OS Homo sapiens.
 XX WO9804720-A1.
 XX 05-FEB-1998.
 XX 18-JUL-1997; 97WO-US12675.
 XX 26-JUL-1996; 96US-0022710.
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 PI Bartido SM, Houghton A, Yu Y;
 XX WPI; 1998-130707/12.
 XX Nucleic acid for genetic immunisation including subcellular
 PT localisation signal - provides better loading of major
 PT histocompatibility complex molecules and increased immune response
 Claim 5; Page 22; 31pp; English.
 XX Peptides AAW52801-05 represent sorting signal regions for various
 CC proteins. AAW52801-04 direct intracellular transport to the endosomes,
 CC while AAW52805 directs intracellular transport to the endoplasmic
 CC reticulum. The specification describes a nucleic acid construct for
 CC genetic immunisation which comprises sequence encoding an antigenic
 CC protein or peptide, and sequence encoding a second protein or peptide
 CC that acts as a sorting signal to direct intracellular transport of the
 CC antigen to the endosome or endoplasmic reticulum. The constructs or
 CC vaccines including them are used to induce an immune response against the
 CC antigen.

XX SQ Sequence 9 AA;
 Query Match 23.5%; Score 4; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 QPLL 8
 Db 4 QPLL 7

RESULT 61

AAV47643
ID AAY47643 standard; Peptide; 9 AA.

XX AC AAY47643;

XX DT 01-DEC-1999 (first entry)

XX DE Immunogenic peptide having a human leukocyte antigen binding motif #2254.
XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX KW immune response; T cell activation; major histocompatibility complex;
XX KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX KW vaccine; immunisation.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9945954-A1.

XX PD 16-SEP-1999.

XX PF 13-MAR-1998; 98WO-US05039.

XX PR 13-MAR-1998; 98WO-US05039.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

XX DR WPI; 1999-551214/46.

XX PT New immunogenic peptides with HLA binding motif, useful in treatment
XX PT and diagnosis of cancers and viral diseases

XX PS Claim 1; Page 117; 150pp; English.

XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX CC having a human major histocompatibility complex (MHC) Class I (also
XX CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX CC response against the antigen from which the peptide is derived.
XX CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX CC normally induced by an antigen in the form of a peptide fragment bound
XX CC to a HLA molecule, rather than the intact foreign antigen itself, and
XX CC are particularly important in tumour rejection and in fighting viral
XX CC infections. The peptides are therefore useful therapeutically to treat
XX CC or prevent viral infections and cancers in mammals (especially humans)
XX CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX CC They can be administered as vaccines to elicit an immune response in
XX CC individuals susceptible or otherwise at risk of viral infection or
XX CC cancer, or used to treat chronic or acute conditions. They are also
XX CC useful diagnostically, and can be used to induce a cytotoxic T cell
XX CC response, by contacting a cytotoxic T cell with the peptide e.g. to
XX CC produce CTLs ex vivo for infusion back into a patient. The
XX CC polynucleotides encoding the immunogenic peptides are also useful
XX CC therapeutically and for immunisation as above.

XX SQ Sequence 9 AA;

Query Match 23.5%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
|||
Db 6 LLQV 9

RESULT 62

AAW93711
ID AAW93711 standard; Peptide; 9 AA.

XX AC AAW93711;

XX DT 28-JUN-1999 (first entry)

XX DE Human breast cancer derived tumour homing peptide 83.

XX KW Tumour homing peptide; tumour; diagnosis; endothelial cell; breast;
XX KW angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic;
XX KW anti-arthritis; NGR receptor; inhibitor; angiogenesis; anticancer drug;
XX KW prognosis; inflammation; regeneration; wounded tissue; targeting;
XX KW macular degeneration; diabetic retinopathy; rheumatoid arthritis;
XX KW occlusive thrombus; human.

XX OS Homo sapiens.

XX PN WO9913329-A1.

XX PD 18-MAR-1999.

XX PF 08-SEP-1998; 98WO-US18895.

XX PR 25-AUG-1998; 98US-0139802.

XX PR 10-SEP-1997; 97US-0926914.

XX PA (BURN-) BURNHAM INST.

XX PI Pasqualini R, Ruoslahti E;

XX DR WPI; 1999-215158/18.

XX PT Identifying molecules that home to angiogenic vasculature used as

XX PT targets for anticancer agents

XX PS Example II; Page 104; 180pp; English.

XX CC This invention describes novel peptides which home to angiogenic
XX CC vasculature, specifically of a tumour and which have anti-tumour,
XX CC anti-inflammatory, anti-angiogenic and anti-arthritis activity. Such
XX CC molecules are identified by treating a purified NGR receptor with a test
XX CC compound and identifying compounds that bind specifically to the NGR
XX CC receptor. The peptides of the invention are inhibitors of angiogenesis
XX CC and can be used to produce conjugates for delivering agents to
XX CC angiogenic vasculature, particularly anticancer drugs or an imaging
XX CC agent, for diagnosis or prognosis. These conjugates may be directed to
XX CC non-tumour angiogenic vasculature, e.g. that present in inflammatory,
XX CC regenerating or wounded tissue, e.g. for treatment of macular
XX CC degeneration, diabetic retinopathy or rheumatoid arthritis. The peptides
XX CC provide specific targeting to tumours, especially their supporting
XX CC vasculature, since the NGR receptor is exposed to the circulation only in
XX CC angiogenic vasculature. Precise targeting should reduce the systemic
XX CC toxicity of anticancer drugs in the conjugates. Complete killing of all
XX CC target cells may not be essential since partial denudation of endothelium
XX CC may result in an occlusive thrombus, and endothelial cells are unlikely
XX CC to become resistant to anticancer agents nor to lose the targeting
XX CC receptor. AAW93622-W93809 and AAW93843-44 are examples of tumour homing
XX CC peptides used in the invention.

XX SQ Sequence 9 AA;

Query Match 23.5%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
|||
Db 4 LLQV 7

RESULT 63

AAB21802

ID AAB21802 standard; Peptide; 9 AA.
 XX AC AAB21802;
 XX
 XX 22-MAR-2001 (first entry)
 DT
 XX Human breast tumour homing peptide #87.
 DE
 XX Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;
 KW breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.
 KW
 XX Homo sapiens.
 OS
 XX WO200042973-A2.
 PN
 XX 27-JUL-2000.
 XX
 XX 21-JAN-2000; 2000WO-US01602.
 PF
 XX 22-JAN-1999; 99US-0235902.
 PR
 XX (BURN-) BURNHAM INST.
 XX
 XX Ellerby HM, Bredesen DE, Pasqualini R, Ruoslahti EI;
 FI
 XX WPI; 2000-499174/44.
 DR
 XX Homing pro-apoptotic conjugate comprising a tumor homing molecule that
 XX selectively homes to a mammalian cell type or tissue linked to an
 PT antimicrobial peptide, useful for the treatment of prostate cancer -
 PT
 XX Example 5; Page 90; 118pp; English.
 PS
 XX The present invention relates to homing pro-apoptotic conjugates,
 CC comprising of a tumour homing molecule that selectively homes to a
 CC mammalian cell type or tissue, linked to an antimicrobial peptide. The
 CC homing pro-apoptotic conjugates are selectively internalised by the
 CC mammalian cell type or tissue and exhibits high toxicity, especially to
 CC angiogenic vasculature. The antimicrobial peptide has low mammalian cell
 CC toxicity when not linked to the tumor homing molecule. The conjugates are
 CC useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and
 CC prostate cancer or melanoma. The present sequence is a homing peptide
 CC isolated in the present invention, which can be conjugated to an
 CC antimicrobial peptide to make the homing pro-apoptotic conjugates of the
 CC present invention.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 23.5%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 LLQV 10
 Db 4 LLQV 7
 RESULT 64
 AAY95224
 ID AAY95224 standard; Peptide; 9 AA.
 XX AC AAY95224;
 XX
 XX 29-AUG-2000 (first entry)
 DT
 XX Anti-platelet glycoprotein Ib human H1b-5 VL CDR3.
 DE
 XX Variable light chain; single chain antibody; scFv; human; H1b-5;
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
 KW antithrombotic; thrombus; therapy; diagnostic; CDR3;
 KW complementarity determining region.
 XX
 XX Homo sapiens.
 OS

XX WO200026667-A1.
 PN
 XX 11-MAY-2000.
 PD
 XX 29-OCT-1999; 99WO-US25495.
 PF
 XX 30-OCT-1998; 98US-0106275.
 PR
 XX (MILL/) MILLER J L.
 PA
 XX Miller JL;
 PI
 XX WPI; 2000-365744/31.
 DR
 XX Isolated nucleic acid molecule encoding anti-human platelet
 PT glycoprotein Ib alpha molecule useful for producing antibodies which
 PT inhibit platelet aggregation -
 XX
 PS Claim 21; Fig 8; 89pp; English.
 XX
 CC The present sequence is that of complementarity determining region
 CC 3 (CDR3) of the light chain variable region (VL) of human single
 CC chain antibody (scFv) H1b-5, which is directed against platelet
 CC glycoprotein Ib (GP1b). The H1b series of scFv antibodies was
 CC isolated from a human synthetic VH and VL scFv library on the
 CC basis of their binding to platelet GPIb. Whether displayed as
 CC surface proteins on a phagemid or secreted as free scFv by
 CC Escherichia coli, the H1b scFv clones are capable of inhibiting
 CC von Willebrand factor-dependent aggregation of platelets. The scFv
 CC are composed of native human protein sequences and are therefore
 CC attractive potential reagents for therapeutic purposes. They
 CC provide a new class of antithrombotic agents, useful for the
 CC prevention of platelet-dependent thrombi in diseased arteries,
 CC bypass grafts, dialysis etc., and can also be used as diagnostic
 CC reagents. Methods of inhibiting aggregation of platelets, of
 CC binding human platelet GPIb alpha and of selecting a VH or VL
 CC region of an antibody that inhibits platelet aggregation are
 CC claimed. Fragments of the scFv VH or VL chain, including CDR
 CC fragments, are also claimed.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 23.5%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LQTP 4
 Db 4 LQTP 7
 RESULT 65
 AAY67365
 ID AAY67365 standard; peptide; 9 AA.
 XX AC AAY67365;
 XX
 XX 25-APR-2000 (first entry)
 DT
 XX Melanosomal protein sorting signal.
 DE
 XX Therapeutic antigen; cytotoxic T lymphocyte; CTL; CTL immune response;
 KW cellular immune response induction method; vaccine; human; tumour;
 KW melanoma glycoprotein 75; melanosomal protein sorting signal.
 XX
 XX Unidentified.
 OS
 XX WO9963945-A2.
 PN
 XX 16-DEC-1999.
 PD
 XX 11-JUN-1999; 99WO-US13146.
 PF

XX 12-JUN-1998; 98US-0089055.
 PR 30-OCT-1998; 98US-0106339.
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 PA Nikolic-Zugic J, Dyall R, Houghton AN;
 PI WPI; 2000-126432/11.
 DR Induction of a cellular immune response to a weakly immunogenic
 PT protein, used to target and kill tumour cells -
 XX Disclosure; Page 7; 44pp; English.
 PS This sequence represents a sorting signal which may be coupled to the
 CC antigen used in the method of the invention. The invention relates to a
 CC method for inducing a cytotoxic T lymphocyte (CTL) immune response to a
 CC non/weakly-immunogenic proteins which are expressed on tumour cells. The
 CC method for inducing a cellular immune response to a non-immunogenic or
 CC weakly immunogenic target peptide expressed on tumour cells of a
 CC mammalian subject comprises administering antigen to induce a cellular
 CC immune response to the target peptide. The antigen comprises an
 CC immunogenic portion having a major histocompatibility complex (MHC)
 CC binding domain which binds to the MHC and an immune recognition domain
 CC which is recognized by T-cells. The antigen is derived from the target
 CC peptide such that the MHC-binding portion binds to MHC with a greater
 CC affinity than the target peptide without material alteration of the
 CC immune recognition portion. The methods are used for inducing a cellular
 CC immune response to a non-immunogenic or weakly immunogenic target peptide
 CC expressed on tumour cells of a mammalian subject. The antigens and
 CC immunogens of the invention, as well as polynucleotides encoding them,
 CC are used in vaccine compositions against tumour cells.
 XX
 SQ Sequence 9 AA;
 Query Match 23.5%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 QPLL 8
 Db |||||
 4 QPLL 7
 RESULT 66
 AAE06380
 ID AAE06380 standard; peptide; 9 AA.
 AC AAE06380;
 XX 25-SEP-2001 (first entry)
 DT Human breast tumour homing peptide #86.
 DE Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide;
 KW antimicrobial peptide; prostate cancer; breast tumour homing molecule;
 KW cytostatic; human.
 XX Homo sapiens.
 OS WO200153342-A1.
 PN 26-JUL-2001.
 PD 16-JAN-2001; 2001WO-US01362.
 PF 21-JAN-2000; 2000US-0489582.
 PR (BURN-) BURNHAM INST.
 PA Ruoslahti EI, Pasqualini R, Arap W, Breddesen DE, Ellerby HM;
 XX Ruoslahti EI, Pasqualini R, Arap W, Breddesen DE, Ellerby HM;
 PI

DR WPI; 2001-451901/48.
 XX Novel chimeric prostate-homing pro-apoptotic peptide, used to treat
 PT prostate cancer, comprises a prostate-homing peptide linked to an
 PT antimicrobial peptide -
 XX Example 5; Page 89; 176pp; English.
 PS The patent discloses novel chimeric prostate-homing pro-apoptotic
 CC peptide which comprises a prostate-homing peptide linked to an
 CC antimicrobial peptide, where the chimeric peptide is selectively
 CC internalised by and exhibits high toxicity to prostate tissue and
 CC where the antimicrobial peptide has low mammalian cell toxicity when
 CC not linked to prostate-homing peptide. The chimeric peptide is used
 CC to direct an antimicrobial peptide in vivo to a prostate cancer, to
 CC induce selective toxicity in vivo in a prostate cancer, and to treat
 CC a patient with prostate cancer. The present sequence is human breast
 CC tumour homing peptide. This sequence is useful in the homing of
 CC pro-apoptotic conjugates of the invention.
 XX Sequence 9 AA;
 SQ Query Match 23.5%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 LLQV 10
 Db |||||
 4 LLQV 7
 RESULT 67
 ABJ15201
 ID ABJ15201 standard; Peptide; 9 AA.
 XX ABJ15201;
 AC 02-JAN-2003 (first entry)
 DT Immunogenic HIV peptide #51.
 DE HIV; gene therapy; vaccine; immunogenic HIV peptide;
 KW cytotoxic T lymphocyte; HIV infection.
 KW Human immunodeficiency virus.
 OS WO200269691-A2.
 PN 12-SEP-2002.
 PD 01-MAR-2002; 2002WO-US06314.
 PF 01-MAR-2001; 2001US-272565P.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (UYBR-) UNIV BROWN RES FOUND.
 XX McNicholl JM, Bond K, Sriwanthana B, Pau C, Degroot A;
 PI WPI; 2002-750429/81.
 DR New immunogenic HIV peptide having one or more epitopes immunoreactive
 XX with cytotoxic T lymphocytes, useful for diagnosing, treating and
 PT monitoring HIV infection in humans -
 PT Claim 6; Page 44; 65pp; English.
 PS The invention comprises immunogenic HIV peptides which contain one or
 CC more epitopes that are immunoreactive with cytotoxic T lymphocytes from
 CC an HIV-positive individual. The immunogenic HIV peptides of the invention
 CC are useful for diagnosing, treating and monitoring HIV infection. The
 CC present amino acid sequence represents an immunogenic HIV peptide of the
 CC invention.

XX Sequence 9 AA; Query Match 23.5%; Score 4; DB 23; Length 9; Best Local Similarity 100.0%; Pred. No. 9.3e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
| | | |
Db 1 LQTP 4

RESULT 68
ABG91962
ID ABG91962 standard; Peptide; 9 AA.
XX
AC ABG91962;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human antibody fragment #146.
XX
KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US49442.
XX
PR 29-DEC-2000; 2000US-258948P.
PR 29-DEC-2000; 2000US-0751181.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR WPI; 2002-674776/72.
XX
PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer -
XX
PS Disclosure; Page 293; 310pp; English.
XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet adhesion or aggregation, for
CC increasing mortality of tumour or leukaemia cells, for increasing the
CC susceptibility of diseased cells to damage by anti-disease, anti-cancer
CC or anti-leukaemia agents, or for decreasing the number of tumour or
CC leukaemia cells in a patient, or in the manufacture of a medicament for
CC the above mentioned purposes. The epitopes are useful for diagnosing and
CC treating diseases such as cancer, leukaemia, autoimmune diseases,
CC inflammatory diseases, cardiovascular diseases such as myocardial
CC infarction, retinopathic diseases and other diseases mediated by abnormal
CC platelet function and diseases caused by sulphated tyrosine-dependent
CC protein-protein interactions. This sequence represents a human antibody

CC fragment of the invention.
XX Sequence 9 AA;
Query Match 23.5%; Score 4; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
| | | |
Db 4 LQTP 7

RESULT 69
ABG91975
ID ABG91975 standard; Peptide; 9 AA.
XX
AC ABG91975;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human antibody fragment #159.
XX
KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US49442.
XX
PR 29-DEC-2000; 2000US-258948P.
PR 29-DEC-2000; 2000US-0751181.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR WPI; 2002-674776/72.
XX
PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer -
XX
PS Disclosure; Page 296; 310pp; English.
XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet adhesion or aggregation, for
CC increasing mortality of diseased cells to damage by anti-disease, anti-cancer
CC or anti-leukaemia agents, or for decreasing the number of tumour or
CC leukaemia cells in a patient, or in the manufacture of a medicament for
CC the above mentioned purposes. The epitopes are useful for diagnosing and
CC treating diseases such as cancer, leukaemia, autoimmune diseases,
CC inflammatory diseases, cardiovascular diseases such as myocardial
CC infarction, retinopathic diseases and other diseases mediated by abnormal
CC platelet function and diseases caused by sulphated tyrosine-dependent
CC platelet function and diseases caused by sulphated tyrosine-dependent

CC protein-protein interactions. This sequence represents a human antibody
 CC fragment of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 23.5%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4
 Db 4 LQTP 7
 ||||

RESULT 70
 ABG94766
 ID ABG94766 standard; Peptide; 9 AA.
 AC
 XX ABG94766;
 AC
 XX 02-DEC-2002 (first entry)
 DT
 XX Replikin sequence identified by the 3-point recognition method #39.
 DE
 XX Replikin; glioma; malignin; anthrax; small pox; antiviral; antibacterial;
 KW 3-point-recognition; vaccine; immunogen; Lethal Factor Protein pX01-107;
 KW Surface Antigen S Precursor Protein.
 KW
 XX Human papillomavirus type 71.
 OS
 XX US2002120106-A1.
 FN
 XX 29-AUG-2002.
 PD
 XX
 XX 26-OCT-2001; 2001US-0984056.
 PF
 XX 27-MAR-2001; 2001US-278761P.
 PR
 XX 09-JUL-2001; 2001US-303396P.
 PR
 XX 04-SEP-1998; 98US-0146755.
 PR
 XX 27-MAR-2001; 2001US-0817144.
 XX
 (BOGO/) BOGOCH S.
 PA (BOGO/) BOGOCH E S.
 PA
 XX Bogoch S, Bogoch ES;
 PI
 XX WPI; 2002-691212/74.
 DR
 XX Isolated Bacillus anthracis and small pox virus peptides (I), also
 PT known as replikins, useful for formulating vaccines for treating
 PT anthrax or small pox, comprise 7 to 50 amino acids -
 XX
 PS Disclosure; Page 3; 16pp; English.
 XX

The invention relates to isolated Bacillus anthracis and small pox virus
 peptides, also known as replikins, comprising 7 to 50 amino acids
 including at least one lysine residue located six to ten residues from a
 second lysine residue, at least one histidine residue, and at least 8%
 lysine residues. The peptides were identified using the 3-point-
 recognition method and based on the replikin sequence isolated from
 glioblastoma cells malignin peptide which is of non-human origin.
 CC Also included are anti-replikin antibodies (or antibody cocktail),
 CC a method of stimulating the immune system of a subject to
 CC produce antibodies to Bacillus anthracis or small pox comprising
 CC administering an effective amount of at least one or more Bacillus
 CC anthracis or small pox replikin and an antisense nucleic acid molecule
 CC complementary to a mRNA encoding a Bacillus anthracis polypeptide
 CC (e.g. Anthrax Lethal Factor Protein pX01-107) comprising a replikin
 CC sequence, an antisense nucleic acid molecule complementary to a mRNA
 CC encoding a Small Pox Virus polypeptide (e.g. Surface Antigen S Precursor
 CC Protein comprising a replikin sequence). The peptides are useful for
 CC stimulating the immune system of a subject to produce antibodies that
 CC bind specifically to Anthrax or small pox polypeptides containing a

CC replikin sequence. The peptides are useful for generating antibodies that
 CC can be used in the treatment and/or prevention of anthrax or small pox.
 CC The peptides are also useful for formulating vaccines for treating
 CC anthrax or small pox. The present sequence is a replikin sequence
 CC isolated by the 3-point-recognition system and sharing structural
 CC similarity with the replikin sequence isolated from glioblastoma cells
 CC malignin.
 XX
 SQ Sequence 9 AA;

Query Match 23.5%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLLQ 9
 Db 4 PLLQ 7
 ||||

RESULT 71
 ABG78271
 ID ABG78271 standard; Peptide; 9 AA.
 XX
 AC ABG78271;
 XX
 XX 15-NOV-2002 (first entry)
 DT
 XX Human Fv molecule hypervariable region related peptide #146.
 DE
 XX Human; Fv molecule; hypervariable region; single chain Fv; cytotstatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX
 OS Homo sapiens.
 XX
 FN WO200259264-A2.
 XX
 PD 01-AUG-2002.
 XX
 XX 31-DEC-2001; 2001WO-US49440.
 PF
 XX 29-DEC-2000; 2000US-0751181.
 PR
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 PA
 XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;
 PI
 XX WPI; 2002-619166/66.
 DR
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favour of other
 PT cells -
 XX
 PS Claim 34; Page 217; 232pp; English.
 XX

The invention relates to a peptide or polypeptide comprising an Fv
 molecule, a construct or fragments or a construct of a fragment with
 enhanced binding characteristics which selectively and/or specifically
 binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention.
 XX

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SQ Sequence 9 AA;
  Query Match      23.5%; Score 4; DB 23; Length 9;
  Best Local Similarity 100.0%; Pred.No. 9.3e+05;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
   ||||
DB 4 LQTP 7

RESULT 72
ABG78284
ID ABG78284 standard; Peptide; 9 AA.
AC ABG78284;
XX
XX
DT 15-NOV-2002 (first entry)
XX
XX Human Fv molecule hypervariable region related peptide #159.
XX
XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
XX Homo sapiens.
OS
XX WO200259264-A2.
PN
XX 01-AUG-2002.
PD
XX 31-DEC-2001; 2001WO-US49440.
PF
XX 29-DEC-2000; 2000US-0751181.
PR
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
PA
XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
PI Plaksin D, Peretz T;
PI
XX WPI; 2002-619166/66.
DR
XX
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favour of other
PT cells -
XX
XX Claim 34; Page 220; 232pp; English.
PS
XX The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention.
XX
XX Sequence 9 AA;
  Query Match      23.5%; Score 4; DB 23; Length 9;
  Best Local Similarity 100.0%; Pred.No. 9.3e+05;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
   ||||
DB 4 LQTP 7

RESULT 74
ABJ01401
ID ABJ01401 standard; Peptide; 9 AA.
AC ABJ01401;
XX
XX 19-SEP-2002 (first entry)
DT
XX
XX 158P1D7 related HLA peptide SEQ ID No 101.
DE
XX
XX Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW cat; cow; horse; human; human; vaccine; gene therapy; human leukocyte antigen;

```

```

Db 4 LQTP 7

RESULT 73
ABP62412
ID ABP62412 standard; Peptide; 9 AA.
XX
XX AC ABP62412;
XX
XX 10-OCT-2002 (first entry)
DT
XX
XX Human immunopeptide to HCV E2 glycoprotein light chain CDR #89.
DE
XX
XX Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX
XX Homo sapiens.
OS
XX WO200259340-A1.
PN
XX 01-AUG-2002.
PD
XX 25-JAN-2002; 2002WO-US02303.
PF
XX 26-JAN-2001; 2001US-264451P.
PR
XX (SCRI ) SCRIPPS RES INST.
PA
XX Maruyama T, Jones IM, Burton DR, Fox RI;
PI WPI; 2002-599801/64.
PI
XX
XX New human immunopolypeptide with binding specificity for certain
PT envelope glycoproteins and nonstructural proteins of hepatitis C virus
PT (HCV), for diagnosing or treating patients having or suspected of
PT having HCV infection -
XX
XX Claim 1; Fig 17; 308pp; English.
PS
XX The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection.
XX
XX Sequence 9 AA;
  Query Match      23.5%; Score 4; DB 23; Length 9;
  Best Local Similarity 100.0%; Pred.No. 9.3e+05;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
   ||||
DB 4 LQTP 7

RESULT 74
ABJ01401
ID ABJ01401 standard; Peptide; 9 AA.
AC ABJ01401;
XX
XX 19-SEP-2002 (first entry)
DT
XX
XX 158P1D7 related HLA peptide SEQ ID No 101.
DE
XX
XX Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW cat; cow; horse; human; human; vaccine; gene therapy; human leukocyte antigen;

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```

KW HLA.
XX Homo sapiens.
XX WO200216593-A2.
XX 28-FEB-2002.
XX 22-AUG-2001; 2001WO-US26276.
XX 22-AUG-2000; 2000US-227098P.
XX 10-APR-2001; 2001US-282739P.
XX (AGEN-) AGENSYS INC.
XX Faxis M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX Challita-eid FM, Jakobovits A;
XX WPI; 2002-425659/45.
XX New compositions comprising a gene (designated 158P1D7), its encoded
XX protein or their modulators, useful for treating or diagnosing cancers,
XX particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX or humans) -
XX Disclosure; Page 129; 181pp; English.
XX The invention relates to a novel nucleic acid, designated 158P1D7. The
XX compositions are useful for treating or diagnosing cancers, particularly
XX bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX horses or humans). The compositions are also useful for monitoring
XX genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX of the invention can be used in gene therapy to treat the said disorders.
XX This sequence represents a human leukocyte antigen (HLA) peptide relating
XX to the 158P1D7 protein of the invention.
XX SQ Sequence 9 AA;
XX Query Match 23.5%; Score 4; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 7 LLQV 10
XX Db ||||
XX 6 LLQV 9
XX RESULT 75
XX ABJ01433
XX ID ABJ01433 standard; Peptide; 9 AA.
XX AC ABJ01433;
XX XX
XX DT 19-SEP-2002 (first entry)
XX DE
XX DE 158P1D7 related HLA peptide SEQ ID No 133.
XX KW Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX HLA.
XX OS Homo sapiens.
XX XX
XX PN WO200216593-A2.
XX XX
XX PD 28-FEB-2002.
XX XX
XX PF 22-AUG-2001; 2001WO-US26276.
XX XX
XX PR 22-AUG-2000; 2000US-227098P.
XX PR 10-APR-2001; 2001US-282739P.
XX XX
XX (AGEN-) AGENSYS INC.
XX Faxis M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX Challita-eid FM, Jakobovits A;
XX WPI; 2002-425659/45.
XX New compositions comprising a gene (designated 158P1D7), its encoded
XX protein or their modulators, useful for treating or diagnosing cancers,
XX particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX or humans) -
XX Disclosure; Page 129; 181pp; English.
XX The invention relates to a novel nucleic acid, designated 158P1D7. The
XX compositions are useful for treating or diagnosing cancers, particularly
XX bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX horses or humans). The compositions are also useful for monitoring
XX genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX of the invention can be used in gene therapy to treat the said disorders.
XX This sequence represents a human leukocyte antigen (HLA) peptide relating
XX to the 158P1D7 protein of the invention.
XX SQ Sequence 9 AA;
XX Query Match 23.5%; Score 4; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 7 LLQV 10
XX Db ||||
XX 6 LLQV 9

```

```

XX Faxis M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX Challita-eid FM, Jakobovits A;
XX WPI; 2002-425659/45.
XX New compositions comprising a gene (designated 158P1D7), its encoded
XX protein or their modulators, useful for treating or diagnosing cancers,
XX particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX or humans) -
XX Disclosure; Page 130; 181pp; English.
XX The invention relates to a novel nucleic acid, designated 158P1D7. The
XX compositions are useful for treating or diagnosing cancers, particularly
XX bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX horses or humans). The compositions are also useful for monitoring
XX genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX of the invention can be used in gene therapy to treat the said disorders.
XX This sequence represents a human leukocyte antigen (HLA) peptide relating
XX to the 158P1D7 protein of the invention.
XX SQ Sequence 9 AA;
XX Query Match 23.5%; Score 4; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 7 LLQV 10
XX Db ||||
XX 1 LLQV 4

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Search completed: November 25, 2003, 18:15:39
Job time : 57.0691 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 : Search time 33.8191 Seconds
(without alignments)
92.715 Million cell updates/sec

Title: US-09-641-801-2

Perfect score: 17

Sequence: 1 LQTPQLQWMEPQGD 17

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

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Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA.*

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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	17	100.0	17	15	US-10-281-652-2
2	6	35.3	12	12	US-10-286-457-195
3	6	35.3	18	9	US-09-864-761-40147
4	5	29.4	12	12	US-10-137-867-452
5	4	23.5	5	12	US-10-168-758-15
6	4	23.5	6	11	US-09-500-700-104
7	4	23.5	7	9	US-09-822-270-12
8	4	23.5	7	12	US-10-342-371-12
9	4	23.5	8	10	US-09-894-018-76
10	4	23.5	8	12	US-10-089-549-17
11	4	23.5	9	7	US-08-344-824-282
12	4	23.5	9	9	US-09-765-086-102
13	4	23.5	9	9	US-09-834-765-48
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18	4	23.5	9	9	US-09-898-541-1
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20	4	23.5	9	10	US-09-984-056-56
21	4	23.5	9	10	US-09-984-057-56
22	4	23.5	9	11	US-09-972-656-30
23	4	23.5	9	12	US-10-375-992-102
24	4	23.5	9	12	US-10-105-232-56
25	4	23.5	9	12	US-10-189-437-56
26	4	23.5	9	12	US-10-277-292-101
27	4	23.5	9	12	US-10-277-292-133
28	4	23.5	9	12	US-10-137-867-288
29	4	23.5	9	12	US-10-280-340-101
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34	4	23.5	10	9	US-09-834-765-468
35	4	23.5	10	10	US-09-908-322-53
36	4	23.5	10	10	US-09-867-852-93
37	4	23.5	10	11	US-09-783-931-53
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39	4	23.5	10	12	US-10-277-292-169
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41	4	23.5	10	12	US-10-277-292-286
42	4	23.5	10	12	US-10-277-292-436
43	4	23.5	10	12	US-10-137-867-274
44	4	23.5	10	12	US-10-280-340-169
45	4	23.5	10	12	US-10-280-340-179
46	4	23.5	10	12	US-10-280-340-286
47	4	23.5	10	12	US-10-280-340-424
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51	4	23.5	11	9	US-09-829-855-234
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53	4	23.5	12	9	US-09-281-717-39
54	4	23.5	12	11	US-09-954-385-193
55	4	23.5	13	11	US-09-992-238-27
56	4	23.5	13	11	US-09-992-238-77
57	4	23.5	14	9	US-09-829-855-217
58	4	23.5	14	12	US-10-271-078-53
59	4	23.5	14	12	US-10-367-405-18
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61	4	23.5	14	15	US-10-120-604-26
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63	4	23.5	14	15	US-10-120-604-85
64	4	23.5	14	15	US-10-294-891-25
65	4	23.5	15	12	US-10-161-791-405
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69	4	23.5	15	12	US-10-281-652-34
70	4	23.5	15	15	US-10-194-985-26
71	4	23.5	16	12	US-10-299-043-2
72	4	23.5	16	15	US-10-174-105A-181
73	4	23.5	17	9	US-09-861-708-1
74	4	23.5	17	9	US-09-864-761-34833
75	4	23.5	18	9	US-09-864-761-45132
76	4	23.5	18	12	US-10-029-386-32086
77	4	23.5	18	12	US-10-029-386-34082
78	4	23.5	18	12	US-10-145-206-153
79	4	23.5	18	12	US-10-350-405-138
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Sequence 30, Appl
Sequence 102, App
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Sequence 597, App
Sequence 468, App
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Sequence 108, App
Sequence 169, App
Sequence 179, App
Sequence 286, App
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Sequence 193, App
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Sequence 33, Appl
Sequence 18, Appl
Sequence 15, Appl
Sequence 26, Appl
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Sequence 85, Appl
Sequence 25, Appl
Sequence 405, App
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Sequence 10, Appl
Sequence 11, Appl
Sequence 34, Appl
Sequence 29, Appl
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Sequence 34933, A
Sequence 45132, A
Sequence 32086, A
Sequence 34082, A
Sequence 153, App
Sequence 138, App
Sequence 26, Appl
Sequence 35260, A
Sequence 43517, A
Sequence 53, Appl
Sequence 4, Appli
Sequence 17, Appl
Sequence 950, App

89 Sequence 1354, Ap
90 Sequence 35404, A
91 Sequence 48956, A
92 Sequence 17, Appl
93 Sequence 18, Appl
94 Sequence 242, App
95 Sequence 11, Appl
96 Sequence 25, Appl
97 Sequence 5, Appl
98 Sequence 5, Appl
99 Sequence 208, App
100 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-2
; Sequence 2, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281.652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641.803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-2

Query Match 100.0%; Score 17; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQLQVMMPEQGD 17
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Db 1 LQTPQLQVMMPEQGD 17

RESULT 2
US-10-286-457-195
; Sequence 195, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286.457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 195
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, ba
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-195

Query Match 35.3%; Score 6; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQP 6
| | | | | |
Db 2 LQTPQP 7

RESULT 3
US-09-864-761-40147
; Sequence 40147, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FC
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864.761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40147
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005343.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4

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; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
US-09-864-761-40147

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Query Match      35.3%; Score 6; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      5 QPLLQV 10
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Db       3 QPLLQV 8

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RESULT 4
US-10-137-867-452
; Sequence 452, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 452
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-452

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Query Match      29.4%; Score 5; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      5 QPLLQ 9
         |||||
Db       7 QPLLQ 11

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RESULT 5
US-10-168-758-15
; Sequence 15, Application US/10168758
; Publication No. US20030207812A1
; GENERAL INFORMATION:
; APPLICANT: Chapdelaine, Marc J
; APPLICANT: Katherine, Knappenberger
; APPLICANT: Steelman, Gary
; APPLICANT: Suchard, Suzanne
; APPLICANT: Sygowski, Linda
; TITLE OF INVENTION: CD45
; FILE REFERENCE: Z70624-1P US

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; CURRENT APPLICATION NUMBER: US/10/168,758
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-168-758-15

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Query Match      23.5%; Score 4; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      13 EPQG 16
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Db       2 EPQG 5

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RESULT 6
US-09-500-700-104
; Sequence 104, Application US/09500700
; Publication No. US20030059767A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: BARBAS III, Carlos F.
; APPLICANT: GOTTESFELD, Joel M.
; APPLICANT: WRIGHT, Peter E.
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
; FILE REFERENCE: SCRIPT1160-4
; CURRENT APPLICATION NUMBER: US/09/500,700
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 08/863,813
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: US 08/676,318
; PRIOR FILING DATE: 1996-12-30
; PRIOR APPLICATION NUMBER: PCT/US95/00829
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: US 08/312,604
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: US 08/183,119
; PRIOR FILING DATE: 1994-01-18
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Modified sequence of finger 2 of zif268
US-09-500-700-104

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Query Match      23.5%; Score 4; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 PQPL 7
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Db       1 PQPL 4

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RESULT 7
US-09-822-270-12
; Sequence 12, Application US/09822270
; Patent No. US20020068697A1
; GENERAL INFORMATION:
; APPLICANT: TOURNIAIRE, ROSELYNE
; APPLICANT: DEMANGE, CAROLINE
; APPLICANT: DERBIN, CLAUDE
; APPLICANT: PERRET, GERARD
; APPLICANT: MAZIE, JEAN-CLAUDE

```

; APPLICANT: PLOUET, JEAN
; APPLICANT: VASSAY, ROGER
; TITLE OF INVENTION: PEPTIDES BLOCKING VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-MEDIA
; TITLE OF INVENTION: ANGIOGENESIS, POLYNUCLEOTIDES ENCODING SAID PEPTIDES AND METHODS
; FILE REFERENCE: 205060US0
; CURRENT APPLICATION NUMBER: US/09/822,270
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/193,396
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-822-270-12

Query Match 23.5%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
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Db 4 LQTP 7

RESULT 8
US-10-342-371-12
; Sequence 12, Application US/10342371
; Publication No. US20030171289A1
; GENERAL INFORMATION:
; APPLICANT: TOURNAIRE, ROSELYNE
; APPLICANT: DEMANGEL, CAROLINE
; APPLICANT: DERBIN, CLAUDE
; APPLICANT: PERRET, GERARD
; APPLICANT: MAZIE, JEAN-CLAUDE
; APPLICANT: PLOUET, JEAN
; APPLICANT: VASSAY, ROGER
; TITLE OF INVENTION: PEPTIDES BLOCKING VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-MEDIA
; TITLE OF INVENTION: ANGIOGENESIS, POLYNUCLEOTIDES ENCODING SAID PEPTIDES AND METHODS
; FILE REFERENCE: 205060US0
; CURRENT APPLICATION NUMBER: US/10/342,371
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US/09/822,270
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/193,396
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-342-371-12

Query Match 23.5%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
|||
Db 4 LQTP 7

RESULT 9
US-09-894-018-76
; Sequence 76, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:

; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Deniw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide
US-09-894-018-76

Query Match 23.5%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
|||
Db 5 PQPL 8

RESULT 10
US-10-089-549-17
; Sequence 17, Application US/10089549
; Publication No. US20030194762A1
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HIGASHIYAMA, Takanobu
; APPLICANT: FUKUDA, Shigeharu
; APPLICANT: MIYAKE, Toshio
; TITLE OF INVENTION: ALPHA-ISOMALTOSE-GLUCOSACCHARIDE-FORMING ENZYME, PROCESS AND I
; TITLE OF INVENTION: SAME
; FILE REFERENCE: KUBOTA=9
; CURRENT APPLICATION NUMBER: US/10/089,549
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: JP 233364/2000
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: JP 234937/2000
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: PCT/JF01/06412
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Bacillus globisporus
US-10-089-549-17

Query Match 23.5%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17
|||
Db 5 PQGD 8

RESULT 11
 US-08-344-824-282
 ; Sequence 282, Application US/08344824
 ; Publication No. US20030152580A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SETTE, Alessandro
 ; APPLICANT: SIDNEY, John
 ; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
 ; NUMBER OF SEQUENCES: 399
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: One Market Plaza, Steuart Street Tower, 20th
 ; STREET: Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/344,824
 ; FILING DATE: 23-NOV-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/278,634
 ; FILING DATE: 21-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bastian, Kevin L.
 ; REGISTRATION NUMBER: 34,774
 ; REFERENCE/DOCKET NUMBER: 14137-80-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 543-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 282:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-344-824-282

 Query Match 23.5%; Score 4; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

 QY 14 PQGD 17
 Db 2 PQGD 5

; NUMBER OF SEQ ID NOS: 235
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 102
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide
 US-09-765-086-102

 Query Match 23.5%; Score 4; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

 QY 7 LLQV 10
 Db 4 LLQV 7

RESULT 13
 US-09-834-765-48
 ; Sequence 48, Application US/09834765
 ; Patent No. US20020055478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mary Paris
 ; APPLICANT: Pia M. Challita-Bid
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Steve Chappell Mitchell
 ; APPLICANT: Daniel E.H. Afar
 ; APPLICANT: Aya Jakobovits
 ; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
 ; TITLE OF INVENTION: AND DETECTION OF CANCER
 ; FILE REFERENCE: 129.6USU1
 ; CURRENT APPLICATION NUMBER: US/09/834,765
 ; CURRENT FILING DATE: 2001-09-21
 ; PRIOR APPLICATION NUMBER: 60/197,647
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 770
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 48
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-834-765-48

 Query Match 23.5%; Score 4; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

 QY 4 PQPL 7
 Db 4 PQPL 7

RESULT 14
 US-09-834-765-130
 ; Sequence 130, Application US/09834765
 ; Patent No. US20020055478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mary Paris
 ; APPLICANT: Pia M. Challita-Bid
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Steve Chappell Mitchell
 ; APPLICANT: Daniel E.H. Afar
 ; APPLICANT: Aya Jakobovits
 ; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
 ; TITLE OF INVENTION: AND DETECTION OF CANCER
 ; FILE REFERENCE: 129.6USU1
 ; CURRENT APPLICATION NUMBER: US/09/834,765
 ; CURRENT FILING DATE: 2001-09-21
 ; PRIOR APPLICATION NUMBER: 60/197,647
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 770


```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-130
```

```
Query Match      23.5%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 PQPL 7
        |||||
Db      6 PQPL 9
```

```
RESULT 15
US-09-834-765-356
; Sequence 356, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 356
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-356
```

```
Query Match      23.5%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 PQPL 7
        |||||
Db      2 PQPL 5
```

```
RESULT 16
US-09-834-765-462
; Sequence 462, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 462
; LENGTH: 9
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-462
```

```
Query Match      23.5%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 PQPL 7
        |||||
Db      6 PQPL 9
```

```
RESULT 17
US-09-834-765-546
; Sequence 546, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 546
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-546
```

```
Query Match      23.5%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 PQPL 7
        |||||
Db      6 PQPL 9
```

```
RESULT 18
US-09-898-541-1
; Sequence 1, Application US/09898541
; Patent No. US20020072504A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Alan
; Bartido, Shirley M.
; Xu, Yiquing
; Wang, Siqun
; TITLE OF INVENTION: Method and Reagents for Genetic
Immunization
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: PO Box 5270
; CITY: Frisco
; STATE: CO
; COUNTRY: USA
; ZIP: 80443-5270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/09/898,541
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: MSK.P-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
TELEFAX: (970) 668-2082
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
DESCRIPTION: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: human
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match 23.5%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 QPLL 8
DB 4 QPLL 7

RESULT 19

US-09-898-541-2
Sequence 2, Application US/09898541
Patent No. US20020072504A1

GENERAL INFORMATION:

APPLICANT: Houghton, Alan
Bartido, Shirley M.
Xu, Yiquing
Wang, Siqun

TITLE OF INVENTION: Method and Reagents for Genetic
Immunization

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Oppedahl & Larson

STREET: PO Box 5270

CITY: Frisco

STATE: CO

COUNTRY: USA

ZIP: 80443-5270

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS 5.0

SOFTWARE: Word Perfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,541

FILING DATE: 02-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Marina T. Larson

REGISTRATION NUMBER: 32,038

REFERENCE/DOCKET NUMBER: MSK.P-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (970) 668-2050
TELEFAX: (970) 668-2082
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
DESCRIPTION: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: human
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-898-541-2

Query Match 23.5%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 QPLL 8
DB 4 QPLL 7

RESULT 20

US-09-984-056-56

Sequence 56, Application US/09984056
Patent No. US20020120106A1

GENERAL INFORMATION:

APPLICANT: BOGOCH, SAMUEL

APPLICANT: BOGOCH, ELENORE S.

TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLIKINS AND METHODS OF USE

FILE REFERENCE: 09425-46903

CURRENT APPLICATION NUMBER: US/09/984,056

CURRENT FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: 60/303,396

PRIOR FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: 60/278,761

PRIOR FILING DATE: 2001-03-27

PRIOR APPLICATION NUMBER: 09/146,755

PRIOR FILING DATE: 1998-09-04

PRIOR APPLICATION NUMBER: 09/817,144

PRIOR FILING DATE: 2001-03-27

PRIOR APPLICATION NUMBER: 08/198,139

PRIOR FILING DATE: 1994-02-17

NUMBER OF SEQ ID NOS: 103

SOFTWARE: PatentIn 2.1

SEQ ID NO 56

LENGTH: 9

TYPE: PRT

ORGANISM: Human papilloamavirus type 71

US-09-984-056-56

Query Match 23.5%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 PLLQ 9
DB 4 PLLQ 7

RESULT 21

US-09-984-057-56

Sequence 56, Application US/09984057
Patent No. US20020151677A1

GENERAL INFORMATION:

APPLICANT: BOGOCH, SAMUEL

APPLICANT: BOGOCH, ELENORE S.

TITLE OF INVENTION: REPLIKIN AND METHODS OF IDENTIFYING

TITLE OF INVENTION: REPLIKIN-CONTAINING SEQUENCES

```

; FILE REFERENCE: 09425-46902
; CURRENT APPLICATION NUMBER: US/09/984,057
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin 2.1
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus type 71
; US-09-984-057-56

Query Match      23.5%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLLQ 9
        ||||
Db      4 PLLQ 7

RESULT 22
US-09-972-656-30
; Sequence 30, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Wei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-972-656-30

Query Match      23.5%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTP 4
        ||||
Db      4 LQTP 7

RESULT 23
US-10-375-992-102
; Sequence 102, Application US/10375992
; Publication No. US20030152578A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego

```

```

; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/10/375,992
; FILING DATE: 27-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-10-375-992-102

Query Match      23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LLQV 10
        ||||
Db      4 LLQV 7

RESULT 24
US-10-105-232-56
; Sequence 56, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: Patentin 2.1
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus type 71
; US-10-105-232-56

Query Match      23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
QY      6 PLLQ 9
Db      4 PLLQ 7

RESULT 25
US-10-189-437-56
; Sequence 56, Application US/10189437
; Publication No. US2003019441A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus type 71
US-10-189-437-56

Query Match      23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLLQ 9
Db      4 PLLQ 7

RESULT 26
US-10-277-292-101
; Sequence 101, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-101

Query Match      23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLLQ 9
Db      4 PLLQ 7

RESULT 27
US-10-277-292-133
; Sequence 133, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-133

Query Match      23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LLQV 10
Db      6 LLQV 9

RESULT 28
US-10-137-867-288
; Sequence 288, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
US-10-137-867-288

Query Match      23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LLQV 10
Db      1 LLQV 4
```

```
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-288

Query Match      23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4
Db 6 LQTP 9

RESULT 29
US-10-280-340-101
; Sequence 101, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-101

Query Match      23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
Db 6 LLQV 9

RESULT 30
US-10-280-340-133
; Sequence 133, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/10/264,374
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/139,802
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-264-374-102

Query Match      23.5%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-133

Query Match      23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
Db 1 LLQV 4

RESULT 31
US-10-264-374-102
; Sequence 102, Application US/10264374
; Publication No. US20030113320A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/10/264,374
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/139,802
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-264-374-102

Query Match      23.5%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      7 LLQV 10
      ||||
Db      4 LLQV 7

RESULT 32
US-08-344-824-393
; Sequence 393, Application US/08344624
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; CITY: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 393:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-393

Query Match      23.5%; Score 4; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 PQGD 17
      ||||
Db      2 PQGD 5

RESULT 33
US-08-424-550B-597
; Sequence 597, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DANSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHRHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK

Query Match      23.5%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LLQV 10
      ||||
Db      1 LLQV 4

US-08-424-550B-597
; Sequence 468, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 468
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-834-765-468

Query Match      23.5%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 4 PQPL 7
| | | |
Db 7 PQPL 10

RESULT 35

US-09-908-322-53
; Sequence 53, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-908-322-53

Query Match 23.5%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
| | | |
Db 1 PQPL 4

RESULT 36

US-09-867-852-93
; Sequence 93, Application US/09867852
; Patent No. US20020147324A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.

; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/867,852
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-04-28
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1994-09-22
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1994-04-13
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-93

Query Match 23.5%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
| | | |
Db 2 PLLQ 5

RESULT 37

US-09-783-931-53
; Sequence 53, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,931
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-783-931-53

Query Match 23.5%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
Db 1 PQPL 4

RESULT 38

US-09-573-822C-108
; Sequence 108, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 108
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG290 at 17-26 and may interact with Sequence
; OTHER INFORMATION: this patent.
US-09-573-822C-108

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
Db 4 PLLQ 7

RESULT 39

US-10-277-292-169
; Sequence 169, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10

; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-169

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 6 LLQV 9

RESULT 40

US-10-277-292-179
; Sequence 179, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-179

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 2 LLQV 5

RESULT 41

US-10-277-292-286
; Sequence 286, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA


```
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 286
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-286

Query Match      23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 1 LLQV 4

RESULT 42
US-10-277-292-424
; Sequence 424, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 424
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-424

Query Match      23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 6 LLQV 9

; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 424
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-424

Query Match      23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 6 LLQV 9

; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 436
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-436

Query Match      23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 7 LLQV 10

; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 436
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-436

Query Match      23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 7 LLQV 10

; APPLICANT: BAKER, KEVIN P.
; APPLICANT: BERESINI, MAUREEN
; APPLICANT: DEFORGE, LAURA
; APPLICANT: DESNOYERS, IUC
; APPLICANT: FILVAROFF, ELLEN
; APPLICANT: GAO, WEI-QIANG
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: GODDARD, AUDREY
; APPLICANT: GODOWSKI, PAUL J.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: SHERWOOD, STEVEN
; APPLICANT: SMITH, VICTORIA
; APPLICANT: STEWART, TIMOTHY A.
; APPLICANT: TUMAS, DANIEL
; APPLICANT: WATANABE, COLIN K
; APPLICANT: WOOD, WILLIAM
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
```

```
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 274
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-274

Query Match      23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PQPL 7
        |||||
Db      6 PQPL 9

RESULT 45
US-10-280-340-169
; Sequence 169, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-169

Query Match      23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LLQV 10
        |||||
Db      6 LLQV 9

RESULT 46
US-10-280-340-179
; Sequence 179, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
```

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; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-179

Query Match      23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LLQV 10
        |||||
Db      2 LLQV 5

RESULT 47
US-10-280-340-286
; Sequence 286, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 286
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-286

Query Match      23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LLQV 10
        |||||
Db      1 LLQV 4

RESULT 48
```

US-10-280-340-424
; Sequence 424, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR FILING DATE: 2000-08-22
; PRIOR FILING DATE: 2000-08-22
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 424
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-424

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
|
|
|
|
Db 6 LLQV 9

RESULT 49
US-10-280-340-436
; Sequence 436, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR FILING DATE: 2000-08-22
; PRIOR FILING DATE: 2000-08-22
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 436
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-436

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
|
|
|
|
Db 7 LLQV 10

RESULT 50
US-10-185-815-89
; Sequence 89, Application US/10185815
; Publication No. US20030096354A1
; GENERAL INFORMATION:
; APPLICANT: Elan Corporation, plc
; APPLICANT: O'Mahony, Daniel
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands
; FILE REFERENCE: E1067-20093
; CURRENT APPLICATION NUMBER: US/10/185,815
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/302,591
; PRIOR FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Segment of CAPHI beta casein precursor
US-10-185-815-89

Query Match 23.5%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
|
|
|
|
Db 7 PQPL 10

RESULT 51
US-09-829-855-233
; Sequence 233, Application US/09829855
; Patent No. US20020065609A1
; GENERAL INFORMATION:
; APPLICANT: Matthew, Ashby N.
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations
; FILE REFERENCE: ASHBY-1
; CURRENT APPLICATION NUMBER: US/09/829,855
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/196063
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/196258
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 233
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured Acidobacterium Sub.Div-1
; NAME/KEY: MISC FEATURE
; LOCATION: (8) ..(8)
; OTHER INFORMATION: Unable to determine
US-09-829-855-233

Db 4 PLLQ 7

RESULT 56

US-09-992-238-27
; Sequence 27, Application US/09992238
; Publication No. US2003005444A1
; GENERAL INFORMATION:
; APPLICANT: BATTAGLINO, PETER
; APPLICANT: FEDER, JOHN N
; APPLICANT: MINTIER, GABE
; APPLICANT: NELSON, THOMAS C
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: WESTPHAL, RYAN
; APPLICANT: CACACE, ANGELA
; APPLICANT: BARBER, LAUREN
; APPLICANT: HAWKEN, DONALD R
; APPLICANT: KORNACKER, MICHAEL G
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGP8RMY8,
; FILE REFERENCE: D0047NP
; CURRENT APPLICATION NUMBER: US/09/992,238
; CURRENT FILING DATE: 2001-11-14
; PRIOR FILING DATE: 2001-09-04
; PRIOR FILING DATE: 2001-07-27
; PRIOR FILING DATE: 2001-02-14
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized
; OTHER INFORMATION: peptide
US-09-992-238-27

Query Match 23.5%; Score 4; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
|||
Db 6 LLQV 9

RESULT 57

US-09-992-238-77
; Sequence 77, Application US/09992238
; Publication No. US2003005444A1
; GENERAL INFORMATION:
; APPLICANT: BATTAGLINO, PETER
; APPLICANT: FEDER, JOHN N
; APPLICANT: MINTIER, GABE
; APPLICANT: NELSON, THOMAS C
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: WESTPHAL, RYAN
; APPLICANT: CACACE, ANGELA
; APPLICANT: BARBER, LAUREN
; APPLICANT: HAWKEN, DONALD R
; APPLICANT: KORNACKER, MICHAEL G
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGP8RMY8,
; FILE REFERENCE: D0047NP
; CURRENT APPLICATION NUMBER: US/09/992,238
; CURRENT FILING DATE: 2001-11-14
; PRIOR FILING DATE: 2001-09-04

; PRIOR APPLICATION NUMBER: 60/308285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/268581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/248285
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-09-992-238-77

Query Match 23.5%; Score 4; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
|||
Db 2 LLQV 5

RESULT 58

US-09-829-855-217
; Sequence 217, Application US/09829855
; Patent No. US20020065609A1
; GENERAL INFORMATION:
; APPLICANT: Matthew, Ashby N.
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations
; FILE REFERENCE: ASHBY-1
; CURRENT APPLICATION NUMBER: US/09/829,855
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/196063
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/196258
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Uncultured GNS bacteria BPC110
US-09-829-855-217

Query Match 23.5%; Score 4; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLL 8
|||
Db 3 QPLL 6

RESULT 59

US-10-271-078-33
; Sequence 33, Application US/10271078
; Publication No. US20030186267A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN LEUCINE-RICH REPEAT DOMAIN CONTAINING PROTEIN, HLG
; FILE REFERENCE: D0157 NP
; CURRENT APPLICATION NUMBER: US/10/271,078
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: U.S. 60/328,478
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 33
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-271-078-33

Query Match 23.5%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
|||
Db 11 PLLQ 14

RESULT 60

US-10-367-405-18
; Sequence 18, Application US/10367405
; Publication No. US20030215438A1

GENERAL INFORMATION:

; APPLICANT: Felix Hausch
; APPLICANT: Gary Gray
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT APPLICATION NUMBER: US/10/367,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 18
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-367-405-18

Query Match 23.5%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
|||
Db 10 PQPL 13

RESULT 61

US-10-256-865-15
; Sequence 15, Application US/10256865
; Publication No. US20030049672A1

GENERAL INFORMATION:

; APPLICANT: Xiao Zhen Zhou
; APPLICANT: Kun Ping Lu
; TITLE OF INVENTION: Methods and Compositions for Regulating
; TITLE OF INVENTION: Protein-Protein Interactions
; FILE REFERENCE: 1440.1034-000
; CURRENT APPLICATION NUMBER: US/10/256,865
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/252,404
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15
; LENGTH: 14
; TYPE: PRT
; ORGANISM: synthetic peptide
US-10-256-865-15

Query Match 23.5%; Score 4; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
|||
Db 9 LQTP 12

RESULT 62

US-10-120-604-26
; Sequence 26, Application US/10120604
; Publication No. US20030096347A1

GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECI
; TITLE OF INVENTION: HGPBMY28 AND HGPBMY29, AND SPLICE VARIANTS THEREOF
; FILE REFERENCE: D0143NP
; CURRENT APPLICATION NUMBER: US/10/120,604
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/283,145
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/283,161
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/288,468
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/300,619
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-604-26

Query Match 23.5%; Score 4; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
|||
Db 9 LQTP 12

RESULT 63

US-10-120-604-69
; Sequence 69, Application US/10120604
; Publication No. US20030096347A1

GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECI
; TITLE OF INVENTION: HGPBMY28 AND HGPBMY29, AND SPLICE VARIANTS THEREOF
; FILE REFERENCE: D0143NP
; CURRENT APPLICATION NUMBER: US/10/120,604
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/283,145
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/283,161
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/288,468
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/300,619
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69

; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-604-69

Query Match 23.5%; Score 4; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4
Db 9 LQTP 12

RESULT 64

US-10-120-604-85
; Sequence 85, Application US/10120604
; Publication No. US20030096347A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: D0143NP
; CURRENT APPLICATION NUMBER: US/10/120,604
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/283,145
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/283,161
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/288,468
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/300,619
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-604-85

Query Match 23.5%; Score 4; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4
Db 9 LQTP 12

RESULT 65

US-10-294-891-25
; Sequence 25, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-25

Query Match 23.5%; Score 4; DB 12; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPOG 16
Db 1 EPOG 4

RESULT 66

US-10-161-791-405
; Sequence 405, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 405:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-405

Query Match 23.5%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PQPL 7
Db 9 PQPL 12

RESULT 67

US-10-360-836-9
; Sequence 9, Application US/10360836
; Publication No. US20030185854A1
; GENERAL INFORMATION:
; APPLICANT: Zavala, Fidel

```
; APPLICANT: Birkett, Ashley
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
; TITLE OF INVENTION: AND MALIGNANCIES
; FILE REFERENCE: 5986/1J876
; CURRENT APPLICATION NUMBER: US/10/360,836
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/354,963
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Plasmodium
US-10-360-836-9

Query Match      23.5%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LLQV 10
        ||||
Db      12 LLQV 15

RESULT 68
US-10-360-836-10
; Sequence 10, Application US/10360836
; Publication No. US20030185854A1
; GENERAL INFORMATION:
; APPLICANT: Zavala, Fidel
; APPLICANT: Birkett, Ashley
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
; TITLE OF INVENTION: AND MALIGNANCIES
; FILE REFERENCE: 5986/1J876
; CURRENT APPLICATION NUMBER: US/10/360,836
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/354,963
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Plasmodium
US-10-360-836-10

Query Match      23.5%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LLQV 10
        ||||
Db      7 LLQV 10

RESULT 69
US-10-360-836-11
; Sequence 11, Application US/10360836
; Publication No. US20030185854A1
; GENERAL INFORMATION:
; APPLICANT: Zavala, Fidel
; APPLICANT: Birkett, Ashley
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
; TITLE OF INVENTION: AND MALIGNANCIES
; FILE REFERENCE: 5986/1J876
; CURRENT APPLICATION NUMBER: US/10/360,836
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/354,963
; PRIOR FILING DATE: 2002-02-08
```

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; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Plasmodium
US-10-360-836-11

Query Match      23.5%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LLQV 10
        ||||
Db      2 LLQV 5

RESULT 70
US-10-281-652-34
; Sequence 34, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-34

Query Match      23.5%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PQPL 7
        ||||
Db      5 PQPL 8

RESULT 71
US-10-194-985-29
; Sequence 29, Application US/10194985
; Publication No. US20030105287A1
; GENERAL INFORMATION:
; APPLICANT: Schaeffer, Michael
; APPLICANT: Schneiderbauer, Michaela
; APPLICANT: Weidler, Sascha
; APPLICANT: Hallek, Michael
; APPLICANT: GSF Forschungszentrum fuer Umwelt und Gesundheit GmbH
; TITLE OF INVENTION: Inhibition of the Proliferation of Cells of the
; TITLE OF INVENTION: Multiple Myeloma
; FILE REFERENCE: 080345-00010005
; CURRENT APPLICATION NUMBER: US/10/194,985
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: DE 19941897.7
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: US 09/625,225
; PRIOR FILING DATE: 2000-07-24
```


; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:p5 peptide
; OTHER INFORMATION: subfragment of Hck binding region of gp130
US-10-194-985-29

Query Match 23.5%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLL 8
Db 6 QPLL 9

RESULT 72
US-10-299-043-2
; Sequence 2, Application US/10299043
; Publication No. US20030158115A1
; GENERAL INFORMATION:
; APPLICANT: TOBACK, F. GARY
; APPLICANT: LIESKE, JOHN C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
; TITLE OF INVENTION: KIDNEY DISEASES ASSOCIATED WITH ADHESION OF CRYSTALS TO
; TITLE OF INVENTION: KIDNEY CELLS
; FILE REFERENCE: 21459/90606
; CURRENT APPLICATION NUMBER: US/10/299,043
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US/09/537,226
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/389,005
; PRIOR FILING DATE: 1995-02-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-299-043-2

Query Match 23.5%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PQPL 7
Db 10 PQPL 13

RESULT 73
US-10-174-105A-181
; Sequence 181, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSHO-PROTEINS USING MOTIF-SPECIFIC,
; TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04

; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 181
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: MOD_RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 9 is phosphorylated
US-10-174-105A-181

Query Match 23.5%; Score 4; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4
Db 11 LQTP 14

RESULT 74
US-09-861-708-1
; Sequence 1, Application US/09861708
; Patent No. US20020098188A1
; GENERAL INFORMATION:
; APPLICANT: KAIBARA, Makoto
; APPLICANT: IWATA, Hiroki
; APPLICANT: TAKIO, Koji
; APPLICANT: DOHMAE, Naoshi
; TITLE OF INVENTION: Blood Coagulation Factor-Activating Protein and Antibody There
; FILE REFERENCE: P21011
; CURRENT APPLICATION NUMBER: US/09/861,708
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: JP 153096/2000
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Unknown Amino Acid
US-09-861-708-1

Query Match 23.5%; Score 4; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 PQGD 17
Db 3 PQGD 6

RESULT 75
US-09-864-761-34833
; Sequence 34833, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1

```
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34833
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009473.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 19
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 30
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 31
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 49
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 29
US-09-864-761-34833
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Query Match 23.5%; Score 4; DB 9; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 6 PLLQ 9

Db 11 PLLQ 14

Search completed: November 25, 2003, 20:25:26
Job time : 35.8191 secs

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 18.5372 Seconds
(without alignments)
38.802 Million cell updates/sec

Title: US-09-641-801-2
Perfect score: 17
Sequence: 1 LQTPQPLLQVMPEQGD 17

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters:	151837
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Minimum DB seq length: 3
Maximum DB seq length: 20
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Post-processing: Listing first 100 summaries

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2: /cgn2_6/ptodata/1/iaa/5E.COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pcp.*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pcp.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	17	100.0	17	4	5	US-09-641-803-2	Sequence 2, Appl
2	6	35.3	18	4	5	PT-US91-05177-19	Sequence 19, Appl
3	5	29.4	7	1	1	US-08-594-447-74	Sequence 74, Appl
4	5	29.4	7	1	1	US-08-541-964-73	Sequence 73, Appl
5	5	29.4	7	2	2	US-08-541-964-73	Sequence 88, Appl
6	5	29.4	4	6	5	US-08-665-647-88	Patent No. 5204326
7	5	29.4	14	6	5	5204336-100	Patent No. 5204326
8	5	29.4	14	6	5	5204336-36	Patent No. 5204326
9	5	29.4	14	6	5	5204336-95	Patent No. 5204326
10	5	29.4	15	6	5	5204336-37	Patent No. 5204326
11	5	29.4	15	6	5	5204336-40	Patent No. 5204326
12	5	29.4	15	6	5	5204336-71	Patent No. 5204326
13	5	29.4	16	6	5	5204336-74	Patent No. 5204326
14	5	29.4	17	6	5	5204336-96	Patent No. 5204326
15	5	29.4	18	6	5	5204336-97	Patent No. 5204326
16	5	29.4	18	6	5	5204336-38	Patent No. 5204326
17	5	29.4	18	6	5	5204336-41	Patent No. 5204326
18	5	29.4	18	6	5	5204336-98	Patent No. 5204326
19	5	29.4	19	6	5	5204336-101	Patent No. 5204326
20	5	29.4	19	6	5	5204336-72	Patent No. 5204326
21	5	29.4	20	6	5	5204336-75	Patent No. 5204326
22	4	23.5	20	6	5	5204336-39	Patent No. 5204326
23	4	23.5	7	1	1	US-08-594-447-75	Sequence 75, Appl
24	4	23.5	7	1	1	US-08-541-964-74	Sequence 74, Appl
25	4	23.5	7	2	2	US-08-541-964-73	Sequence 40, Appl
26	4	23.5	7	2	2	US-08-665-647-89	Sequence 89, Appl
27	4	23.5	7	2	2	US-09-160-126-3	Sequence 3, Appl
28	4	23.5	7	4	5	US-08-757-4258-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1

US-09-641-803-2
; Sequence 2, Application US/09641803
; Patent No. 650798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-2

Query Match 100.0%; Score 17; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQLQVMEPQGD 17
Db 1 LQTPQLQVMEPQGD 17

RESULT 2

PCT-US91-05177-19
; Sequence 19, Application PC/TUS9105177
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathy L
; TITLE OF INVENTION: GAMMA-CARBOXYLASE AND METHODS OF USE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05177
; FILING DATE: 1991.0722
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/557,220
; FILING DATE: 23-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.544PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031

; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; FRAGMENT TYPE: internal
PCT-US91-05177-19

Query Match 35.3%; Score 6; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPQPLL 8
Db 1 TPQPLL 6

RESULT 3

US-08-594-447-74
; Sequence 74, Application US/08594447
; Patent No. 5776716
; GENERAL INFORMATION:
; APPLICANT: Ron, Dorit
; APPLICANT: Napolitano, Eugene W.
; APPLICANT: Voronova, Anna F.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH
; TITLE OF INVENTION: BLOCKTHE INTERACTION OF FYN WITH PKC-THETA, AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,447
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSH
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /label= PRK1-3
US-08-594-447-74

Query Match 29.4%; Score 5; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MEPOG 16
Db 1 MEPOG 5

RESULT 4
US-08-541-964-73
; Sequence 73, Application US/08541964
; Patent No. 5783405
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; APPLICANT: Kauvar, Lawrence M.
; APPLICANT: Napolitano, Eugene W.
; TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS
; TITLE OF INVENTION: OF SIGNAL TRANSDUCTION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW-STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,964
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /label= PK1-3
US-08-541-964-73
Query Match 29.4%; Score 5; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 MEPQG 16
Db 1 MEPQG 5
RESULT 5
US-08-665-647-88
; Sequence 88, Application US/08665647
; Patent No. 5935803
; GENERAL INFORMATION:
; APPLICANT: Dasquez, Nicki J.
; APPLICANT: Ron, Dorit
; APPLICANT: Voronova, Anna F.
; APPLICANT: Napolitano, Eugene W.
; TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS
; TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,647
; FILING DATE: 18-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /label= PK1-3
US-08-665-647-88
Query Match 29.4%; Score 5; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 MEPQG 16
Db 1 MEPQG 5
RESULT 6
5204326-100
; Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:100:
; LENGTH: 9
5204326-100
Query Match 29.4%; Score 5; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQTPQ 5
Db 3 LQTPQ 7
RESULT 7
5204326-36
; Patent No. 5204326

; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIIHITO;SHIMIZU, FUMIO
 ; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
 ;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
 ; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
 ; METABOLISM IMPROVING AGENT
 ; NUMBER OF SEQUENCES: 147
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/493,359
 ; FILING DATE: 14-MAR-1990
 ; SEQ ID NO:36:
 ; LENGTH: 14
 5204326-36

Query Match 29.4%; Score 5; DB 6; Length 14;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5
 |||||
 Db 2 LQTPQ 6

RESULT 8

5204326-95
 ; Patent No. 5204326
 ; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIIHITO;SHIMIZU, FUMIO
 ; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
 ;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
 ; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
 ; METABOLISM IMPROVING AGENT
 ; NUMBER OF SEQUENCES: 147
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/493,359
 ; FILING DATE: 14-MAR-1990
 ; SEQ ID NO:95:
 ; LENGTH: 14
 5204326-95

Query Match 29.4%; Score 5; DB 6; Length 14;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5
 |||||
 Db 2 LQTPQ 6

RESULT 9

5204326-37
 ; Patent No. 5204326
 ; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIIHITO;SHIMIZU, FUMIO
 ; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
 ;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
 ; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
 ; METABOLISM IMPROVING AGENT
 ; NUMBER OF SEQUENCES: 147
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/493,359
 ; FILING DATE: 14-MAR-1990
 ; SEQ ID NO:37:
 ; LENGTH: 15
 5204326-37

Query Match 29.4%; Score 5; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5
 |||||
 Db 3 LQTPQ 7

RESULT 10

5204326-40
 ; Patent No. 5204326
 ; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIIHITO;SHIMIZU, FUMIO
 ; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
 ;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
 ; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
 ; METABOLISM IMPROVING AGENT
 ; NUMBER OF SEQUENCES: 147
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/493,359
 ; FILING DATE: 14-MAR-1990
 ; SEQ ID NO:40:
 ; LENGTH: 15
 5204326-40

Query Match 29.4%; Score 5; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5
 |||||
 Db 3 LQTPQ 7

RESULT 11

5204326-71
 ; Patent No. 5204326
 ; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIIHITO;SHIMIZU, FUMIO
 ; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
 ;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
 ; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
 ; METABOLISM IMPROVING AGENT
 ; NUMBER OF SEQUENCES: 147
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/493,359
 ; FILING DATE: 14-MAR-1990
 ; SEQ ID NO:71:
 ; LENGTH: 15
 5204326-71

Query Match 29.4%; Score 5; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5
 |||||
 Db 3 LQTPQ 7

RESULT 12

5204326-74
 ; Patent No. 5204326
 ; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIIHITO;SHIMIZU, FUMIO
 ; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
 ;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
 ; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
 ; METABOLISM IMPROVING AGENT
 ; NUMBER OF SEQUENCES: 147
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/493,359
 ; FILING DATE: 14-MAR-1990
 ; SEQ ID NO:74:
 ; LENGTH: 15
 5204326-74

Query Match 29.4%; Score 5; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5
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 Db 3 LQTPQ 7

```
Db          6 LQTPQ 10

RESULT 16
5204326-96
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:96:
; LENGTH: 16
5204326-96

Query Match          29.4%; Score 5; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTPQ 5
        |||||
Db      4 LQTPQ 8

RESULT 14
5204326-97
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:97:
; LENGTH: 17
5204326-97

Query Match          29.4%; Score 5; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTPQ 5
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Db      5 LQTPQ 9

RESULT 15
5204326-38
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:38:
; LENGTH: 18
5204326-38

Query Match          29.4%; Score 5; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTPQ 5
        |||||

Db          6 LQTPQ 10

RESULT 17
5204326-98
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:98:
; LENGTH: 18
5204326-98

Query Match          29.4%; Score 5; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTPQ 5
        |||||
Db      6 LQTPQ 10

RESULT 18
5204326-101
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:101:
; LENGTH: 18
5204326-101

Query Match          29.4%; Score 5; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTPQ 5
        |||||
Db      6 LQTPQ 10

RESULT 18
5204326-101
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:101:
; LENGTH: 18
5204326-101

Query Match          29.4%; Score 5; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTPQ 5
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Wed Nov 26 09:07:00 2003

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Qy      1 LQTPQ 5
Db      6 LQTPQ 10

RESULT 19
5204326-72
;PATENT NO. 5204326
;APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
;MITSURU;SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
;TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
;METABOLISM IMPROVING AGENT
;NUMBER OF SEQUENCES: 147
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/493,359
;FILING DATE: 14-MAR-1990
;SEQ ID NO:72:
;LENGTH: 19
5204326-72
Query Match      29.4%; Score 5; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LQTPQ 5
Db      7 LQTPQ 11

RESULT 20
5204326-75
;PATENT NO. 5204326
;APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
;MITSURU;SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
;TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
;METABOLISM IMPROVING AGENT
;NUMBER OF SEQUENCES: 147
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/493,359
;FILING DATE: 14-MAR-1990
;SEQ ID NO:75:
;LENGTH: 19
5204326-75
Query Match      29.4%; Score 5; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LQTPQ 5
Db      7 LQTPQ 11

RESULT 21
5204326-39
;PATENT NO. 5204326
;APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
;MITSURU;SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
;TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
;METABOLISM IMPROVING AGENT
;NUMBER OF SEQUENCES: 147
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/493,359
;FILING DATE: 14-MAR-1990
;SEQ ID NO:39:
;LENGTH: 20
5204326-39
Query Match      29.4%; Score 5; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LQTPQ 5
Db      7 LQTPQ 11

RESULT 22
US-08-594-447-75
; Sequence 75, Application US/08594447
; Patent No. 5776716
; GENERAL INFORMATION:
; APPLICANT: Ron, Dorit
; APPLICANT: Napolitano, Eugene W.
; APPLICANT: Voronova, Anna F.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH
; TITLE OF INVENTION: BLOCKTHE INTERACTION OF PYN WITH PKC-THETA, AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,447
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TLEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLESCULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /label= PRK2-3
US-08-594-447-75
Query Match      23.5%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 EPOG 16
Db      2 EPOG 5

RESULT 23
US-08-541-964-74
; Sequence 74, Application US/08541964
; Patent No. 5783405
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; APPLICANT: Kauvar, Lawrence M.
```


APPLICANT: Napolitano, Eugene W.
TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS
TITLE OF INVENTION: OF SIGNAL TRANSDUCTION
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW-STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1889
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,964
FILING DATE: 10-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22550-20025.23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030 MRSNFORSWSH
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..7
OTHER INFORMATION: /label= PRK2-3
US-08-541-964-74

Query Match 23.5%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPQG 16
Db 2 EPQG 5

RESULT 24
US-08-666-473-40
Sequence 40, Application US/08666473
Patent No. 5843713
GENERAL INFORMATION:
APPLICANT: YOSHIDA, Aruto
APPLICANT: TAKEUCHI, Makoto
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,473
FILING DATE: 19-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP95/02238
FILING DATE: 01-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-22101
FILING DATE: 09-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-269111
FILING DATE: 01-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/837
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-666-473-40

Query Match 23.5%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPQP 6
Db 4 TPQP 7

RESULT 25
US-08-665-647-89
Sequence 89, Application US/08665647
Patent No. 5935803
GENERAL INFORMATION:
APPLICANT: Dasquez, Nicki J.
APPLICANT: Ron, Dorit
APPLICANT: Voronova, Anna F.
APPLICANT: Napolitano, Eugene W.
TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS
TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1889
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,647
FILING DATE: 18-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22550-20025.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168

Wed Nov 26 09:07:00 2003

TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..7
OTHER INFORMATION: /label= PRK2-3
US-08-665-647-89

Query Match 23.5%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQG 16
|||
Db 2 EPQG 5

RESULT 26
US-09-160-126-3
; Sequence 3, Application US/09160126
; Patent No. 5962417
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Park, Hee-young
; TITLE OF INVENTION: Methods of Modulating Melanin Synthesis
; FILE REFERENCE: BU95-59A2
; CURRENT APPLICATION NUMBER: US/09/160,126
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: PCT/US97/04752
; EARLIER FILING DATE: 1997-03-27
; EARLIER APPLICATION NUMBER: 08/623,364
; EARLIER FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-160-126-3

Query Match 23.5%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLL 8
|||
Db 1 QPLL 4

RESULT 27
US-08-757-425B-62
; Sequence 62, Application US/08757425B
; Patent No. 6506660
; GENERAL INFORMATION:
; APPLICANT: Fastrez, Jacques
; TITLE OF INVENTION: Chimeric Target Molecules Having A Regulatable Activity
; FILE REFERENCE: 100390-09640
; CURRENT APPLICATION NUMBER: US/08/757,425B
; CURRENT FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mimotope

US-08-757-425B-62

Query Match 23.5%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17
|||
Db 2 PQGD 5

RESULT 28

US-08-757-425B-63
; Sequence 63, Application US/08757425B
; Patent No. 6506660
; GENERAL INFORMATION:
; APPLICANT: Fastrez, Jacques
; TITLE OF INVENTION: Chimeric Target Molecules Having A Regulatable Activity
; FILE REFERENCE: 100390-09640
; CURRENT APPLICATION NUMBER: US/08/757,425B
; CURRENT FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mimotope
US-08-757-425B-63

Query Match 23.5%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17
|||
Db 2 PQGD 5

RESULT 29

US-09-822-270-12
; Sequence 12, Application US/09822270
; Patent No. 6559126
; GENERAL INFORMATION:
; APPLICANT: TOURNAIRE, ROSELYNE
; APPLICANT: DEMANGEL, CAROLINE
; APPLICANT: DERBIN, CLAUDE
; APPLICANT: PERRET, GERARD
; APPLICANT: MAZIE, JEAN-CLAUDE
; APPLICANT: FLOUET, JEAN
; APPLICANT: VASSAY, ROGER
; TITLE OF INVENTION: PEPTIDES BLOCKING VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-MI
; FILE REFERENCE: 205060US0
; CURRENT APPLICATION NUMBER: US/09/822,270
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/193,396
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-822-270-12

Query Match 23.5%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
|||
DB 4 LQTP 7

RESULT 30
US-08-350-260A-362
; Sequence 362, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-362

Query Match

23.5%; Score 4; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
|||
DB 4 LQTP 7

RESULT 31
US-08-350-260A-452
; Sequence 452, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 452:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-350-260A-452

Query Match 23.5%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
|
|
|
|
Db 4 LQTP 7

RESULT 32

US-08-350-260A-453
; Sequence 453, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 453:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-453

Query Match 23.5%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
|
|
|
|
Db 4 LQTP 7

RESULT 33

US-08-350-260A-458
; Sequence 458, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 453:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids

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; INFORMATION FOR SEQ ID NO: 458:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 8 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-350-260A-458

Query Match      23.5%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTP 4
Db      4 LQTP 7

RESULT 34
US-08-350-260A-460
; Sequence 460, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107

; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 460:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 8 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-350-260A-460

Query Match      23.5%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTP 4
Db      4 LQTP 7

RESULT 35
US-08-350-260A-515
; Sequence 515, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
```

us-09-641-801-2.oligo.rai

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 515:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-515

Query Match      23.5%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    1 LQTP 4
Db     4 LQTP 7

RESULT 36
US-08-350-260A-520
; Sequence 520, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:

```

```
/
/ NAME: Bartnicki, Audrey L.
/ REGISTRATION NUMBER: 40,499
/ REFERENCE/DOCKET NUMBER: 28111/32372A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ INFORMATION FOR SEQ ID NO: 362:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-104-337A-362

Query Match      23.5%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
Db 4 LQTP 7

RESULT 38
US-09-104-337A-452
; Sequence 452, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 362:
```

```
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ INFORMATION FOR SEQ ID NO: 452:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 452:
US-09-104-337A-452

Query Match      23.5%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
Db 4 LQTP 7

RESULT 39
US-09-104-337A-453
; Sequence 453, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 453:
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SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 458:
US-09-104-337A-458
Query Match 23.5%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQTP 4
Db 4 LQTP 7
RESULT 41
US-09-104-337A-460
Sequence 460, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific binding pairs
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 460:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 460:

SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 453:
US-09-104-337A-453
Query Match 23.5%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQTP 4
Db 4 LQTP 7
RESULT 40
US-09-104-337A-458
Sequence 458, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific binding pairs
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 458:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid

US-09-104-337A-460

Query Match 23.5%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LQTP 4
Db 4 LQTP 7

RESULT 42

US-09-104-337A-515
; Sequence 515, Application US/09104337A
; Patent No. 6492160

GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond

TITLE OF INVENTION: Methods for producing members of specific binding pairs

NUMBER OF SEQUENCES: 600

CORRESPONDENCE ADDRESS:

ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994

APPLICATION NUMBER: GB 9110549.4

FILING DATE: 15-MAY-1991

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

APPLICATION NUMBER: PCT/GB92/00883

FILING DATE: 15-MAY-1992

APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 24-MAR-1993

APPLICATION NUMBER: US 08/150,002

FILING DATE: 31-MAR-1994

APPLICATION NUMBER: US 08/307,619

FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bartnicki, Audrey L.

REGISTRATION NUMBER: 40,499

REFERENCE/DOCKET NUMBER: 28111/32372A

TELEPHONE: 312-474-6300

INFORMATION FOR SEQ ID NO: 515:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 515:

US-09-104-337A-515

Query Match

23.5%; Score 4; DB 4; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LQTP 4
Db 4 LQTP 7

RESULT 43

US-09-104-337A-520

; Sequence 520, Application US/09104337A

; Patent No. 6492160

GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond

TITLE OF INVENTION: Methods for producing members of specific binding pairs

NUMBER OF SEQUENCES: 600

CORRESPONDENCE ADDRESS:

ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A

FILING DATE: 25-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/350,260

FILING DATE: 05-DEC-1994

APPLICATION NUMBER: GB 9110549.4

FILING DATE: 15-MAY-1991

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

APPLICATION NUMBER: PCT/GB92/00883

FILING DATE: 15-MAY-1992

APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 24-MAR-1993

APPLICATION NUMBER: US 08/150,002

FILING DATE: 31-MAR-1994

APPLICATION NUMBER: US 08/307,619

FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bartnicki, Audrey L.

REGISTRATION NUMBER: 40,499

REFERENCE/DOCKET NUMBER: 28111/32372A

TELEPHONE: 312-474-6300

INFORMATION FOR SEQ ID NO: 520:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 520:

US-09-104-337A-520

Query Match

23.5%; Score 4; DB 4; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LQTP 4
|
|
|
|
Db 4 LQTP 7

RESULT 44
US-08-594-447-52
; Sequence 52, Application US/08594447
; Patent No. 5776716
; GENERAL INFORMATION:
; APPLICANT: Ron, Dorit
; APPLICANT: Napolitano, Eugene W.
; APPLICANT: Voronova, Anna F.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH
; TITLE OF INVENTION: BLOCKTHE INTERACTION OF FYN WITH PKC-THETA, AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,964
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..9
; OTHER INFORMATION: /label= theta-V3-2
US-08-541-964-51

Query Match 23.5%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQG 16
|
|
|
|
Db 4 EPQG 7

RESULT 46
US-08-665-647-66
; Sequence 66, Application US/086656647
; Patent No. 5935803
; GENERAL INFORMATION:
; APPLICANT: Dasquez, Nicki J.
; APPLICANT: Ron, Dorit
; APPLICANT: Voronova, Anna F.
; APPLICANT: Napolitano, Eugene W.
; TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS
; TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

QY 1 LQTP 4
|
|
|
|
Db 4 LQTP 7

RESULT 45
US-08-541-964-51
; Sequence 51, Application US/08541964
; Patent No. 5783405
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; APPLICANT: Kauvar, Lawrence M.
; APPLICANT: Napolitano, Eugene W.
; TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS

Query Match 23.5%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQG 16
|
|
|
|
Db 4 EPQG 7

RESULT 45
US-08-541-964-51
; Sequence 51, Application US/08541964
; Patent No. 5783405
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; APPLICANT: Kauvar, Lawrence M.
; APPLICANT: Napolitano, Eugene W.
; TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS

```

; APPLICATION NUMBER: US/08/665,647
; FILING DATE: 18-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFORSHWSH
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..9
; OTHER INFORMATION: /label=theta-V3-2
;
US-08-665-647-66

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Query Match      23.5%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      13 EPOG 16
        ||||
Db       4 EPOG 7

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RESULT 47

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US-08-350-260A-356
; Sequence 356, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134

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; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 356:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-350-260A-356

```

```

Query Match      23.5%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 LQTP 4
        ||||
Db       4 LQTP 7

```

RESULT 48

```

US-08-350-260A-365
; Sequence 365, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9

```

;
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 365:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-365

Query Match 23.5%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LQTP 4
Db 4 LQTP 7

RESULT 49

US-08-350-260A-373
; Sequence 373, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Anuwa
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4

;
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-373

Query Match 23.5%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LQTP 4
Db 4 LQTP 7

RESULT 50

US-08-318-856A-37
; Sequence 37, Application US/08318856A
; Patent No. 5972351
; GENERAL INFORMATION:
; APPLICANT: Adrian V.S. Hill, et al.
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
; TITLE OF INVENTION: RESTRICTED CTL EPTOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
; TITLE OF INVENTION: ANTIGENS (AS AMENDED)
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1+
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,856A
; FILING DATE: October 3, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 08 068.8
; FILING DATE: April 3, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 17 704.7
; FILING DATE: August 20, 1992

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB93/00711
; FILING DATE: April 5, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 263-PP1R1577US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-318-856A-37

Query Match      23.5%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTP 4
        ||||
Db      5 LQTP 8

RESULT 51
US-08-159-339A-1062
; Sequence 1062, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1062:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-1062

Query Match      23.5%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 PQGD 17
        ||||
Db      2 PQGD 5

RESULT 52
US-09-139-802-102
; Sequence 102, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/139,802
; CURRENT FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 08/926,914
; EARLIER FILING DATE: 1997-09-10
; EARLIER APPLICATION NUMBER: 08/710,067
; EARLIER FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; US-09-139-802-102

Query Match      23.5%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LLQV 10
        ||||
Db      4 LLQV 7

RESULT 53
US-09-230-199-1
; Sequence 1, Application US/09230199
; Patent No. 6294378
; GENERAL INFORMATION:
; APPLICANT: Houghton, Alan
; APPLICANT: Bartido, Shirley M.
; APPLICANT: Xu, Yiquing
; APPLICANT: Wang, Siqun
; TITLE OF INVENTION: Method and Reagents for Genetic
; TITLE OF INVENTION: Immunization
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: PO Box 5270
; CITY: Frisco
; STATE: CO
; COUNTRY: USA
; ZIP: 80443-5270
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/230,199
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/12675
FILING DATE: 18-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: MSK-P-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
TELEFAX: (970) 668-2082
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: human
US-09-230-199-1

Query Match 23.5%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLL 8
Db 4 QPLL 7

RESULT 54
US-09-230-199-2
Sequence 2, Application US/09230199
Patent No. 6294379
GENERAL INFORMATION:
APPLICANT: Houghton, Alan
APPLICANT: Bartigo, Shirley M.
APPLICANT: Xu, Yiquing
APPLICANT: Wang, Siqun
TITLE OF INVENTION: Method and Reagents for Genetic
TITLE OF INVENTION: Immunization
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: PO Box 5270
CITY: Frisco
STATE: CO
COUNTRY: USA
ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/230,199
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/12675
FILING DATE: 18-JUL-1997
ATTORNEY/AGENT INFORMATION:

NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: MSK-P-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
TELEFAX: (970) 668-2082
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: human
US-09-230-199-2

Query Match 23.5%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLL 8
Db 4 QPLL 7

RESULT 55
US-08-737-109-5
Sequence 5, Application US/08737109
Patent No. 6455688
GENERAL INFORMATION:
APPLICANT: SLABAS, Antoni Ryszard
APPLICANT: ELBOROUGH, Kieran Michael
APPLICANT: BRIGHT, Simon William Jonathan
APPLICANT: FENTIM, Philip Anthony
TITLE OF INVENTION: Plant Gene Specifying Acetyl Coenzyme A
TITLE OF INVENTION: Carboxylase and Transformed Plants Containing Same
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,109
FILING DATE: 21-OCT-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/00846
FILING DATE: 02-MAY-1994
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Avena sativa
US-08-737-109-5

Query Match 23.5%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQG 16
 ||||
Db 4 EPQG 7

RESULT 56

US-09-659-786-102
; Sequence 102, Application US/09659786
; Patent No. 6491894
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/659,786
; CURRENT FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-659-786-102

Query Match 23.5%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
 ||||
Db 4 LLQV 7

RESULT 57

US-09-104-337A-356
; Sequence 356, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

INFORMATION FOR SEQ ID NO: 356:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 356:

US-09-104-337A-356

Query Match 23.5%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
 ||||
Db 4 LQTP 7

RESULT 58

US-09-104-337A-365
; Sequence 365, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 365:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 365:
US-09-104-337A-365

```

```

Query Match      23.5%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LQTP 4
Db      4 LQTP 7

```

RESULT 59

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US-09-104-337A-373
; Sequence 373, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4

```

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; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 373:
US-09-104-337A-373

```

```

Query Match      23.5%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY      1 LQTP 4
Db      4 LQTP 7

```

RESULT 60

```

US-08-926-914-102
; Sequence 102, Application US/08926914
; Patent No. 6576239
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: both

```


; MOLECULE TYPE: peptide
US-08-926-914-102

Query Match 23.5%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
|||
Db 4 LLQV 7

RESULT 61

US-08-310-912A-93
; Sequence 93, Application US/08310912A
; Patent No. 5981730
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,912A
; FILING DATE: September 22, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/254001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254

INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-310-912A-93

Query Match 23.5%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
|||
Db 2 PLLQ 5

RESULT 62

US-08-159-339A-971
; Sequence 971, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:

INFORMATION FOR SEQ ID NO: 971:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-971

Query Match 23.5%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17
|||
Db 6 PQGD 9

RESULT 63

US-08-159-339A-1070
; Sequence 1070, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254

;;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1070:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-1070

Query Match 23.5%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 14 PQGD 17
Db 2 PQGD 5

RESULT 64
US-08-841-089-93
; Sequence 93, Application US/08841089
; Patent No. 6127607
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Skaskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-liang
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy

;;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,089
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,360
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-841-089-93

Query Match 23.5%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 6 PLLQ 9
Db 2 PLLQ 5

RESULT 65
US-08-981-392-53
; Sequence 53, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE

APPLICANT: ISA K. MUSHAWAR

TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,446
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 597:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-446-597

Query Match 23.5%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 LLQV 10
|||
Db 1 LLQV 4

RESULT 69

US-08-467-344A-597
Sequence 597, Application US/08467344A
Patent No. 6586568
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 597:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 597:
US-08-467-344A-597

Query Match 23.5%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 LLQV 10
|||
Db 1 LLQV 4

RESULT 70

PCT-US95-04570-93
Sequence 93, Application PC/TUS9504570
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04570-93

Query Match 23.5%; Score 4; DB 5; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0; Mismatches 0;
Matches 4; Conservative 0;

QY 6 PLLQ 9
|||
Db 2 PLLQ 5

RESULT 71
PCT-US95-04589-93
; Sequence 93, Application PC/TUS9504589
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-liang
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 201
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04589
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,360
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04589-93

Query Match 23.5%; Score 4; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0; Mismatches 0;
Matches 4; Conservative 0;

QY 6 PLLQ 9
|||
Db 2 PLLQ 5

RESULT 72
US-09-183-846A-24
; Sequence 24, Application US/09183846A
; Patent No. 6255046
; GENERAL INFORMATION:
; APPLICANT: Richard J. Bucala et al.

Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0; Mismatches 0;
Matches 4; Conservative 0;

QY 5 QPLL 8
|||
Db 2 QPLL 5

RESULT 73
US-08-339-214-56
; Sequence 56, Application US/08339214
; Patent No. 6348334
; GENERAL INFORMATION:
; APPLICANT: Nagata, Shigikazu
; APPLICANT: Suda, Takashi
; APPLICANT: Takahashi, Tomoniro
; APPLICANT: Nakamura, No. 6348334io
; TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
; TITLE OF INVENTION: Encoding the Same
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,214
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.

Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0; Mismatches 0;
Matches 4; Conservative 0;

QY 5 QPLL 8
|||
Db 2 QPLL 5

Query Match 23.5%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0; Mismatches 0;
Matches 4; Conservative 0;

QY 5 QPLL 8
|||
Db 2 QPLL 5

RESULT 73
US-08-339-214-56
; Sequence 56, Application US/08339214
; Patent No. 6348334
; GENERAL INFORMATION:
; APPLICANT: Nagata, Shigikazu
; APPLICANT: Suda, Takashi
; APPLICANT: Takahashi, Tomoniro
; APPLICANT: Nakamura, No. 6348334io
; TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
; TITLE OF INVENTION: Encoding the Same
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,214
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.

Wed Nov 26 09:07:00 2003

REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /label= peptide
OTHER INFORMATION: /note= "peptide 1"
US-08-339-214-56

Query Match 23.5%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VMME 13
|||
Db 2 VMME 5

RESULT 74
5204326-35
Patent No. 5204326
APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:35:
; LENGTH: 12
5204326-35

Query Match 23.5%; Score 4; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTPQ 5
|||
Db 1 QTPQ 4

RESULT 75
5204326-94
Patent No. 5204326
APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:94:
; LENGTH: 12
5204326-94

Query Match 23.5%; Score 4; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QTPQ 5
|||
Db 1 QTPQ 4

Search completed: November 25, 2003, 20:15:57
Job time : 19.5372 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 : Search time 16.5638 Seconds
(without alignments)
104.507 Million cell updates/sec

Title: us-09-641-801-3
Perfect score: 18
Sequence: 1 DQPPVEKPLQLPFQVQS 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	27.8	9	2	S66419
2	5	27.8	15	2	S20410
3	4	22.2	15	2	A60221
4	4	22.2	17	2	B44873
5	4	22.2	19	2	S59485
6	4	22.2	19	2	S59486
7	4	22.2	20	2	S11416
8	3	16.7	6	2	PC4392
9	3	16.7	7	2	S71299
10	3	16.7	7	2	S68004
11	3	16.7	7	2	PT0283
12	3	16.7	8	2	PT0030
13	3	16.7	8	2	I48935
14	3	16.7	9	2	G58502
15	3	16.7	9	2	A61620
16	3	16.7	10	1	RHAQ1
17	3	16.7	10	2	A32543
18	3	16.7	10	2	C35389
19	3	16.7	10	2	A60476
20	3	16.7	10	2	A61007
21	3	16.7	10	2	B61218
22	3	16.7	10	2	C54226
23	3	16.7	10	2	PA0116
24	3	16.7	10	2	PS0220
25	3	16.7	11	2	YHRT
26	3	16.7	11	2	YHHT
27	3	16.7	11	2	YHBO
28	3	16.7	11	2	YHAE
29	3	16.7	11	2	YHJFHY

30	3	16.7	11	2	PC2254	cytochrome P450 3A
31	3	16.7	12	2	S10059	tachykinin - Afric
32	3	16.7	12	2	S07436	tachykinin - Afric
33	3	16.7	12	2	C64030	hypothetical prote
34	3	16.7	12	2	T46794	hypothetical prote
35	3	16.7	12	2	A35585	cytokinin-binding
36	3	16.7	13	2	S21152	tryptophyllin-rela
37	3	16.7	13	2	A05174	tryptophyllin-13
38	3	16.7	13	2	PT0331	Ig heavy chain CRD
39	3	16.7	13	2	G61458	Ig lambda chain V-
40	3	16.7	13	2	A39836	aggrican - bovine
41	3	16.7	14	2	I39753	nitrogenase (EC 1.
42	3	16.7	14	2	PS0371	hypothetical prote
43	3	16.7	14	2	I49514	Bl44 protein A - m
44	3	16.7	15	2	PA0003	nucleoside-diphosp
45	3	16.7	15	2	I58116	Dp116 - human
46	3	16.7	15	2	S29207	avenin gamma-4 - o
47	3	16.7	15	2	PQ0681	photosystem I 19.0
48	3	16.7	15	2	B39109	hypothetical 1.5K
49	3	16.7	15	2	S24138	alkaline proteinas
50	3	16.7	15	2	S39012	proteinase - therm
51	3	16.7	15	2	S21238	hydrogensulfite re
52	3	16.7	15	2	E56819	PS I complex subun
53	3	16.7	15	2	A56891	gamma 1 gliadin -
54	3	16.7	15	2	B56891	gamma 2 gliadin -
55	3	16.7	15	2	PA0053	protein QP200006 -
56	3	16.7	15	2	PA0051	protein QP200016 -
57	3	16.7	15	2	PA0088	protein QP200051 -
58	3	16.7	15	2	PA0071	superoxide dismuta
59	3	16.7	15	2	JN0263	antigen (clone PV1
60	3	16.7	15	2	PC1313	small granule S6 c
61	3	16.7	15	2	F57789	galbladder stone
62	3	16.7	15	4	I38032	hypothetical MNI/T
63	3	16.7	16	1	A49761	locustapyrokinin -
64	3	16.7	16	2	D58501	26K kidney and gal
65	3	16.7	16	2	D45193	zinc finger protei
66	3	16.7	16	2	D83865	hypothetical prote
67	3	16.7	17	2	S66198	alcohol dehydrogen
68	3	16.7	17	2	PN0587	tyrosine 3-monooxy
69	3	16.7	17	2	S50901	chlorophyll a/b-b1
70	3	16.7	17	2	S66364	sodium-translocati
71	3	16.7	17	2	A42920	fatty acid ethyl e
72	3	16.7	17	2	S10786	enamelin, 26K - bo
73	3	16.7	17	2	PD0005	very-high-density
74	3	16.7	17	4	I51887	hypothetical EMSR1
75	3	16.7	18	2	PN0149	beta-gliadine 13 -
76	3	16.7	18	2	S52125	gamma2-gliadin P25
77	3	16.7	18	2	S29166	guinaldine oxidore
78	3	16.7	18	2	S10452	hypothetical prote
79	3	16.7	18	2	B57789	kidney stone matri
80	3	16.7	18	2	S26664	microtubule-associ
81	3	16.7	19	1	EW5MAN	anconvenin - Strept
82	3	16.7	19	2	I49422	L-lactate dehydrog
83	3	16.7	19	2	PS0186	superoxide dismuta
84	3	16.7	19	2	C56049	superoxide dismuta
85	3	16.7	19	2	PA0012	superoxide dismuta
86	3	16.7	19	2	FC1251	tesin II - rat (f
87	3	16.7	19	2	C21182	4K prothoracicotro
88	3	16.7	19	2	A37968	neural surface pro
89	3	16.7	20	2	S21176	testosterone beta
90	3	16.7	20	2	S65135	xanthine dehydroge
91	3	16.7	20	2	S36842	acylaminoacyl-pept
92	3	16.7	20	2	A60100	fimbrial antigen C
93	3	16.7	20	2	PS0028	flagellar motor sw
94	3	16.7	20	2	S33867	quinaldic acid 4-o
95	3	16.7	20	2	B39089	hydrogenase (EC 1.
96	3	16.7	20	2	D25507	proteinase inhibit
97	3	16.7	20	2	A61276	superoxide dismuta
98	3	16.7	20	2	A41439	acid ribonuclease
99	3	16.7	20	2	A60897	class I histocompa
100	3	16.7	20	2	A60802	25K acrosomal auto

ALIGNMENTS

RESULT 1

S66419
tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C:Accession: S66419
R:Kuwabara, T.
FBS Lett. 371, 195-198, 1995
A:Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of spinacia oleracea (spinach)
A:Reference number: S66419; PMID:7672127
A:Accession: S66419
A:Molecule type: protein
A:Residues: 1-9 <KOW>

Query Match 27.8%; Score 5; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDVEK 8
|||
DB 5 PDVEK 9

RESULT 2

S20410
protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)
N:Alternate names: LHCI protein kinase
C:Species: chloroplast Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: S20410
R:Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.
FBS Lett. 298, 33-35, 1992
A:Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cytochrome b6/f complex in spinach chloroplasts
A:Reference number: S20410; PMID:92183823; PMID:1544419
A:Accession: S20410
A:Molecule type: protein
A:Residues: 1-15 <GAL>
C:Genetics:
A:Genome: chloroplast
C:Function:
A:Description: is responsible for the regulation of energy distribution between photosystems I and II
A:Note: does not exhibit redox-controlled activation
C:Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphotransferase

Query Match 27.8%; Score 5; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDVEK 8
|||
DB 5 PDVEK 9

RESULT 3

A60221
apolipoprotein A-I - common carp (fragment)
C:Species: Cyprinus carpio (common carp)
C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Dec-1993
C:Accession: A60221
R:Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.
J. Neurochem. 55, 1237-1243, 1990
A:Title: Fish apolipoprotein-A-I has heparin binding activity: implication for nerve regeneration
A:Reference number: A60221; PMID:90376100; PMID:2118944
A:Accession: A60221
A:Molecule type: protein
A:Residues: 1-15 <HAR>
A:Note: protein from plasma and from optic nerve yielded the same sequence
C:Keywords: lipid binding; lipoprotein

Query Match 22.2%; Score 4; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPP 4
|||
DB 1 DQPP 4

RESULT 4

B44873
caldesmon - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 04-Mar-2000
C:Accession: B44873
R:Kebebe, M.; Hornick, T.
Arch. Biochem. Biophys. 288, 538-542, 1991
A:Title: Determination of the phosphorylation sites of smooth muscle caldesmon by pro-
tein kinase C
A:Reference number: A44873; PMID:91378498; PMID:1898046
A:Accession: B44873
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <IKE>
A:Experimental source: skeletal myosin
A:Note: sequence extracted from NCBI backbone (NCBIP:63202)
C:Superfamily: caldesmon

Query Match 22.2%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9
|||
DB 8 VEKP 11

RESULT 5

S59485
hydroxyproline-rich cell wall glycoprotein (42K and others) - kidney bean (fragment)
C:Species: Phaseolus vulgaris (kidney bean)
C:Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 05-Dec-1998
C:Accession: S59485; S59484; S59483
R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A:Title: Specificity in the immobilisation of cell wall proteins in response to differ-
ent pH values
A:Reference number: S59481; PMID:96011753; PMID:7548825
A:Accession: S59485
A:Molecule type: protein
A:Residues: 1-19 <WOJ>
A:Note: hydroxyproline-rich cell wall glycoprotein, 42K
A:Accession: S59484
A:Molecule type: protein
A:Residues: 1-15 <WOW>
A:Note: hydroxyproline-rich cell wall glycoprotein, 84K
A:Accession: S59483
A:Molecule type: protein
A:Residues: 1-14 <WOF>
A:Note: hydroxyproline-rich cell wall glycoprotein, 136K, minor component
C:Superfamily: proline-rich protein 3
C:Keywords: glycoprotein; hydroxyproline
F:6,11,16/Modified site: hydroxyproline (Pro) #status experimental

Query Match 22.2%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9
|||
DB 7 VEKP 10

RESULT 6

S59486
cell wall protein, 22K - kidney bean (fragment)

C;Species: Phaseolus vulgaris (kidney bean)
 C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C;Accession: S59486
 R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
 Plant Mol. Biol. 28, 1075-1087, 1995
 A;Title: Specificity in the immobilisation of cell wall proteins in response to different
 A;Reference number: S59481; MUID:96011753; PMID:7548825
 A;Accession: S59486
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-19 <WOJ>

Query Match 22.2%; Score 4; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPD 5
 DB 3 QPPD 6

RESULT 7
 S11416
 ribosomal protein L6, cytosolic [validated] - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jul-2000
 C;Accession: S11416
 R;Wittmann-Liebold, B.; Geissler, A.W.; Lin, A.; Wool, I.G.
 J. Supramol. Struct. 12, 425-433, 1979
 A;Title: Sequence of the amino-terminal region of rat liver ribosomal proteins S4, S6, S
 A;Reference number: S11413; MUID:80252792; PMID:398910
 A;Accession: S11416
 A;Molecule type: protein
 A;Residues: 1-20 <WIT>
 A;Note: the protein is designated as ribosomal protein L6
 C;Keywords: protein biosynthesis; ribosome

Query Match 22.2%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXPD 10
 DB 6 EXPD 9

RESULT 8
 PC4392
 whey glycoprotein WGP-88 - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 10-Nov-1997 #sequence_revision 10-Nov-1997 #text_change 07-May-1999
 C;Accession: PC4392
 R;Hwangbo, S.; Azuma, N.; Kurisaki, J.; Kanno, C.
 Biosci. Biotechnol. Biochem. 61, 1568-1574, 1997
 A;Title: Purification and characterization of novel whey glycoprotein WGP-88 which binds
 A;Reference number: PC4392; MUID:97480944; PMID:9339560
 A;Accession: PC4392
 A;Molecule type: protein
 A;Residues: 1-6 <HWA>
 A;Experimental source: milk
 C;Comment: This protein binds to the monoclonal antibody to PAS-4 glycoprotein.

Query Match 16.7%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QVQ 17
 DB 4 QVQ 6

RESULT 9
 S71299
 ICL2 protein - Paramecium tetraurelia (fragment)
 C;Species: Paramecium tetraurelia
 C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
 C;Accession: S71299
 R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
 Eur. J. Biochem. 238, 121-128, 1996
 A;Title: Characterization of centrin genes in Paramecium.
 A;Reference number: S71298; MUID:96248429; PMID:8665928
 A;Accession: S71299
 A;Molecule type: protein
 A;Residues: 1-7 <MAD>
 A;Experimental source: strain d4-2
 C;Genetics:
 A;Genetic code: SGCS

Query Match 16.7%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
 DB 2 QPP 4

RESULT 10
 S68004
 hucolin, 75K chain - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C;Accession: S68004
 R;Edgar, P.F.
 PEST Lett. 375, 159-161, 1995
 A;Title: Hucolin, a new corticosteroid-binding protein from human plasma with structu
 A;Reference number: S68004; MUID:96087107; PMID:7498469
 A;Accession: S68004
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-7 <EDG>

Query Match 16.7%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQ 12
 DB 5 DLQ 7

RESULT 11
 PT0283
 Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0283
 R;Yamada, M.; Massman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
 A;Reference number: PT0222; MUID:91108337; PMID:1899102
 A;Accession: PT0283
 A;Molecule type: DNA
 A;Residues: 1-7 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
 DB 5 QPP 7

RESULT 12

PT0030
 inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)
 N;Alternate names: inulase
 C;Species: Aspergillus ficuum
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-May-1999
 C;Accession: PT0030
 R;Etalalibi, M.; Baratti, J.C.
 Agric. Biol. Chem. 54, 61-68, 1990
 A;Title: Molecular and kinetic properties of Aspergillus ficuum inulinases.
 A;Reference number: PT0030; MUID:90344234; PMID:1369526
 A;Accession: PT0030
 A;Molecule type: protein
 A;Residues: 1-8 <ET>
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 16.7%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQP 3
 |||
 DB 4 DQP 6

RESULT 13

I48935
 apolipoprotein A-II - western wild mouse (fragment)
 C;Species: Mus spretus (western wild mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C;Accession: I48935
 R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maerzaki, Y.; Nadeau, J.H.
 Mamm. Genome 5, 349-355, 1994
 A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
 A;Reference number: I48934; MUID:94319082; PMID:8043949
 A;Accession: I48935
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-8 <RS>
 A;Cross-references: EMBL:U05692; NID:g497011; PIDN:AAB60463.1; PID:g642827

Query Match 16.7%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EKP 9
 |||
 DB 1 EKP 3

RESULT 14

G58502
 kidney and bladder stone protein - unidentified bacterium (fragment)
 C;Species: unidentified bacterium
 C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
 C;Accession: G58502
 R;Binette, J.P.; Binette, M.B.
 submitted to the Protein Sequence Database, October 1996
 A;Description: The proteins of kidney and gallbladder stones.
 A;Reference number: A58501
 A;Accession: G58502
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <BIN>
 A;Experimental source: human kidney stone, bladder stone
 A;Note: a secondary sequence AAKENPKD was also found

Query Match 16.7%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
 |||

Db 3 PDV 5

RESULT 15

A61620
 locustamyotropin III - migratory locust
 C;Species: Locusta migratoria (migratory locust)
 C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
 C;Accession: A61620
 R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
 Insect Biochem. Mol. Biol. 22, 447-452, 1992
 A;Title: Isolation, identification and synthesis of locustamyotropin III and IV, two
 A;Reference number: A61620
 A;Accession: A61620
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <SCH>
 C;Keywords: amidated carboxyl end; neuropeptide
 F;9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 QPF 14
 |||
 DB 3 QPF 5

RESULT 16

RHA01
 gonadoliberin I - American alligator
 N;Alternate names: gonadotropin-releasing hormone I
 C;Species: Alligator mississippiensis (American alligator)
 C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
 C;Accession: A60066
 R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swan
 Regul. Pept. 33, 105-116, 1991
 A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains
 A;Reference number: A60066; MUID:91352338; PMID:1882082
 A;Accession: A60066
 A;Molecule type: protein
 A;Residues: 1-10 <LOV>
 C;Superfamily: gonadoliberin
 C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13
 |||
 DB 7 LQP 9

RESULT 17

A32543
 cardioexcitatory neuropeptide - desert locust
 C;Species: Schistocerca gregaria (desert locust)
 C;Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 18-Aug-2000
 C;Accession: A32543
 R;Robb, S.; Packman, L.C.; Evans, P.D.
 Biochem. Biophys. Res. Commun. 160, 850-856, 1989
 A;Title: Isolation, primary structure and bioactivity of Schistocerca gregaria, a FMRF-ar
 A;Reference number: A32543; MUID:89246543; PMID:2719702
 A;Accession: A32543
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <ROB>
 C;Superfamily: unassigned animal peptides
 C;Keywords: amidated carboxyl end; neuropeptide

F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PDV 6
|||
Db 1 PDV 3

RESULT 18

C35389
urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)
C;Species: Morganella morganii
C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 23-Jun-1993
C;Accession: C35389
R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A;Title: Morganella morganii urease: purification, characterization, and isolation of gene
A;Reference number: A35389; MUID:90264298; PMID:2345135
A;Accession: C35389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <HUA>
C;Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEK 8
|||
Db 8 VEK 10

RESULT 19

A60476
S-layer protein - Bacillus thuringiensis (fragment)
C;Species: Bacillus thuringiensis
C;Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 12-Mar-1993
C;Accession: A60476
R;Luckevich, M.D.; Beveridge, T.J.
J. Bacteriol. 171, 6656-6667, 1989
A;Title: Characterization of a dynamic S layer on Bacillus thuringiensis.
A;Reference number: A60476; MUID:90078111; PMID:2592346
A;Accession: A60476
A;Molecule type: protein
A;Residues: 1-10 <LUC>
C;Comment: The S-layer, or surface array, is the outermost component of several archaea

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PDV 6
|||
Db 6 PDV 8

RESULT 20

A61007
hementin (EC 3.4.-.-) - Amazon leech (fragment)
C;Species: Haementeria ghilianii (Amazon leech)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C;Accession: A61007
R;Swadesh, J.K.; Huang, I.Y.; Budzynski, A.Z.
J. Chromatogr. 502, 359-369, 1990
A;Title: Purification and characterization of hementin, a fibrinogenolytic protease from
A;Reference number: A61007; MUID:90256973; PMID:2187898
A;Accession: A61007
A;Molecule type: protein
A;Residues: 1-10 <SWA>

C;Keywords: anticoagulant; hydrolase; saliva

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDL 11
|||
Db 8 PDL 10

RESULT 21

B61218
alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)
C;Species: Haynaldia villosa, Dasyphyrum villosum
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999
C;Accession: B61218
R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.
Biochem. Genet. 29, 207-211, 1991
A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Hayn.
A;Reference number: A61218; MUID:91315394; PMID:1859356
A;Accession: B61218
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SHE>
C;Keywords: seed; storage protein

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LQP 13
|||
Db 8 LQP 10

RESULT 22

C54226
light-harvesting protein B-830 alpha-3 chain - Chromatium purpuratum (fragment)
C;Species: Chromatium purpuratum
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C;Accession: C54226
R;Kerfeld, C.A.; Yeates, T.O.; Thornber, J.P.
Biochemistry 33, 2178-2184, 1994
A;Title: Purification and characterization of the peripheral antenna of the purple-su
A;Reference number: A54226; MUID:94162224; PMID:8117674
A;Accession: C54226
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <KER>
C;Keywords: antenna complex; light-harvesting polypeptide

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 VQS 18
|||
Db 8 VQS 10

RESULT 23

PA0116
ferredoxin-NADP reductase (EC 1.18.1.2) - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 03-Jun-2002
C;Accession: PA0116
R;Kamo, M.; Tsugita, A.
submitted to JFID, March 1995
A;Reference number: PA0114
A;Accession: PA0116
A;Molecule type: protein
A;Residues: 1-10 <KAM>

A:Experimental source: leaf
C:Keywords: NADP; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEX 8
|||
Db 1 VEX 3

RESULT 24

PS0220
ferredoxin-NADP reductase (EC 1.18.1.2) - rice (fragment)

C:Species: Oryza sativa (rice)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
C:Accession: PS0220
R:Uchiyama, Y.; Tsugita, A.
submitted to JIPID, August 1991
A:Reference number: PS0205
A:Accession: PS0220
A:Molecule type: protein
A:Residues: 1-10 <UCH>
C:Keywords: NADP; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEX 8
|||
Db 1 VEX 3

RESULT 25

YHRT
morphogenetic neuropeptide - rat

C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelestis

A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: A01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>
R:Biir, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator
C:Superfamily: unassigned animal peptides
C:Keywords: growth factor; hormone; hypothalamus; intestine; neuroglutamic acid
F:1/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
|||
Db 1 QPP 3

RESULT 26

YHUU
morphogenetic neuropeptide - human

C:Species: Homo sapiens (man)

C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: B01427; A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981

A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelestis
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: B01427

A:Molecule type: protein
A:Residues: 1-11 <BOD>
R:Biir, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981

A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator
C:Superfamily: unassigned animal peptides

C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuroglutamic acid
F:1/Modified site: blocked amino end (Gln) (probably pyroglutamic acid) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
|||
Db 1 QPP 3

RESULT 27

YHBO
morphogenetic neuropeptide - bovine

C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: C01427; A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981

A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelestis
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: C01427

A:Molecule type: protein
A:Residues: 1-11 <BOD>
R:Biir, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981

A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator
C:Superfamily: unassigned animal peptides

C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuroglutamic acid
F:1/Modified site: blocked amino end (Gln) (probably pyroglutamic acid) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
|||
Db 1 QPP 3

RESULT 28

YHXA
morphogenetic neuropeptide - sea anemone (Anthopleura elegantissima)

N:Alternate names: head activator
C:Species: Anthopleura elegantissima

C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A93900; A01427
R:Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: A93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4

DB 1 QPP 3

RESULT 29

YHJPHY

morphogenetic neuropeptide - Hydra attenuata

N;Alternate names: head activator

C;Species: Hydra attenuata

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: B93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4

DB 1 QPP 3

RESULT 30

PC2254

Cytochrome P450 3A - savannah baboon (fragment)

C;Species: Papio hamadryas doguera (savannah baboon)

C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 19-May-2000

C;Accession: PC2254

R;Ohmori, S.; Kudo, S.; Nakasa, H.; Horie, T.; Kitada, M.

Biol. Pharm. Bull. 17, 1584-1588, 1994

A;Title: Purification and characterization of cytochrome P450 3A enzyme from hepatic mid

A;Reference number: PC2254; MUID:95253110; PMID:7735199

A;Accession: PC2254

A;Molecule type: protein

A;Residues: 1-11 <OHM>

A;Experimental source: liver

Query Match 16.7%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDL 11

DB 5 PDL 7

RESULT 31

S10059

tachykinin - African tree frog (Kassina maculata)

N;Alternate names: hylambates-kassinin

C;Species: Kassina maculata

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Sep-2000

C;Accession: S10059

R;Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.

Biomed. Res. 2, 613-617, 1981

A;Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, i

A;Reference number: S07436

A;Accession: S10059

A;Molecule type: protein

A;Residues: 1-12 <YAS>

A;Experimental source: skin

A;Note: the source is designated as Hylambates maculatus

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 16.7%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10

DB 4 KPD 6

RESULT 32

S07436

tachykinin - African tree frog (Kassina maculata)

N;Alternate names: hylambatin

C;Species: Kassina maculata

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Sep-2000

C;Accession: S07436

R;Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.

Biomed. Res. 2, 613-617, 1981

A;Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, i

A;Reference number: S07436

A;Accession: S07436

A;Molecule type: protein

A;Residues: 1-12 <YAS>

A;Experimental source: skin

A;Note: the source is designated as Hylambates maculatus

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 16.7%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPD 5

DB 2 PPD 4

RESULT 33

C64030

hypothetical protein H11451 - Haemophilus influenzae (strain Rd KW20)

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C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 10-Oct-1997
C:Accession: C64030
R:Flaischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.;
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: C64030
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-12 <TIGR>
A:Cross-references: GB:U32823; GB:L42023; NID:g1574281; PID:g1574296; TIGR:HI1451

Query Match 16.7%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPD 5
Db 9 PPD 11

RESULT 34
T46794
hypothetical protein [imported] - Haloarcula marismortui (fragment)
C:Species: Haloarcula marismortui
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
C:Accession: T46794
R:Arndt, E.
FEBS Lett. 267, 193-198, 1990
A:Title: Nucleotide sequence of four genes encoding ribosomal proteins from the 'S10 and
A:Reference number: S10731; MUID:90336772; PMID:2143141
A:Accession: T46794
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-12 <ARN>
A:Cross-references: EMBL:X55311; NID:g43610; PIDN:CAA39015.1; PID:g43611

Query Match 16.7%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQ 12
Db 7 DLQ 9

RESULT 35
A35585
cytokinin-binding factor 1 - durum wheat
C:Species: Triticum durum (durum wheat)
C:Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993
C:Accession: A35585
R:Brinegar, A.C.; Cooper, G.; Stevens, A.; Hauer, C.R.; Shabanowitz, J.; Hunt, D.F.; Fox
Proc. Natl. Acad. Sci. U.S.A. 85, 5927-5931, 1988
A:Title: Characterization of a benzyladenine binding-site peptide isolated from a wheat
by mass spectrometry.
A:Reference number: A35585; MUID:88320357; PMID:3413067
A:Accession: A35585
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <BRI>

Query Match 16.7%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LQP 13
Db 3 LQP 5

RESULT 36
S21152
tryptophyllin-related peptide - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S21152
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspaner, G.; Kreil,
FEBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of
A:Reference number: S21152; MUID:923339502; PMID:1633846
A:Accession: S21152
A:Molecule type: protein
A:Residues: 1-13 <MIG>
A:Experimental source: skin
C:Superfamily: unassigned animal peptides

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 EXP 9
Db 2 EXP 4

RESULT 37
A05174
tryptophyllin-13 - Rohde's leaf frog
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Aug-2000
C:Accession: A05174
R:Montecucchi, P.C.; Gozzini, L.; Erspaner, V.
Int. J. Pept. Protein Res. 27, 175-182, 1986
A:Reference number: A05174
A:Accession: A05174
A:Molecule type: protein
A:Residues: 1-13 <MON>
C:Superfamily: unassigned animal peptides
C:Keywords: pyroglutamic acid; skin
P:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 EXP 9
Db 2 EXP 4

RESULT 38
PT0331
Ig heavy chain CRD3 region (clone J2-121) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0331
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0331
A:Molecule type: DNA
A:Residues: 1-13 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFQ 15

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```

Db      11 PFQ 13
||||
RESULT 39
Ig lambda chain V-II region (AZI) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C:Accession: G61458; P10159
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-assc
A:Reference number: A61458; MUID:90039128; PMID:2478651
A:Accession: G61458
A:Molecule type: protein
A:Residues: 1-13 <BRO>
C:Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycop
C:Keywords: heterotetramer; immunoglobulin

Query Match      16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QPP 4
      |||
Db      6 QPP 8
      |||

RESULT 40
A39836
aggrecan - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 24-Jun-1993
C:Accession: A39836
R:Sandy, J.D.; Neame, P.J.; Boynton, R.E.; Flannery, C.R.
J. Biol. Chem. 266, 8683-8685, 1991
A:Title: Catabolism of aggrecan in cartilage explants. Identification of a major cleavag
A:Reference number: A39836; MUID:91224956; PMID:2026585
A:Accession: A39836
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <SAN>

Query Match      16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KPD 10
      |||
Db      10 KPD 12
      |||

RESULT 41
I39753
nitrogenase (EC 1.18.6.1) - Azospirillum brasilense (fragment)
N:Alternate names: dinitrogenase reductase
C:Species: Azospirillum brasilense
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jan-2001
C:Accession: I39753
R:Zhang, Y.; Burris, R.H.; Roberts, G.P.
J. Bacteriol. 174, 3364-3369, 1992
A:Title: Cloning, sequencing, mutagenesis, and functional characterization of draT and d
A:Reference number: I39751; MUID:92250433; PMID:1577701
A:Accession: I39753
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14 <RES>
A:Cross-references: GB:M87319; NID:gl42411; PIDN:AAA22182.1; PID:gl42414
C:Keywords: AIP; nitrogen fixation; oxidoreductase

Query Match      16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KPD 10
      |||
Db      10 KPD 12
      |||

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 DLQ 12
      |||
Db      3 DLQ 5
      |||

RESULT 42
PS0371
hypothetical protein (psaC region) - Synechococcus sp. (fragment)
C:Species: Synechococcus sp.
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C:Accession: PS0371
R:Rhial, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.
Gene 112, 123-128, 1992
A:Title: The psac genes of Synechococcus sp. FCC7002 and Cyanophora paradoxa: cloning
A:Reference number: JS0694; MUID:92201692; PMID:1551590
A:Accession: PS0371
A:Molecule type: DNA
A:Residues: 1-14 <RHI>
A:Cross-references: GB:M86238; NID:gl54574; PIDN:AAA27351.1; PID:g552030

Query Match      16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 LQP 13
      |||
Db      12 LQP 14
      |||

RESULT 43
I49514
B144 protein A - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49514
R:Tauge, I.; Shen, F.
Immunogenetics 26, 378-380, 1987
A:Title: A gene in the H-2S: H-2D interval of the major histocompatibility complex whi
A:Reference number: I49514; MUID:88031493; PMID:3117682
A:Accession: I49514
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-14 <RES>
A:Cross-references: GB:M18187; NID:gl92097; PIDN:AAA37272.1; PID:gl92098

Query Match      16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 DLQ 12
      |||
Db      3 DLQ 5
      |||

RESULT 44
PA0003
nucleoside-diphosphate kinase (EC 2.7.4.6) - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Nov-1994 #sequence_revision 06-Jan-1995 #text_change 15-Mar-1996
C:Accession: PA0003
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensi
A:Reference number: PA0001
A:Accession: PA0003
A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Experimental source: leaf and callus
C:Superfamily: nucleoside-diphosphate kinase
C:Keywords: phosphotransferase

```

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPD 10
|||
Db 11 KPD 13

RESULT 45

I58116
Dp116 - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I58116
R;Byers, T.J.; Lidov, H.G.; Kunkel, L.M.
Nature Genet. 4, 77-81, 1993
A;Title: An alternative dystrophin transcript specific to peripheral nerve.
A;Reference number: I58116; MUID:93291881; PMID:18513330
A;Accession: I58116
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-15 <RES>
A;Cross-references: GB:S62617; NID:G386224; PIDN:AB271159.1; PID:G386225
C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystroph

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQ 12
|||
Db 11 DLQ 13

RESULT 46

S29207
avenin gamma-4 - oat (fragment)
N;Alternate names: CIP-1; coeliac immunoreactive protein 1
C;Species: Avena sativa (oat)
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C;Accession: S29207
R;Rocher, A.; Collilla, F.; Ortiz, M.L.; Mendez, E.
FEBS Lett. 310, 37-40, 1992
A;Title: Identification of the three major coeliac immunoreactive proteins and one alpha
A;Reference number: S29207; MUID:92405739; PMID:1526282
A;Accession: S29207
A;Molecule type: protein
A;Residues: 1-15 <ROC>
A;Experimental source: endosperm
C;Superfamily: gliadin
C;Keywords: prolamin; seed

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QPF 14
|||
Db 13 QPF 15

RESULT 47

PQ0681
photosystem I 19.0K D1 chain - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C;Accession: PQ0681
R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.
Plant Physiol. 102, 1259-1267, 1993
A;Title: Molecular heterogeneity of photosystem I. psad, psae, psaf, psah and psal are a
A;Reference number: PQ0667; MUID:94105345; PMID:8278548
A;Accession: PQ0681

A;Molecule type: protein
A;Residues: 1-15 <OBO>
C;Superfamily: photosystem I chain II
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEX 8
|||
Db 2 VEX 4

RESULT 48

B39109
hypothetical 1.5K protein - hepatitis C virus
N;Alternate names: hypothetical protein 2
C;Species: hepatitis C virus
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C;Accession: B39109; JQ1585
R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Teka
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identific
A;Reference number: A39109; MUID:91156678; PMID:1705704
A;Accession: B39109
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-15 <HAN>
A;Cross-references: GB:M58406
R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992
A;Title: Cloning and sequencing of the structural region and expression of putative c
A;Reference number: JQ1584; MUID:92300349; PMID:1318944
A;Accession: JQ1585
A;Molecule type: genomic RNA
A;Residues: 1-15 <KUM>
A;Experimental source: strain U.K.

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
|||
Db 5 QPP 7

RESULT 49

S24138
alkaline proteinase (EC 3.4.21.-) - Thermus sp. (strain Rt41A) (fragment)
C;Species: Thermus sp.
A;Variety: strain Rt41A
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: S24138
R;Peek, K.; Daniel, R.M.; Monk, C.; Parker, L.; Coolbear, T.
Eur. J. Biochem. 207, 1035-1044, 1992
A;Title: Purification and characterization of a thermostable proteinase isolated from
A;Reference number: S24138; MUID:92362605; PMID:1499549
A;Accession: S24138
A;Molecule type: protein
A;Residues: 1-15 <PEE>
A;Experimental source: strain Rt41a
C;Keywords: hydrolase; serine proteinase

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 VQS 18
|||
Db 2 VQS 4

RESULT 50

S39012
 Proteinase - Thermus sp.
 C:Species: Thermus sp.
 C>Date: 18-Feb-1994 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
 C:Accession: S39012
 R:Freeman, S.A.; Peek, K.; Prescott, M.; Daniel, R.
 Biochem. J. 295, 463-469, 1993
 A:Title: Characterization of a chelator-resistant proteinase from *Thermus* strain R-4A2.
 A:Reference number: S39012; MUID:94058984; PMID:8240244
 A:Accession: S39012
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <PRE>
 A>Note: 13-Ala was also found

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 VQS 18
 |||
 Db 2 VQS 4

RESULT 51

S21238
 hydrogensulfite reductase (EC 1.8.99.3) beta chain - Desulfovibrio vulgaris (fragment)
 N:Alternate names: bisulfite reductase; desulfofuscidin; desulfurubidin; desulfovibridin;
 C:Species: Desulfovibrio vulgaris
 C>Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
 C:Accession: S21238
 R:Pierik, A.J.; Duyvis, M.G.; van Helvoort, J.M.L.M.; Wolbert, R.B.G.; Hagen, W.R.
 Eur. J. Biochem. 205, 111-115, 1992
 A:Title: The third subunit of desulfovibridin-type dissimilatory sulfite reductases.
 A:Reference number: S21197; MUID:92209491; PMID:1555572
 A:Accession: S21238
 A:Molecule type: protein
 A:Residues: 1-15 <PIE>
 A:Experimental source: strain Hildenborough
 C:Genetics:

A:Gene: dsbB
 C:Complex: heterohexamer; two alpha, two beta and two gamma chains
 C:Function:
 A:Description: catalyzes the six-electron reduction of sulfite to sulfide
 A:Pathway: the terminal oxidase in the sulfate-reduction pathway
 C:Keywords: heterohexamer; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
 |||
 Db 10 EXP 12

RESULT 52

E56819
 PS I complex subunit 8 - cucumber (fragment)
 C:Species: Cucumis sativus (cucumber)
 C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
 C:Accession: E56819
 R:Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.
 Biochim. Biophys. Acta 1059, 141-148, 1991
 A:Title: Characterization of genes that encode subunits of cucumber PS I complex by N-te
 A:Reference number: A56819; MUID:91355209; PMID:1883835
 A:Accession: E56819
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <IWA>

A>Note: sequence extracted from NCBI backbone (NCBIP:58606)

Query Match

16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FOV 16
 |||
 Db 8 FOV 10

RESULT 53

A56891
 gamma 1 gliadin - wheat (fragment)
 C:Species: Triticum sp. (wheat)
 C>Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 08-Dec-1995
 C:Accession: A56891
 R:Sjostrom, H.; Friis, S.U.; Noren, O.; Anthonsen, D.
 Clin. Chim. Acta 207, 227-237, 1992
 A:Title: Purification and characterisation of antigenic gliadins in coeliac disease.
 A:Reference number: A56891; MUID:93009000; PMID:1395028
 A:Contents: Kadett
 A:Accession: A56891
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <SJO>
 A>Note: sequence extracted from NCBI backbone (NCBIP:119387)

Query Match

16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QVO 17
 |||
 Db 9 QVO 11

RESULT 54

B56891
 gamma 2 gliadin - wheat (fragment)
 C:Species: Triticum sp. (wheat)
 C>Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 08-Dec-1995
 C:Accession: B56891
 R:Sjostrom, H.; Friis, S.U.; Noren, O.; Anthonsen, D.
 Clin. Chim. Acta 207, 227-237, 1992
 A:Title: Purification and characterisation of antigenic gliadins in coeliac disease.
 A:Reference number: A56891; MUID:93009000; PMID:1395028
 A:Contents: Kadett
 A:Accession: B56891
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <SJO>
 A>Note: sequence extracted from NCBI backbone (NCBIP:119388)

Query Match

16.7%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QVO 17
 |||
 Db 9 QVO 11

RESULT 55

PA0053
 protein QF200006 - fungus (*Fusarium sporotrichioides*) (fragment)
 C:Species: *Fusarium sporotrichioides*
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C:Accession: PA0053
 R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotr*;
 A:Reference number: PA0051
 A:Accession: PA0053

A;Molecule type: protein
A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
|||
Db 4 EXP 6

RESULT 56

PA0051
protein QF200016 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0051
R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PA0051
A;Accession: PA0051
A;Molecule type: protein
A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEX 8
|||
Db 2 VEX 4

RESULT 57

PA0088
protein QF200051 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0088
R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PA0051
A;Accession: PA0088
A;Molecule type: protein
A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
|||
Db 2 KPD 4

RESULT 58

PA0071
superoxide dismutase (EC 1.15.1.1) (Fe/Mn) - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0071
R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PA0051
A;Accession: PA0071
A;Molecule type: protein
A;Residues: 1-15 <CHO>
C;Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C;Keywords: metalloprotein; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDL 11
|||
Db 5 PDL 7

RESULT 59

JN0263
antigen (clone PV12) - Plasmodium vivax (fragment)
C;Species: Plasmodium vivax
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Sep-1997
C;Accession: JN0263; S21344
R;Ray, P.; Sharma, Y.D.
Biochem. Biophys. Res. Commun. 184, 668-672, 1992
A;Title: Molecular cloning and serological characterization of a new Plasmodium vivax antigen
A;Reference number: JN0263; MUID:92246949; PMID:1575740
A;Accession: JN0263
A;Molecule type: DNA
A;Residues: 1-15 <RAY>
A;Cross-references: GB:X53681; NID:gl0084; PID:gl0085

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQP 3
|||
Db 1 DQP 3

RESULT 60

PC1313
small granule S6 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)
C;Species: Tachyplesus tridentatus
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: PC1313
R;Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; J. Biochem. 114, 307-316, 1993
A;Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridentatus) granules
A;Reference number: PC1309; MUID:94110249; PMID:8282718
A;Accession: PC1313
A;Molecule type: protein
A;Residues: 1-15 <SHI>
C;Comment: This protein contributes to a self-defense system against invaders.

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
|||
Db 1 EXP 3

RESULT 61

F57789
gallbladder stone matrix protein 2, 41K - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 03-May-1996
C;Accession: F57789
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, February 1996
A;Description: The proteins of gallbladder stones.
A;Reference number: A57789
A;Accession: F57789
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <BIN>

A;Note: 9-Phe was also found

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
|||
Db 4 KPD 6

RESULT 62

I38032
hypothetical MN1/TEL mutant fusion protein type I - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C;Accession: I38032
R;Buijs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.
Oncogene 10, 1511-1519, 1995
A;Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion
A;Reference number: I38031; MUID:95249265; PMID:7731705
A;Accession: I38032
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-15 <BUI>
A;Cross-references: EMBL:X85025; NID:9971467; PIDN:CAA59398.1; PID:9971468
C;Comment: This sequence is the chimeric product of a translocation mutation.
C;Genetics:
A;Gene: MN1/ETV6; MN1/TEL
A;Map position: 22q11/12p13
C;Keywords: fusion protein

Query Match 16.7%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13
|||
Db 9 LQP 11

RESULT 63

A49761
locustapyrokinin - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 08-Dec-1995
C;Accession: A49761
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.
Gen. Comp. Endocrinol. 81, 97-104, 1991
A;Title: Isolation, primary structure, and synthesis of locustapyrokinin: a myotropic peptide
A;Reference number: A49761; MUID:91224474; PMID:2026322
A;Accession: A49761
A;Molecule type: protein
A;Residues: 1-16 <SCH>
C;Comment: This neuropeptide stimulates contractions in an isolated cockroach hindgut as
C;Superfamily: pyrokinin
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental
F;16/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 QPF 14
|||
Db 10 QPF 12

RESULT 64

D58501
26K kidney and gallbladder stone protein - unidentified bacterium (fragment)
C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C;Accession: D58501
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A;Description: The proteins of kidney and gallbladder stones.
A;Reference number: A58501
A;Accession: D58501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <BIN>
A;Experimental source: human kidney and gallbladder stones

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred.No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
|||
Db 4 KPD 6

RESULT 65

D45193
zinc finger protein ZNF60 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 01-Jan-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: D45193
R;Lichter, P.; Bray, P.; Ried, T.; Dawid, I.B.; Ward, D.C.
Genomics 13, 999-1007, 1992
A;Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile
A;Reference number: A43284; MUID:92372070; PMID:1505991
A;Accession: D45193
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-16 <LIC>
A;Cross-references: GB:M88369; NID:9340475; PIDN:AAA61327.1; PID:9340476
A;Note: sequence extracted from NCBI backbone (NCBIN:111662, NCBIP:111664)

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred.No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
|||
Db 5 EXP 7

RESULT 66

D83865
hypothetical protein BH1724 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: D83865
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H.
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83865
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-16 <STO>
A;Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05443.1; GSPDB:G
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1724

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred.No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
|||
Db 10 PDV 12

```

RESULT 67
S66198
alcohol dehydrogenase (EC 1.1.1.1) class III - garden pea (fragment)
C;Species: Pisum sativum (garden pea)
C;Date: 14-Feb-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C;Accession: S66198
R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.;
FEBS Lett. 367, 237-240, 1995
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. M
zyme.
A;Reference number: S66191; MUID:95331382; PMID:7607314
A;Accession: S66198
A;Molecule type: protein
A;Residues: 1-17 <HJE>
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match          16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DVE 7
    |||
Db 15 DVE 17

RESULT 68
PN0587
tyrosine 3-monooxygenase (EC 1.14.16.2) type 3 and 4 - Japanese macaque (fragment)
N;Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase
C;Species: Macaca fuscata (Japanese macaque)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 31-Mar-2000
C;Accession: PN0587
R;Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
Biochem. Biophys. Res. Commun. 195, 158-165, 1993
A;Title: Increased heterogeneity of tyrosine hydroxylase in humans.
A;Reference number: PN0575; MUID:93371398; PMID:7689834
A;Accession: PN0587
A;Molecule type: genomic RNA
A;Residues: 1-17 <ICH>
A;Cross-references: GB:L14801
A;Experimental source: kidney
C;Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosy
C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: bipterin; monooxygenase; oxidoreductase

Query Match          16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LQP 13
    |||
Db 15 LQP 17

RESULT 69
S50901
chlorophyll a/b-binding protein Lhcb4 - spinach (fragment)
N;Alternate names: light-harvesting complex LHCIIa protein
C;Species: Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999
C;Accession: S50901
R;Walters, R.G.; Ruban, A.V.; Horton, P.
Eur. J. Biochem. 226, 1063-1069, 1994
A;Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclo
A;Reference number: S50900; MUID:95112835; PMID:7813461
A;Accession: S50901
A;Molecule type: protein
A;Residues: 1-17 <WAL>
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: cnlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosys

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Query Match          16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LQP 13
    |||
Db 4 LQP 6

RESULT 70
S66364
sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) gamma-1 chain - Vib
C;Species: Vibrio alginolyticus
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C;Accession: S66364
R;Beattie, P.; Tan, K.; Bourne, R.M.; Leach, D.; Rich, P.R.; Ward, F.B.
FEBS Lett. 356, 333-338, 1994
A;Title: Cloning and sequencing of four structural genes for the Na(+)-translocating
A;Reference number: S51013; MUID:95104445; PMID:7805867
A;Accession: S66364
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <BEA>
C;Keywords: oxidoreductase

Query Match          16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QVQ 17
    |||
Db 15 QVQ 17

RESULT 71
A42920
fatty acid ethyl ester synthase-II - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C;Accession: A42920
R;Bora, P.S.; Wu, X.; Spilburg, C.A.; Lange, L.G.
J. Biol. Chem. 267, 13217-13221, 1992
A;Title: Purification and characterization of fatty acid ethyl ester synthase-II from
A;Reference number: A42920; MUID:92317032; PMID:1618826
A;Accession: A42920
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-17 <BOR>
A;Experimental source: myocardium
A;Note: sequence extracted from NCBI backbone (NCBIP:107742)

Query Match          16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPD 5
    |||
Db 3 PPD 5

RESULT 72
S10786
enamelin, 26K - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C;Accession: S10786
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a
A;Reference number: S10780; MUID:90336641; PMID:2379503
A;Accession: S10786
A;Molecule type: protein

```

A;Residues: 1-17 <STR>
C;Keywords: enamel; phosphoprotein

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
|||
Db 3 QPP 5

RESULT 73

PD0005
very-high-density lipoprotein - sand crayfish (fragment)
N;Alternate names: VHDL
C;Species: Ibacus ciliatus (sand crayfish)
C;Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999
C;Accession: PD0005
R;Komatsu, M.; Ando, S.
BioSci. Biotechnol. Biochem. 62, 459-463, 1998
A;Title: A very-high-density lipoprotein with clotting ability from hemolymph of sand ch
A;Reference number: PD0005; MUID:98233268; PMID:9571775
A;Accession: PD0005
A;Molecule type: protein
A;Residues: 1-17 <KOW>
C;Comment: This protein plays an important role in the defense process of crustacea, it a

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13
|||
Db 1 LQP 3

RESULT 74

I51887
hypothetical EWSR1/FLI1 mutant fusion protein, type 1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C;Accession: I51887
R;Downing, J.R.; Head, D.R.; Parham, D.M.; Douglass, E.C.; Hulshof, M.G.; Link, M.P.; Mc
Am. J. Pathol. 143, 1294-1300, 1993
A;Title: Detection of the (11;22)(q24;q12) translocation of Ewing's sarcoma and peripher
A;Reference number: I51887; MUID:94056652; PMID:8238248
A;Accession: I51887
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-17 <DOW>
A;Cross-references: GB:S66911; NID:G440935; PIDN:AAB28655.1; PID:G440936
C;Comment: This sequence is the chimeric product of a translocation mutation.
C;Genetics:
A;Gene: EWSR1/FLI1; EWS/FLI-1
A;Map position: 22q12/11q24
C;Keywords: fusion protein

Query Match 16.7%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDL 11
|||
Db 10 PDL 12

RESULT 75

PN0149
beta-Gliadine 13 - Aegilops longissima (fragment)
C;Species: Aegilops longissima
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PN0149

R;Odintsova, T.I.; Egorov, T.A.
Biokhimiia 55, 509-516, 1990
A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin
A;Reference number: PN0146; MUID:90283493; PMID:2354218
A;Accession: PN0149
A;Molecule type: protein
A;Residues: 1-18 <ODI>
A;Experimental source: strain K-202
C;Superfamily: gliadin

Query Match 16.7%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13
|||
Db 8 LQP 10

Search completed: November 25, 2003, 18:28:15
Job time : 18.5638 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 8.71277 Seconds
(without alignments)
97.154 Million cell updates/sec

Title: US-09-641-801-3
Perfect score: 18
Sequence: 1 DQPPDVEKPLQPFQVQS 18

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	16.7	7	UF04_MOUSE	P38642 mus musculus
2	3	16.7	9	LMT3_LOCOMI	P41489 locusta mig
3	3	16.7	10	FARP_PANRE	P82660 panagrellus
4	3	16.7	10	FARP_LOCOMI	P38553 locusta mig
5	3	16.7	10	GONI_ALLMI	P37041 alligator m
6	3	16.7	10	SLAP_BACTG	F49325 bacillus th
7	3	16.7	10	UPA2_HUMAN	P30088 homo sapien
8	3	16.7	10	URE3_MORMO	P17339 morganella
9	3	16.7	11	MORN_HUMAN	P01163 homo sapien
10	3	16.7	12	HS9A_RAT	P82995 rattus norv
11	3	16.7	12	TKN1_KASMA	P08613 kassina mac
12	3	16.7	12	TKN2_KASMA	P08614 kassina mac
13	3	16.7	13	E121_LITRU	P82097 litoria rub
14	3	16.7	13	E122_LITRU	P82098 litoria rub
15	3	16.7	13	IDHP_RAT	P56574 rattus norv
16	3	16.7	13	PEDI_HYDAT	P80578 hydra atten
17	3	16.7	13	SODM_CANFA	P54712 canis famil
18	3	16.7	13	TY13_PHYRO	P04096 phyllomedus
19	3	16.7	14	MARI_ALTPS	P29399 alteromonas
20	3	16.7	15	HS11_PINPS	P81083 pinus pinas
21	3	16.7	15	MK1_FALPR	P80408 palomena pr
22	3	16.7	15	MK2A_FALPR	P80409 palomena pr
23	3	16.7	15	ONC1_ONCMY	P83287 oncorhynch
24	3	16.7	15	PSAO_CUCSA	F42052 cucumis sat
25	3	16.7	15	VORA_METTM	P80907 methanobact
26	3	16.7	16	LPK1_LOCOMI	P20404 locusta mig
27	3	16.7	16	MK2B_FALPR	P80410 palomena pr
28	3	16.7	16	MK3_FALPR	P80411 palomena pr
29	3	16.7	16	MPX_SOLTU	P80501 solanum tub
30	3	16.7	18	SODM_MYCHA	P80582 mycobacteri
31	3	16.7	18	UC21_MAIZE	P80627 zea mays (m
32	3	16.7	19	LANC_STRSQ	P38655 streptomyc
33	3	16.7	20	ACPH_BOVIN	P80227 bos taurus

ALIGNMENTS

RESULT 1

34	1	16.7	20	1	BULB_NAPPS	P80554 narcissus p
35	1	16.7	20	1	CHP_THICU	P80486 thioacillu
36	1	16.7	20	1	CP35_FAFSP	P80056 papio sp. (
37	1	16.7	20	1	DER6_DERPT	P49277 dermatophag
38	1	16.7	20	1	SODM_HORVU	P28524 hordeum vul
39	1	16.7	20	1	TRYL_STREX	P80420 streptomyc
40	1	11.1	5	1	TUFT_HUMAN	P01858 homo sapien
41	2	11.1	5	1	SUGA_ACHDO	P19991 acheta dome
42	2	11.1	6	1	ACPH_RABIT	P25154 oryctolagus
43	2	11.1	6	1	OVN_DEPDE	P25985 leptinotars
44	2	11.1	7	1	TRFI_PSEPU	P36414 pseudomonas
45	2	11.1	7	1	FAR1_HELTI	P41871 helisoma tr
46	2	11.1	7	1	FAR4_PANRE	P41875 panagrellus
47	2	11.1	7	1	FARB_CALVO	P41866 calliphora
48	2	11.1	7	1	LANC_CARUI	P36960 carnobacter
49	2	11.1	7	1	PPH2_LYCES	P83379 lycopersico
50	2	11.1	7	1	TPFY_PACDA	P83455 pachymedusa
51	2	11.1	7	1	UH11_RAT	P56576 rattus norv
52	2	11.1	7	1	UN06_PINPS	P81675 pinus pinas
53	2	11.1	8	1	ACT_CARMA	P80709 carcinus ma
54	2	11.1	8	1	AKHG_GRYBI	P14086 gryllus bim
55	2	11.1	8	1	AKH_LIBAU	P25418 libellula a
56	2	11.1	8	1	AKH_MEML	P25423 melolontha
57	2	11.1	8	1	ALL2_CARMA	P81815 carcinus ma
58	2	11.1	8	1	ALL5_CALVO	P41841 calliphora
59	2	11.1	8	1	ANG2_BOTJA	Q10582 bothrops ja
60	2	11.1	8	1	HTFI_PERAM	P04548 periplaneta
61	2	11.1	8	1	LCK3_LEUMA	P21142 leucophaea
62	2	11.1	8	1	LCK6_LEUMA	P19988 leucophaea
63	2	11.1	8	1	NPB_BOVIN	P15507 bos taurus
64	2	11.1	8	1	PLP_BRANA	P81707 brassica na
65	2	11.1	8	1	PPK2_PERAM	P82692 periplaneta
66	2	11.1	8	1	PPK3_PERAM	P82618 periplaneta
67	2	11.1	8	1	UC26_MAIZE	P80632 zea mays (m
68	2	11.1	8	1	UH09_RAT	P56575 rattus norv
69	2	11.1	8	1	UPA1_HUMAN	P30087 homo sapien
70	2	11.1	9	1	AL10_CARMA	P81813 carcinus ma
71	2	11.1	9	1	CCAP_CARMA	P38556 carcinus ma
72	2	11.1	9	1	COW_CONVE	P83047 conus ventr
73	2	11.1	9	1	COXE_THUOB	P80975 thunnus obe
74	2	11.1	9	1	FAR3_PENMO	P83318 penaeus obe
75	2	11.1	9	1	FAR4_CALVO	P83319 penaeus mon
76	2	11.1	9	1	FAR4_PENMO	P41859 calliphora
77	2	11.1	9	1	FARS_ASCSU	P83170 ascaris suu
78	2	11.1	9	1	FRFI_SARBU	P83350 sarcophaga
79	2	11.1	9	1	HUTU_KLEAE	P12381 klebsiella
80	2	11.1	9	1	KNL3_BOMVA	P83058 bombina var
81	2	11.1	9	1	LMTP_LOCOMI	P31799 locusta mig
82	2	11.1	9	1	OXYT_BUFRE	P42995 bufo regula
83	2	11.1	9	1	PPH1_LYCES	P83380 lycopersico
84	2	11.1	9	1	PTSP_BOMMO	P82003 bombyx mori
85	2	11.1	9	1	RT33_BOVIN	P82926 bos taurus
86	2	11.1	9	1	UHA2_HUMAN	P40929 homo sapien
87	2	11.1	9	1	ULAE_HUMAN	P31931 homo sapien
88	2	11.1	9	1	ULAH_HUMAN	P31934 homo sapien
89	2	11.1	9	1	UPA6_HUMAN	P30092 homo sapien
90	2	11.1	9	1	YBFR_AZOV1	P25925 azotobacter
91	2	11.1	10	1	AH3_PRUSE	P29261 prunus sero
92	2	11.1	10	1	AKHG_LOCOMI	P81626 locusta mig
93	2	11.1	10	1	ANG1_BOTJA	Q10581 bothrops ja
94	2	11.1	10	1	ANGT_BOVIN	P01017 bos taurus
95	2	11.1	10	1	ANGT_CHICK	P01018 gallus gall
96	2	11.1	10	1	APE_CAGPI	P80474 capnocytoph
97	2	11.1	10	1	BPF2_BOTIN	P30422 bothrops in
98	2	11.1	10	1	BPF2_BOTJA	P01022 bothrops ja
99	2	11.1	10	1	BPP8_BOTIN	P30426 bothrops in
100	2	11.1	10	1	BPP_VIPAS	P31351 vipera aspi

```

UF04 MOUSE
ID UF04 MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=9500907; Wichter L.L., He C., Selkirk J.K.;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON TER
SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPD 5
Db 3 PPD 5

RESULT 2
LMT3 LOCMI
ID LMT3 LOCMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family."
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QPF 14
Db 3 QPF 5

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RESULT 3
FAR6 PANRE
ID FAR6 PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRamide-like neuropeptide PF6 (NGAPQFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RC Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of RMRamide-related
peptides (FARPs) from free-living nematode, Panagrellus redivivus."
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 10
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QPF 14
Db 5 QPF 7

RESULT 4
FARP LOCMI
ID FARP LOCMI STANDARD; PRT; 10 AA.
AC P38553;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Schistoflrfamide (PDVDFLRF-amide) (Cardioexcitatory neuropeptide).
OS Locusta migratoria (Migratory locust), and
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004, 7010;
RN [1]
RP SEQUENCE.
RC SPECIES=L.migratoria; TISSUE=Brain;
RX MEDLINE=93324430; PubMed=7687352;
RA Schoofs L., Holman G.M., Veelaert D., Amelinckx M.,
RA de Loof A.;
RT "Isolation, identification, and synthesis of PDVDFLRFamide
RT (Schistoflrfamide) in Locusta migratoria and its association with the
RT male accessory glands, the salivary glands, the heart, and the
RT oviduct."
RL Peptides 14:409-421(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=S.gregaria; TISSUE=Thoracic nervous system;
RX MEDLINE=89246543; PubMed=2719702;
RA Robb S., Packman L.C., Evans P.D.;
RT "Isolation, primary structure and bioactivity of schistoflrf-amide, a
RT FMRP-amide-like neuropeptide from the locust, Schistocerca
RT gregaria."
RL Biochem. Biophys. Res. Commun. 160:850-856(1989).
CC -!- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL
OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND
OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.

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OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE.
RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson B.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
DR PIR: C35389; C35389.
KW Hydrolase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEK 8
Db 8 VEK 10

RESULT 9
MORN HUMAN
ID MORN HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuropeptide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]_TaxID=9606, 10116, 9913, 6110, 6087;
RP SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuropeptide, the head activator,
RT from coelenterates to humans.";
RL Nature 293:579-580(1981).
RN [2]
RP SEQUENCE.
RC SPECIES=A.elegantissima, and H.attenuata;
RX Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
RT hydra.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RP SYNTHESIS.
RX MEDLINE=82050803; PubMed=7297679;
RA Bitt C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuropeptide, the head activator from hydra.";
RL FEBS Lett. 131:317-321(1981).
RN [4]
RP FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
RT in the G2/mitosis transition.";
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
CC IN THE G2/MITOSIS TRANSITION.

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CC -!- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
DR PIR: A01427; YHRT.
DR PIR: A93900; YHXA.
DR PIR: B01427; YHUU.
DR PIR: B93900; YHJPHY.
DR PIR: C01427; YHBO.
DR GK; P01163; -.
KW Growth factor; Cell cycle; Mitosis; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
Db 1 QPP 3

RESULT 10
HS9A_RAT
ID HS9A_RAT STANDARD; PRT; 12 AA.
AC P82995;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heat shock protein HSP 90-alpha (Fragment).
GN HSPCA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=21589773; PubMed=11732320;
RA Langer T., Fasold H.;
RT "Isolation and quantification of the heat shock protein 90 alpha and
RT beta isoforms from rat liver.";
RL Protoplasma 218:54-56(2001).
CC -!- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
DR InterPro: IPR001404; Hsp90.
DR PROSITE: PS00298; HSP90; PARTIAL.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD_RES 4 4
FT MOD_RES 6 6
FT MOD_RES 12 12
FT NON_TER 12 12
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1432 MW; DE47C322CAB6C1B6 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQP 3
Db 8 DQP 10

RESULT 11
TKN1_KASMA
ID TKN1_KASMA STANDARD; PRT; 12 AA.
AC P08613;
DT 01-AUG-1988 (Rel. 08, Created)

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DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hylambates kassinin ((Gl2,Pro5)kassinin).
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8414;
RN [1]_TaxID=8414;
RN SEQUENCE.
RP TISSUE=Skin secretion;
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
RT hylambatin, in the skin of the African rhacophorid frog Hylambates
RT maculatus.", 2:613-617(1981).
RL Biomed. Res. 2:613-617(1981).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S10059; S10059.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 12 12
FT SEQUENCE 12 AA; 1376 MW; 3E756D279DD6DAB7 CRC64;
SQ
Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 KPD 10
Db 4 KPD 6
RESULT 12
TKN2_KASMA STANDARD; PRT; 12 AA.
ID TKN2_KASMA
AC P08614;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hylambatin.
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8414;
RN [1]_TaxID=8414;
RN SEQUENCE.
RP TISSUE=Skin secretion;
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
RT hylambatin, in the skin of the African rhacophorid frog Hylambates
RT maculatus.", 2:613-617(1981).
RL Biomed. Res. 2:613-617(1981).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S07436; S07436.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.

DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 12 12
FT SEQUENCE 12 AA; 1441 MW; 3287CD2F0DD40AB7 CRC64;
SQ
Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PPD 5
Db 2 PPD 4
RESULT 13
E121_LITRU STANDARD; PRT; 13 AA.
ID E121_LITRU
AC P82097;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RN SEQUENCE.
RP TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.",
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 13 13
FT SEQUENCE 13 AA; 1599 MW; C1808EF326F57322 CRC64;
SQ
Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PDV 6
Db 10 PDV 12
RESULT 14
E122_LITRU STANDARD; PRT; 13 AA.
ID E122_LITRU
AC P82098;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 2.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RN SEQUENCE.
RP TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.",
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.

KW Amphibian defense peptide; Amidation.
FT MOD_RES 13 13 AMIDATION
SQ SEQUENCE 13 AA; 1598 MW; C1808EF33B357322 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
DB 10 PDV 12

RESULT 15
IDHP_RAT STANDARD; PRT; 13 AA.
AC P56574;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Isocitrate dehydrogenase [NADP], mitochondrial (EC 1.1.1.42)
DE (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP) (ICD-M) (Fragment).
GN IDH2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J., Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: PLAYS A ROLE IN INTERMEDIARY METABOLISM AND ENERGY PRODUCTION. IT MAY TIGHTLY ASSOCIATE OR INTERACT WITH THE PYRUVATE DEHYDROGENASE COMPLEX (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2) + NADPH.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN (SPOT P8) IS: 9.0, ITS MW IS: 42 kDa.
CC -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE DEHYDROGENASES FAMILY.
DR InterPro; IPR001804; Iscdh.
DR PROSITE; PS00470; IDH_IDMH; PARTIAL.
KW Oxidoreductase; NADP; Glyoxylate bypass; Tricarboxylic acid cycle; Mitochondrion.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1526 MW; 5FB81031723E02C3 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEK 8
DB 7 VEK 9

RESULT 16
PEDI_HYDAT STANDARD; PRT; 13 AA.
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pedin.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;

RN [1]
RP SEQUENCE
RA MEDLINE=96232307; PubMed=8674432;
RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active peptides from Hydra vulgaris.";
RL Development 122:1941-1948(1996).
CC -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT DEVELOPMENT.
KW Morphogen.
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
DB 9 PDV 11

RESULT 17
SODM_CANFA STANDARD; PRT; 13 AA.
ID SODM_CANFA
AC P54712;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).
GN SOD2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Manganese (By similarity).
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
DR HSC-2DPAGE; P54712; DOG.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Manganese; Mitochondrion.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1476 MW; 9C9651DE8BE0672A CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDL 11
DB 5 PDL 7

RESULT 18
TY13_PHYRO STANDARD; PRT; 13 AA.
ID TY13_PHYRO
AC P04096;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-13.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]_
RN SEQUENCE.
RA Montecucchi P.C., Gorzini L., Erspamer V.;
RT "Primary structure determination of a tryptophan-containing
RT tridecapeptide from Phyllomedusa rohdei.";
RL Int. J. Pept. Protein Res. 27:175-182(1986).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; A05174; A05174.
KW Amphibian defense peptide; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 7 EXP 9
Db 2 EXP 4

RESULT 19
MARI_ALTSP
ID MARI_ALTSP STANDARD; PRT; 14 AA.
AC P2939;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Marinostatin C-2 (Marinostatin C-1; Marinostatin D).
OS Alteromonas sp. (strain B-10-31).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Alteromonas.
OX NCBI_TaxID=29456;
RN [1]_
RN SEQUENCE, AND ACTIVE SITE.
RX MEDLINE=92176155; PubMed=1794974;
RA Takano R., Imada C., Kanei K., Hara S.;
RT "The reactive site of marinostatin, a proteinase inhibitor from
RT marine Alteromonas sp. B-10-31."
RL J. Biochem. 110:856-858(1991).
CC -!- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
CC NOT TRYPSIN.
KW Serine protease inhibitor; Pyrrolidone carboxylic acid.
FT PEPTIDE 1 14 MARINOSTATIN C-2.
FT PEPTIDE 3 14 MARINOSTATIN C-1.
FT PEPTIDE 4 14 MARINOSTATIN D.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 6 7 REACTIVE BOND.
SQ SEQUENCE 14 AA; 1644 MW; 6B7CEFP2EF32E44 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 QPF 14
Db 1 QPF 3

RESULT 20
HSII_PINPS
ID HSII_PINPS STANDARD; PRT; 15 AA.
AC P81083;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable class I heat shock protein (water stress responsive protein
DE 3) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]_
RN SEQUENCE.
RA TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water deficit-responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]_
RN SEQUENCE.
RA TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
RN [3]_
RN REVISION TO 1.
RA Frigerio J.-M.;
RL Submitted (SEP-2001) to the SWISS-PROT data bank.
CC -!- SUBUNIT: FORMS OLIGOMERIC STRUCTURES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- INDUCTION: By water stress.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT N144) IS: 6.1. ITS MW IS: 17 kDa.
CC -!- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
CC FAMILY.
CC -!- SIMILARITY: PLANTS HAVE FOUR CLASSES OF HSP20: CLASS I AND II
CC WHICH ARE CYTOPLASMIC; CLASS III WHICH IS IN THE CHLOROPLAST
CC AND CLASS IV WHICH IS IN THE ENOMEMBRANE. THIS PROTEIN BELONGS
CC TO CLASS I.
DR InterPro; IPR002068; Hsp20.
DR PROSITE; PS01031; HSP20; PARTIAL.
KW Heat shock; Multigene family.
FT NON_TER 1 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1847 MW; 87FC504C2EB1F2B7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFQ 15
Db 12 PFQ 14

RESULT 21
MK1_PALPR
ID MK1_PALPR STANDARD; PRT; 15 AA.
AC P80408;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metanikowin I.
OS Palomena prasina (Green shield bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Panheteroptera; Pentatomomorpha; Pentatomidae;
OC Palomena.
OX NCBI_TaxID=55431;
RN [1]_
RN SEQUENCE.
RA TISSUE=Hemolymph;
RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect

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RT Palomena prasina: identification of a unique family of proline-rich
RT peptides and of a novel insect defensin."
RL J. Insect Physiol. 42:81-89(1996).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
CC BACTERIA.
CC -!- INDUCTION: By bacterial infection.
KW Antibiotic; Insect immunity.
SQ SEQUENCE 15 AA; 1838 MW; 214078663CE46299 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
DB 3 KPD 5

RESULT 22
MK2A_PALPR STANDARD; PRT; 15 AA.
AC P80409;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metanikowin IIA.
OS Palomena prasina (Green shield bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Panheteroptera; Pentatomomorpha; Pentatomidae;
OC Palomena
OX NCBI_TaxID=55431;
RN [1]
RP TISSUE=Hemolymph;
RC Cherysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RA "The inducible antibacterial peptides of the hemipteran insect
RT Palomena prasina: identification of a unique family of proline-rich
RT peptides and of a novel insect defensin."
RL J. Insect Physiol. 42:81-89(1996).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
CC BACTERIA.
CC -!- INDUCTION: By bacterial infection.
KW Antibiotic; Insect immunity.
SQ SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
DB 3 KPD 5

RESULT 23
ONCL_ONCMY STANDARD; PRT; 15 AA.
AC P83287;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Oncorhynchin 1 (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin;
RC Fernandes J.M.O., Smith V.J., Kemp G.D.;
RA "Purification and N-terminal sequencing of a 3 kDa antibacterial

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RT peptide from skin secretions of rainbow trout."
RL Submitted (MAY-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacterium P.citreus.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003795; F:antimicrobial peptide activity; NAS.
DR GO; GO:0006805; P: xenobiotic metabolism; NAS.
KW Antibiotic.
FT UNSURE 4 4 OR G.
FT UNSURE 9 9 OR T.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1601 MW; 43C25028DBC12B7C CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVE 7
DB 9 DVE 11

RESULT 24
PSAO_CUCSA STANDARD; PRT; 15 AA.
AC F42052;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem I reaction centre subunit 8 (Photosystem I 17.5 kDa
DE protein) (Fragment).
GN PSAM.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE.
RC TISSUE=Cotyledon;
RX MEDLINE=91355209; PubMed=1883835;
RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;
RT "Characterization of genes that encode subunits of cucumber PS I
RT complex by N-terminal sequencing."
RL Biochim. Biophys. Acta 1059:141-148(1991).
CC -!- FUNCTION: ESSENTIAL FOR THE ACTIVITY OF NADP PHOTOREDUCTION.
DR PIR; E56819; E56819.
KW Photosystem I; Photosynthesis; Chloroplast; Thylakoid; Membrane.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1714 MW; CA0BF5DAD403D9F4 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FOV 16
DB 8 FOV 10

RESULT 25
VORA_METTM STANDARD; PRT; 15 AA.
AC P80907;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ketosovalerate oxidoreductase subunit VORA (EC 1.-.-.-) (VOR) (2-
DE oxoisovalerate oxidoreductase alpha chain) (2-oxoisovalerate-
DE ferredoxin oxidoreductase alpha subunit) (Fragment).
GN VORA.

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OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
in Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 244:862-868(1997).
CC -!- SUBUNIT: HETEROTRIMER OF THE VORA, VORB AND VORC SUBUNITS.
CC -!- MISCELLANEOUS: As a pH optimum of 9.7 and an optimal temperature
of 75 degrees Celsius.
KW Oxidoreductase.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1779 MW; 31320B6531C4528F CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
DB 7 KPD 9

RESULT 26
LPK1_LOGMI
ID LPK1_LOGMI STANDARD; PRT; 16 AA.
AC P20404;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 1 (LOM-PK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX MEDLINE=91224474; PubMed=2026322;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
myotropic peptide of Locusta migratoria.";
RL Gen. Comp. Endocrinol. 81:97-104(1991).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A49761; A49761.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1827 MW; A178BDC0A0AFDD6 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 QPF 14
DB 10 QPF 12

RESULT 27
MK2B_PALPR
ID MK2B_PALPR STANDARD; PRT; 16 AA.
AC P80410;
DT 01-NOV-1995 (Rel. 32, Created)

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DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metelnikowin IIB.
OS Palomena prasina (Green shield bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
OC Palomena.
OX NCBI_TaxID=55431;
RN [1]
RP SEQUENCE.
RX TISSUE=Hemolymph;
RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect
Palomena prasina: identification of a unique family of proline-rich
peptides and of a novel insect defensin.";
RL J. Insect Physiol. 42:81-89(1996).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
BACTERIA.
CC -!- INDUCTION: By bacterial infection.
KW Antibiotic; Insect immunity.
SQ SEQUENCE 16 AA; 2040 MW; AF21407D063B9462 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
DB 3 KPD 5

RESULT 28
MK3_PALPR
ID MK3_PALPR STANDARD; PRT; 16 AA.
AC P80411;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metelnikowin III.
OS Palomena prasina (Green shield bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
OC Palomena.
OX NCBI_TaxID=55431;
RN [1]
RP SEQUENCE.
RX TISSUE=Hemolymph;
RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect
Palomena prasina: identification of a unique family of proline-rich
peptides and of a novel insect defensin.";
RL J. Insect Physiol. 42:81-89(1996).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
BACTERIA.
CC -!- INDUCTION: By bacterial infection.
KW Antibiotic; Insect immunity.
SQ SEQUENCE 16 AA; 2024 MW; A9E3835D063B9462 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
DB 3 KPD 5

RESULT 29
MMPX_SOLTU
ID MMPX_SOLTU STANDARD; PRT; 16 AA.
AC P80501;

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DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Unidentified mitochondrial matrix protein (Fragment).
OS Solanum tuberosum (potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE
RC TISSUE=Tuber;
RX MEDLINE=97077345; PubMed=8919912;
RA Jansch L., Kruit V., Schmitz U.K., Braun H.P.;
RT "New insights into the composition, molecular mass and stoichiometry
of the protein complexes of plant mitochondria.";
RL Plant J. 9:357-368(1996).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
KW Mitochondrion.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1768 MW; C58D4DB48AA18B8D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEK 8
   |||
DB 9 VEK 11

RESULT 30
SODM MYCHA
ID _SODM_MYCHA STANDARD; PRT; 18 AA.
AC P80582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1) (Fragment).
GN SODA OR SOD.
OS Mycobacterium habana.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1784;
RN [1]
RP SEQUENCE.
RC STRAIN=TMC 5135;
RX MEDLINE=96262709; PubMed=8704977;
RA Bist D., Mehrotra J., Dhindsa M.S., Singh N.B., Sinha S.;
RT "A major T-cell-inducing cytosolic 23 kDa protein antigen of the
vaccine candidate Mycobacterium habana is superoxide dismutase.";
RL Microbiology 142:1375-1383(1996).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Manganese (By similarity).
CC -!- SUBUNIT: Homodimer (Probable).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Manganese.
FT NON_TER 18
SQ SEQUENCE 18 AA; 1883 MW; A4161A3DAC93F710 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDL 11
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Db 6 PDL 8

RESULT 31
UC21 MAIZE
ID _UC21_MAIZE STANDARD; PRT; 18 AA.
AC P80627;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 443)
  (Fragment).
DE Zea mays (Maize).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
RL Theor. Appl. Genet. 93:957-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.9, ITS MW IS: 26.5 KDa.
CC -!- SIMILARITY: TO L-ASCORBATE PEROXIDASES.
DR Maize-2DPAGE; P80627; COLEOPTILE.
DR MaizeDB; 123953; -.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1938 MW; F32F6FEF038BAB8A CRC64;

Query Match 16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEK 8
   |||
DB 15 VEK 17

RESULT 32
LANC STRSQ
ID _LANC_STRSQ STANDARD; PRT; 19 AA.
AC P38655;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lanthibiotic anconevin.
OS Streptomyces sp. (strain A647P-2).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1931;
RN [1]
RP SEQUENCE.
RA Wakamiya T., Ueki Y., Shiba T., Kido Y., Motoki Y.;
RT "The structure of anconevin, a new peptide inhibitor of angiotensin I
  converting enzyme.";
RL Tetrahedron Lett. 26:665-668(1985).
CC -!- FUNCTION: ACTS AS INHIBITOR OF ANGIOTENSIN I CONVERTING ENZYME.
CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of
  Thr, and Ser into dehydrated AA and the formation of thioether
  bonds with cysteine or the formation of dialkylamine bonds with
  lysine. This is followed by membrane translocation and cleavage of
  the modified precursor.
CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
DR PIR; A61284; EWSMAN.
KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.
FT CROSSLNK 1 18
   Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 4 14
   Lanthionine (Ser-Cys).
FT CROSSLNK 5 11
   Beta-methylanthionine (Cys-Thr).

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FT CROSSLINK      6      19      Lysinoalanine (Ser-Lys).
SQ SEQUENCE      19 AA; 2033 MW;  F434299E2736286A CRC64;

Query Match      16.7%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 VQS 18
DB      2 VQS 4

RESULT 33
ACPH_BOVIN
ID ACPH_BOVIN      STANDARD;      PRT;      20 AA.
AC P80227;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
GN APEH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Lens;
RX MEDLINE=93387316; PubMed=8375399;
RA Sharma K.K., Ortworth B.J.;
RT "Bovine lens acylpeptide hydrolase. Purification and characterization
of a tetrameric enzyme resistant to urea denaturation and proteolytic
inactivation.";
RL Eur. J. Biochem. 216:631-637(1993).
CC -1- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -1- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
+ peptide.
CC -1- SUBUNIT: Homotetramer.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR PIR; S36842; S36842.
DR InterPro; IPR002471; Prol endopep_ser.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KM Hydrolase.
FT NON_TER      1      1
FT NON_TER      20     20
SQ SEQUENCE      20 AA; 2325 MW;  B9D028BA8378F624 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KPD 10
DB      1 KPD 3

RESULT 34
BULB_NARPS
ID BULB_NARPS      STANDARD;      PRT;      20 AA.
AC P80554;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Bulb protein (Fragment).
OS Narcissus pseudonarcissus (Daffodil).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OC Narcissus.
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OX NCBI_TaxID=39639;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Golden Harvest; TISSUE=Bulb;
RA Partis M.D., Barker P., Thomas B.;
RL Submitted (FEB-1996) to the SWISS-PROT data bank.
FT UNSUBRE      2      2
FT NON_TER      20     20
SQ SEQUENCE      20 AA; 2077 MW;  76212FF3A468AD38 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PDV 6
DB      2 PDV 4

RESULT 35
CHP_THICU
ID CHP_THICU      STANDARD;      PRT;      20 AA.
AC P80486;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chemoheterotroph-specific protein (Fragment).
OS Thiobacillus cuprinus.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Thiomonas.
OX NCBI_TaxID=36860;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 5494;
RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
RL Submitted (SEP-1995) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
CC CHEMOHETEROTROPHICALLY.
FT NON_TER      20     20
FT NON_TER      20     20
SQ SEQUENCE      20 AA; 2167 MW;  E5BAEC1BA3238A0A CRC64;

Query Match      16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KPD 10
DB      17 KPD 19

RESULT 36
CP35_PAPSP
ID CP35_PAPSP      STANDARD;      PRT;      20 AA.
AC P80056;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome P450 3A5 (EC 1.14.14.1) (CYP11A5) (P450 FA) (6-beta-
testosterone hydroxylase) (Fragment).
DE Papio sp. (Baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=61183;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=92174920; PubMed=1541278;
RA Dalet-Beluche I., Boulenc X., Fabre G., Maurel P., Bonfils C.;
RL "Purification of two cytochrome P450 isoforms related to CYP2A and
CYP3A gene families from monkey (baboon, Papio papio) liver
microsomes. Cross reactivity with human forms.";
RL Eur. J. Biochem. 204:641-648 (1992).
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CC -!- FUNCTION: 6-BETA-TESTOSTERONE HYDROXYLASE.
CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -!- INDUCTION: By phenobarbital.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR InterPro: IPR001128; Cytochrome P450.
DR PROSITE: PS00086; CYTOCHROME P450; PARTIAL.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2226 MW; 3FEF8B6E2BC0F36 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDL 11
Db 5 PDL 7

RESULT 37
DER6_DERPT STANDARD; PRT; 20 AA.
AC P49277;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mite allergen Der P 6 [EC 3.4.21.-] (Der P VI) (DP5) (Fragment).
GN DERP6.
OS Dermatophagoides pteronyssinus (House-dust mite).
CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
CC Acariformes; Sarcophormes; Astigmata; Psoroptidia; Analgoidea;
CC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6956;
RN [1]
RP SEQUENCE.
RX MEDLINE=93327207; PubMed=8334537;
RA Yasueda H., Mita H., Akiyama K., Shida T., Ando T., Sugiyama S.,
RA Yamakawa H.;
RT "Allergens from Dermatophagoides mites with chymotryptic activity.";
RL Clin. Exp. Allergy 23:384-390(1993).
CC -!- CATALYTIC ACTIVITY: Specificity similar to chymotrypsin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR MEROPS: S01.187; -.
DR InterPro: IPR001254; Ser. protease Try.
DR PROSITE: PS00240; TRYPSIN_DOM; PARTIAL.
DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
KW Hydrolase; Serine protease; Allergen.
FT UNSURE 1
FT UNSURE 6
FT UNSURE 10
FT UNSURE 11
FT UNSURE 17
FT NON_TER 20
SQ SEQUENCE 20 AA; 2082 MW; 26D5F39E06639983 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFQ 15
Db 13 PFQ 15

RESULT 38
SODM_HORVU STANDARD; PRT; 20 AA.
ID SODM_HORVU
AC P28524;

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DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).
GN SODA.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. CM 72; TISSUE=Root;
RA Hurkman W.J., Tao H.P., Tanaka C.K.;
RT "germin-like polypeptides increase in barley roots during salt
RT stress.";
RL Plant Physiol. 97:366-374(1991).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Manganese (By similarity).
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
CC InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; sodfe; 1.
DR PROSITE: PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Manganese; Mitochondrion.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2152 MW; 7F7CAE8DFF1C9657 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDL 11
Db 7 PDL 9

RESULT 39
TRYL_STREX STANDARD; PRT; 20 AA.
AC P80420;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin-like protease (EC 3.4.21.-) (Fragment).
OS Streptomyces exfoliatus (Streptomyces hydrogenans).
CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
CC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1905;
RN [1]
RP SEQUENCE.
RC STRAIN=SMF13;
RX MEDLINE=95291424; PubMed=7773379;
RA Kim I.S., Lee K.J.;
RT "Physiological roles of leupeptin and extracellular proteases in
RT mycelium development of Streptomyces exfoliatus SMF13.";
RL Microbiology 141:1017-1025(1995).
CC -!- FUNCTION: INVOLVED IN MYCELIUM DIFFERENTIATION.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2A.
DR MEROPS: S01.101; -.
DR InterPro: IPR001254; Ser. protease Try.
DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2129 MW; 4568F56D0E7393AF CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFQ 15
Db 13 PFQ 15

RESULT 40

ACPH HUMAN
ID TUFT HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;
RA Nishioka K., Constantinopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsin.";
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
RN IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
effect of leucophilic gamma globulin (leucokinin) on the phagocytic
activity of human polymorphonuclear leucocyte.";
RL Biochemistry 6:3386-3392(1967).
CC -!- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
ACTIVITY OF NEUTROPHILS.
CC PIR: A02147; A02147.
DR MI; 191150; -
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006909; P:phagocytosis; NAS.
SQ SEQUENCE 4 AA; 501 MW; 74176321C000000000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KP 9
Db 2 KP 3

RESULT 41

SUGA ACHDO
ID SUGA ACHDO STANDARD; PRT; 5 AA.
AC P19931;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Subesophageal ganglion pentapeptide.
OS Acheta domesticus (House cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Acheta.
OX NCBI_TaxID=6997;
RN [1]
RN SEQUENCE.
RA Wicker C.;
RT "Isolation and structure of a peptide isolated from the
subesophageal ganglion of Acheta domesticus (orthoptera).";
RL Comp. Biochem. Physiol. 88C:185-187(1987).

CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
CC GANGLIA.
DR PIR; JS0319; JS0319.
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PF 14
Db 4 PF 5

RESULT 42

ACPH RABIT
ID ACPH RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
GN APEH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN SEQUENCE.
RX TISSUE=Muscle;
RX MEDLINE=92222120; PubMed=1807161;
RA Krishna R.G., Chin C.Q., Wold F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
unblocking with N-acylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199:45-50(1991).
CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
+ peptide.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR PIR; A49792; A49792.
DR MEROPS; S09.004; -
DR InterPro; IPR002471; Prol endopep_ser.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QV 16
Db 4 QV 5

RESULT 43

OVN LEPDE
ID OVN LEPDE STANDARD; PRT; 6 AA.
AC P42985;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Oviductal motility stimulating peptide (Leb-OVM).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;

OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
 OC Chrysomelini; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=91271080; PubMed=2052497;
 RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
 RA Proost P., Torrekens S., de Loof A.;
 RT "Isolation, identification and synthesis of novel oviductal motility
 RT stimulating head peptide in the Colorado potato beetle, *Leptinotarsa*
 RT *decemlineata*.";
 RL Peptides 12:31-36 (1991).
 CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC OVIDUCT.
 KW Neuropeptide; Amidation.
 FT MOD_RES 6 6 AMIDATION.
 SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 8 KP 9
 DB 4 KP 5
 RESULT 44
 ID TRPI_PSEPU STANDARD; PRT; 6 AA.
 AC P36414;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TrpBA operon transcriptional activator (fragment).
 GN TRPI.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PPG1 C1S;
 RX MEDLINE=89335826; PubMed=2503057;
 RA Eberly L., Crawford I.P.;
 RT "DNA sequence of the tryptophan synthase genes of *Pseudomonas*
 RT *putida*.";
 RL Biochimie 71:521-531 (1989).
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
 CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
 CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
 CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; X13299; CAA31660.1; -;
 DR InterPro; IPR000847; HTH_LysR.
 DR PROSITE; PS00044; HTH_LYSR_FAMILY; PARTIAL.
 KW Tryptophan biosynthesis; Transcription regulation; Activator;
 KW DNA-binding.
 FT NON_TER 6 6
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 DL 11
 DB 4 DL 5
 RESULT 45
 ID FARL_HELTI STANDARD; PRT; 7 AA.
 AC P41871;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide GDPFIRF-amide.
 OS Helisoma trivolvis (Snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymnaeidae; Planorbidae; Helisoma.
 OX NCBI_TaxID=27815;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, *Helisoma*
 RT *trivolvis*.";
 RL Peptides 15:31-36 (1994).
 CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
 CC THE KIDNEY, MANTLE AND SKIN.
 CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 13 PF 14
 DB 3 PF 4
 RESULT 46
 ID FAR4_PANRE STANDARD; PRT; 7 AA.
 AC P41875;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRFamide-like neuropeptide PF4 (KPNFIRF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=95232026; PubMed=7716079;
 RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
 RA Thim L., Kubiak T.M., Martin R.A., Geary T.G.;
 RT "Isolation and preliminary biological characterization of
 RT KPNFIRFamide, a novel FMRFamide-related peptide from the free-living
 RT nematode, *Panagrellus redivivus*.";
 RL Peptides 16:87-93 (1995).
 CC -!- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT
 CC MUSCLE TENSION INCREASE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7 7 AMIDATION.

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SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KP 9
Db 1 KP 2

RESULT 47
FARB CALVO STANDARD; PRT; 7 AA.
AC P41866;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 11.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRamides) from the blowfly
RT Calliphora vomitoria.;
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; B44787; B44787.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 926 MW; 69D40699C444AB700 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PD 5
Db 1 PD 2

RESULT 48
LANC CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin U149 (Fragment).
OS Carnobacterium sp. (strain UI49).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
CC ACTIVE ON GRAM-POSITIVE BACTERIA.
KW Antibiotic; Bacteriocin; Lantibiotic.
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FT NON TER 7 7
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
Db 5 QP 6

RESULT 49
PPH2 LYCES STANDARD; PRT; 7 AA.
AC P83379;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Purple acid phosphatase isozyme LeSAP2 (EC 3.1.3.2) (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
RP GLYCOSYLATION.
RC STRAIN=cv. Moneymaker; TISSUE=Seed;
RX MEDLINE=22361242; PubMed=12473124;
RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
RT "Purification and characterization of two secreted purple acid
RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon
RT esculentum) cell cultures.";
RL Eur. J. Biochem. 269:6278-6286(2002).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Glycosylated.
CC -!- MISCELLANEOUS: In L. esculentum there are at least two isozymes of
CC purple acid phosphatase.
KW Hydrolase; Glycoprotein.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DL 11
Db 6 DL 7

RESULT 50
TPFY PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryphtophyllin-1 (pdt-1).
OS Pachymedusa dancicolor (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE=Skin secretion;
```

Chen T.B., Orr D.F., Shaw C.;
 RA "Pachymedusa danielcolor tryptophyllin-1 (Pdt-1): structural
 RT characterization, pharmacological activity and cloning of precursor
 RT cDNA.";

RL Submitted (SEP-2002) to the SWISS-PROT data bank.
 CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
 CC smooth muscle.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.

CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
 DR GO: GO:000576; C:extracellular; NAS.
 DR GO: GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.
 KW Amphibian defense peptide; Amidation; Hydroxylation.
 FT MOD_RES 3 3 HYDROXYLATION.
 FT MOD_RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PP 4
 Db 2 PP 3

RESULT 51
 UH11_RAT
 ID UH11_RAT STANDARD; PRT; 7 AA.
 AC P56576;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.

RC STRAIN=Wistar; TISSUE=Heart;
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
 RA Jungblut P.R.;

RL Submitted (SEP-1998) to the SWISS-PROT data bank.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC -!- PROTEIN IS: 8.5, ITS MW IS: 42 KDa.
 FT UNSURE 2 2 OR A.
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 QS 18
 Db 1 QS 2

RESULT 52
 UN06_PINPS
 ID UN06_PINPS STANDARD; PRT; 7 AA.
 AC P81675;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of needles (N141) (Fragment).
 OS Pinus pinaster (Maritime pine).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.

TISSUE=Needle;
 RC MEDLINE=99274088; PubMed=10344291;
 RX Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;

RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";

RL Electrophoresis 20:1098-1108(1999).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC -!- PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
 FT NON_TER 1 1
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 823 MW; 69D7672448B5740 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PF 14
 Db 6 PF 7

RESULT 53
 ACT_CARMA
 ID ACT_CARMA STANDARD; PRT; 8 AA.
 AC P80709;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 34, Last annotation update)
 DE Actin (Fragment).
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 CC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.

RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
 RA Baghdassarian D.;

RL "A transaldolase. An enzyme implicated in crab steroidogenesis.";
 RT Endocrine 5:23-32(1996).
 CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
 CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
 CC IN ALL EUKARYOTIC CELLS.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
 CC 6.8, ITS MW IS: 46 kDa.
 CC -!- SIMILARITY: Belongs to the actin family.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin like.
 DR PROSITE; PS00406; ACTINS_1; PARTIAL.
 DR PROSITE; PS00432; ACTINS_2; PARTIAL.
 DR PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
 KW Structural protein.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAEB3 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DV 6
 Db 3 DV 4

RESULT 54
 AKHG_GRYBI
 ID AKHG_GRYBI STANDARD; PRT; 8 AA.
 AC P14086;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
of a peptide with adipokinetic activity from the corpora cardiaca of
the cricket Gryllus bimaculatus.";
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A28004;
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QV 16
DB 1 QV 2

RESULT 55
AKH_LIBAU
ID AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
concentrating hormone family isolated and sequenced from a
dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.

DR PIR; S10596; S10596.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QV 16
DB 1 QV 2

RESULT 56
AKH_MELML
ID AKH_MELML STANDARD; PRT; 8 AA.
AC P25423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Melolontha melolontha (Cockchafer),
OS Geotrues stercorosus (Dor beetle), and
OS Pachoda marginata (flower beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;
OC Scarabaeidae; Melolonthinae; Melolontha.
OX NCBI_TaxID=7061, 7087, 7058;
RN [1]
RP SEQUENCE.
RC SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
RX MEDLINE=91248100; PubMed=2039445;
RA Gaede G.;
RT "A unique charged tyrosine-containing member of the adipokinetic
hormone/red-pigment-concentrating hormone peptide family isolated and
sequenced from two beetle species.";
RL Biochem. J. 275:671-677(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;
RX MEDLINE=92265187; PubMed=1586453;
RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
RT "Primary structures of neuropeptides isolated from the corpora
cardiaca of various cetonid beetle species determined by
pulsed-liquid phase sequencing and tandem fast atom bombardment mass
spectrometry.";
RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A58641; A58641.
DR PIR; S15422; S15422.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1022 MW; 867AB75AB544736 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PD 5
DB 6 PD 7

RESULT 57

AL12_CARMA STANDARD; PRT; 8 AA.
 ID _ALL2_CARMA
 AC P81815;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 12.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.; and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab *Carcinus maenas*.
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Multigene family.
 KW Neuropeptide; Multigene family.
 SQ SEQUENCE 8 AA; 913 MW; 672879CDBC569AB7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PD 5

Db 1 PD 2

RESULT 58

ALL5_CALVO STANDARD; PRT; 8 AA.
 ID _ALL5_CALVO
 AC P41841;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93211980; PubMed=8460157;
 RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
 RA Thorpe A.;
 RT "Callatostatins: neuropeptides from the blowfly *Calliphora vomitoria*
 RT with sequence homology to cockroach allatostatins."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
 RN [2]
 RP CHARACTERIZATION, AND HYDROXYLATION.
 RX TISSUE=Head;
 RC MEDLINE=94342269; PubMed=8063725;
 RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
 RT "[Hyp3]Met-callatostatin. Identification and biological properties of
 RT a novel neuropeptide from the blowfly *Calliphora vomitoria*."
 RL J. Biol. Chem. 269:21059-21066(1994).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
 CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
 CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
 CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
 CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
 CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

DR

PIR; E47393; E47393.
 KW Neuropeptide; Amidation; Hydroxylation.
 FT MOD RES 3 3 HYDROXYLATION (20%).
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB47768 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PP 4

Db 2 PP 3

RESULT 59

ANG2_BOTJA STANDARD; PRT; 8 AA.
 ID _ANG2_BOTJA
 AC Q10582;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide II (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B., Dallie Lucca J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake *Bothrops jararaca*."
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PF 14

Db 7 PF 8

RESULT 60

HTF1_PERAM STANDARD; PRT; 8 AA.
 ID _HTF1_PERAM
 AC P04548;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-I)
 DE (Pea-CAH-I) (LeD-CC-I) (Hypertrehalosaemic neuropeptide I).
 OS Periplaneta americana (American cockroach),
 OS Leptinotarsa decemlineata (Colorado potato beetle), and
 OS Blattella orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattellidae; Periplaneta.
 OX NCBI_TaxID=6978; 7539, 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,

RA Rinehart K.L. Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P. americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=B. orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A44960; A44960.
 DR PIR; A49823; A49823.
 DR PIR; S08995; S08995.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 QV 16
 DB 1 QV 2

RESULT 61
 LCK3_LEUMA
 ID LCK3_LEUMA STANDARD; PRT; 8 AA.
 AC P21142;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE Leucokinin III (I-III).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 CC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;

RT "Primary structure and synthesis of two additional neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RT Cephalomyotropins.";
 RL Comp. Biochem. Physiol. 84C:271-276(1986).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DQ 2
 DB 1 DQ 2

RESULT 62
 LCK6_LEUMA
 ID LCK6_LEUMA STANDARD; PRT; 8 AA.
 AC P19988;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leucokinin VI (I-VI).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 CC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RA MEDLINE=87052651; PubMed=2877794;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
 RT myotropic peptides of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 89C:27-30(1987).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
 CC HELIOTHIS ZEA ADIPOKINETIC HORMONE.
 DR PIR; JS0316; JS0316.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 935 MW; 9D6365B5E9D5A5A6 CRC64;
 Query Match 11.1%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 QS 18
 DB 1 QS 2

RESULT 63
 NPB_BOVIN
 ID NPB_BOVIN STANDARD; PRT; 8 AA.
 AC P15507;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropeptide B.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 CC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;


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RN NCBI_TaxID=6978;
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR Interpro; IPR001484; Pyrokinin.
KW PROSITE; PS00539; PYROKININ; FALSE NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
|||
DB 4 QP 5

RESULT 64
PLP_BRANA STANDARD; PRT; 8 AA.
ID_PLP_BRANA
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Plastidial lipid-associated protein (fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. TOPAZ; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;
RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
RA Murphy D.J.;
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RT pollen coat of Brassica napus.";
RL Planca 208:588-598(1999).
CC -!- FUNCTION: MAY PLAY A STRUCTURAL ROLE IN THE ELAIOPLAST, A TAPETUM-
CC SPECIFIC PLASTIDIAL LIPID ORGANELLE.
CC -!- TISSUE SPECIFICITY: TAPETUM OF ANTHEIRS.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DV 6
|||
DB 3 DV 4

RESULT 65
PPK2_PERAM STANDARD; PRT; 8 AA.
ID_PPK2_PERAM
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.

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OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR Interpro; IPR001484; Pyrokinin.
KW PROSITE; PS00539; PYROKININ; FALSE NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
|||
DB 2 PP 3

RESULT 66
PPK3_PERAM STANDARD; PRT; 8 AA.
ID_PPK3_PERAM
AC P82618;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach.";
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

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Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PF 14
DB 3 PF 4

RESULT 67
UC26 MAIZE STANDARD; PRT; 8 AA.
AC P80632;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Tourret P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.0, ITS MW IS: 57.2 kDa.
DR Maize-2DPAGE; P80632; COLEOPTILE.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQ 2
DB 5 DQ 6

RESULT 68
UH09 RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RT Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQ 2
DB 5 DQ 6

QY 17 QS 18
DB 5 QS 6

RESULT 69
UPAL HUMAN STANDARD; PRT; 8 AA.
ID UPAL_HUMAN
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON_TER 1
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQ 2
DB 1 DQ 2

RESULT 70
AL10 CARMA STANDARD; PRT; 9 AA.
ID AL10_CARMA
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9
FT MOD_RES 9
SQ SEQUENCE 9 AA; 963 MW; 372D79DCB4776C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQ 2
DB 1 DQ 2

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Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 QP 3
DB 3 QP 4

RESULT 71
CCAP_CARMA STANDARD; PRT; 9 AA.
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RN SEQUENCE.
RP SPECIES=C.maenas; TISSUE=Pericardial organs;
RC Stangier J., Hilbich C., Beyreuther K., Keller R.;
RA "Unusual cardioactive peptide (CCAP) from pericardial organs of the
RT shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579 (1987).
RN [2]
RN SEQUENCE.
RP SPECIES=M.sexta;
RC MEDLINE=93050243; PubMed=1426284;
RX Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RA "Primary structure of a cardioactive neuropeptide from the tobacco
RT hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168 (1992).
RN [3]
RN SEQUENCE.
RP SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RX MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
RT molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074 (1993).
CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
CC INTO THE HEMOLYMPH.
DR PIR; A26363; A26363.
DR PIR; S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
FT MOD RES 9 9
FT SEQUENCE 9 AA; 959 MW; CSA861A9CDD44EB9 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PF 14
DB 1 PF 2

RESULT 72
COW_CORVE STANDARD; PRT; 9 AA.
AC P83047;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Contryphan-Vn.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=117992;
RN [1]
RN SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RP TISSUE=Venom;
RC MEDLINE=21547785; PubMed=11688995;
RX Massilia G.R., Schinina M.E., Ascenzi P., Politicelli F.;
RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
RT snail Conus ventricosus.";
RL Biochem. Biophys. Res. Commun. 288:908-913 (2001).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1088.6; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Amidation; D-amino acid.
FT DISULFID 3 9
FT MOD RES 5 5
FT MOD RES 9 9
FT SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KP 9
DB 6 KP 7

RESULT 73
COWE_THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide via (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RN SEQUENCE.
RP TISSUE=Heart;
RC MEDLINE=97454291; PubMed=9310366;
RX Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103 (1997).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
FT SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;

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Best Local Similarity 100.0%; Pred.No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3

Db 3 QP 4

RESULT 74

FAR3 PENMO
ID FAR3 PENMO STANDARD; PRT; 9 AA.
AC P83318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP3 (AQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupem J., Krungkarn C., Longyant S.,
RA Chaivithangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.

Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred.No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3

Db 2 QP 3

RESULT 75

FAR4 CALVO
ID FAR4 CALVO STANDARD; PRT; 9 AA.
AC P41859;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CallifMRamide 4.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated callifMRamides) from the blowfly
Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; D41978; D41978.

KW Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KP 9

Db 1 KP 2

Search completed: November 25, 2003, 18:17:23
Job time : 9.71277 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 43.3723 Seconds
(without alignments)
107.095 Million cell updates/sec

Title: US-09-641-801-3

Perfect score: 18

Sequence: 1 DQPPDVEXPDLPQFFQVQS 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	5	27.8	15	8	Q972K8	Q972K8 spinacia ol
2	4	22.2	11	2	Q9S618	Q9S618 prochloroco
3	4	22.2	11	6	Q8HYM4	Q8HYM4 felis silve
4	4	22.2	13	2	Q9R3R6	Q9R3R6 prochloroco
5	4	22.2	15	12	Q86174	Q86174 human coron
6	4	22.2	17	2	Q9LB06	Q9LB06 prochloroco
7	4	22.2	17	6	Q9TRW1	Q9TRW1 oryctolagus
8	4	22.2	17	12	Q919B0	Q919B0 human papil
9	4	22.2	18	2	Q9X3E9	Q9X3E9 prochloroco
10	4	22.2	18	2	Q67971	Q67971 synecococc
11	4	22.2	18	2	Q9R4E0	Q9R4E0 pseudomonas
12	4	22.2	18	6	P82674	P82674 bos taurus
13	4	22.2	18	10	Q9S8G8	Q9S8G8 psophocarpu
14	4	22.2	18	12	Q919D5	Q919D5 human papil
15	4	22.2	18	12	Q919B3	Q919B3 human papil
16	4	22.2	18	12	Q919B5	Q919B5 human papil

17	4	22.2	18	12	Q919B7	Q919B7 human papil
18	4	22.2	18	12	Q919C5	Q919C5 human papil
19	4	22.2	18	12	Q919D1	Q919D1 human papil
20	4	22.2	18	12	Q919D3	Q919D3 human papil
21	4	22.2	18	12	Q919B9	Q919B9 human papil
22	4	22.2	18	12	Q919A8	Q919A8 human papil
23	4	22.2	18	12	Q919C7	Q919C7 human papil
24	4	22.2	18	12	Q919C9	Q919C9 human papil
25	4	22.2	18	13	Q13167	Q13167 xiphias gla
26	4	22.2	19	2	Q9R7I3	Q9R7I3 prochloroco
27	4	22.2	19	10	Q9S8G9	Q9S8G9 psophocarpu
28	4	22.2	20	2	Q67964	Q67964 prochloroco
29	4	22.2	20	2	Q9X3M3	Q9X3M3 prochloroco
30	4	22.2	20	2	Q67966	Q67966 prochloroco
31	4	22.2	20	2	Q9R4L9	Q9R4L9 streptomyc
32	4	22.2	20	10	Q9S8H0	Q9S8H0 psophocarpu
33	4	22.2	20	11	Q91X54	Q91X54 mus musculu
34	3	16.7	8	6	Q95M23	Q95M23 sus scrofa
35	3	16.7	8	11	Q62528	Q62528 mus spratus
36	3	16.7	9	2	Q9EZ14	Q9EZ14 sodalis glo
37	3	16.7	9	2	Q9R7J5	Q9R7J5 streptomyc
38	3	16.7	9	4	Q9UCS8	Q9UCS8 homo sapien
39	3	16.7	9	4	Q16605	Q16605 homo sapien
40	3	16.7	9	10	Q9FX10	Q9FX10 lilium long
41	3	16.7	9	10	P82429	P82429 nicotiana t
42	3	16.7	9	13	Q8AYL5	Q8AYL5 carassius a
43	3	16.7	9	13	Q8AUM7	Q8AUM7 carassius a
44	3	16.7	9	16	Q935G1	Q935G1 salmorella
45	3	16.7	10	2	Q9XBH3	Q9XBH3 bacillus ce
46	3	16.7	10	8	Q8SHA8	Q8SHA8 rhampoleon
47	3	16.7	10	13	Q9PRY8	Q9PRY8 triakis scy
48	3	16.7	11	2	Q47606	Q47606 escherichia
49	3	16.7	11	2	Q47604	Q47604 escherichia
50	3	16.7	11	7	Q19718	Q19718 homo sapien
51	3	16.7	11	10	Q8RV30	Q8RV30 zea mays (m
52	3	16.7	11	13	Q8UUP1	Q8UUP1 xenopus lae
53	3	16.7	12	4	Q9UC37	Q9UC37 homo sapien
54	3	16.7	12	4	Q8IVH0	Q8IVH0 homo sapien
55	3	16.7	12	8	P92457	P92457 ephedra sp.
56	3	16.7	12	10	P82328	P82328 pisum sativ
57	3	16.7	12	12	Q88577	Q88577 theiler's e
58	3	16.7	12	12	Q88578	Q88578 theiler's e
59	3	16.7	12	12	Q88579	Q88579 theiler's e
60	3	16.7	12	12	Q88575	Q88575 theiler's e
61	3	16.7	12	12	Q88580	Q88580 theiler's e
62	3	16.7	12	12	Q88582	Q88582 theiler's e
63	3	16.7	12	12	Q88581	Q88581 theiler's e
64	3	16.7	12	12	Q88576	Q88576 theiler's e
65	3	16.7	13	11	Q88176	Q88176 mus musculu
66	3	16.7	13	11	Q8CJ33	Q8CJ33 mus musculu
67	3	16.7	13	12	Q67604	Q67604 squash leaf
68	3	16.7	13	13	Q8JJ32	Q8JJ32 ficedula al
69	3	16.7	14	2	Q55326	Q55326 synecococc
70	3	16.7	14	2	Q43905	Q43905 azospirillu
71	3	16.7	14	2	P81715	P81715 streptomyc
72	3	16.7	14	3	P90342	P90342 saccharomyc
73	3	16.7	14	3	Q8U1G2	Q8U1G2 ashbya goss
74	3	16.7	14	4	Q9P2A2	Q9P2A2 homo sapien
75	3	16.7	14	4	Q96Q50	Q96Q50 homo sapien
76	3	16.7	14	4	Q16045	Q16045 homo sapien
77	3	16.7	14	11	Q9Z1H4	Q9Z1H4 mus musculu
78	3	16.7	15	2	Q9R531	Q9R531 thermus ch
79	3	16.7	15	3	Q9UR63	Q9UR63 emericeia
80	3	16.7	15	3	Q9URCS	Q9URCS saccharomyc
81	3	16.7	15	4	Q08947	Q08947 homo sapien
82	3	16.7	15	4	Q9UCV1	Q9UCV1 homo sapien
83	3	16.7	15	5	Q26159	Q26159 plasmodium
84	3	16.7	15	5	Q9TWQ2	Q9TWQ2 tachypleus
85	3	16.7	15	8	Q9AT15	Q9AT15 lycopersico
86	3	16.7	15	10	Q9AT15	Q9AT15 lycopersico
87	3	16.7	15	10	Q9S8N8	Q9S8N8 hordeum vul
88	3	16.7	15	10	Q9S8V2	Q9S8V2 triticum ae
89	3	16.7	15	10	Q9S8V3	Q9S8V3 triticum ae

90 Q09936 nicotiana t
 91 Q9quy3 rattus sp.
 92 Q9r4l3 mycobacteri
 93 Q9r596 micrococcus
 94 Q9ur86 candida par
 95 Q9uc65 homo sapien
 96 Q9ud41 homo sapien
 97 Q9twn7 toxoplasma
 98 Q9tr97 oryctolagus
 99 Q33429 anas platyr
 100 Q9t2r0 solanum tub

ALIGNMENTS

RESULT 1
 Q9T2K8 PRELIMINARY; PRT; 15 AA.
 AC Q9T2K8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE LHCII kinase, 64 kDa kinase (Fragment).
 OS Spinacia oleracea (Spinach).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=92183823; PubMed=1544419;
 RA Gal A., Herrmann R.G., Lottspeich F., Ohad I.;
 RT "Phosphorylation of cytochrome b6 by the LHC II kinase associated with
 the cytochrome complex.";
 RL FEBS Lett. 298:33-35(1992).
 FT NON_TER 1
 FT NON_TER 15
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1556 MW; 6E00A4F917DDF33E CRC64;

Query Match 27.8%; Score 5; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDVEK 8
 Db 5 PDVEK 9

RESULT 2
 Q9S618 PRELIMINARY; PRT; 11 AA.
 AC Q9S618;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Cytochrome b6/f complex subunit IV (Fragment).
 GN PETD.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=1220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Urbach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 sorted from the Sargasso Sea and Gulf Stream.";
 RL Limnol. Oceanog. 43:1615-1630(1998).
 DR EMBL; AF070132; AAD20740.1; -.
 FT NON_TER 11
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 KPDL 11
 Db 6 KPDL 9

RESULT 3

Q8HYM4 PRELIMINARY; PRT; 11 AA.
 AC Q8HYM4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Coagulation factor IX (Fragment).
 GN F9.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Susott E.E., Rollo W.A., Venta P.J., Ewart S.L.;
 RT "Characterization of 8 Feline Type I Markers.";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF459805; AAO15586.1; -.
 FT NON_TER 1
 FT NON_TER 11
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1169 MW; 9C8E7EFCFA05B02CA CRC64;

Query Match 22.2%; Score 4; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDVE 7
 Db 3 PDVE 6

RESULT 4

Q9R3R6 PRELIMINARY; PRT; 13 AA.
 AC Q9R3R6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Cytochrome b6/f complex subunit IV (Fragment).
 GN PETD.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=1220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Urbach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 sorted from the Sargasso Sea and Gulf Stream.";
 RL Limnol. Oceanog. 43:1615-1630(1998).
 DR EMBL; AF070222; AAD23275.1; -.
 DR EMBL; AF070221; AAD23273.1; -.
 FT NON_TER 13
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1522 MW; 4CDE4CC38013B763 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
 Db 6 KPDL 9

```

RESULT 5
Q66174
ID Q66174 PRELIMINARY; PRT; 15 AA.
AC Q66174;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Surface protein (Fragment).
OS Human coronavirus (strain 229E).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11137;
RN [1]_TaxID=11137;
RP SEQUENCE FROM N.A.
RC STRAIN=229E;
RX MEDLINE=89366667; PubMed=2701946;
RA Raabe T., Sidell S.;
RT "Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA
RT 5 unique regions.";
RL Nucleic Acids Res. 17:6387-6387(1989).
DR EMBL; X15654; CAA33680.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1834 MW; 8CE369AE77DC4015 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 8 DVEK 11

RESULT 6
Q9LB06
ID Q9LB06 PRELIMINARY; PRT; 17 AA.
AC Q9LB06;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]_TaxID=1220;
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070156; AAD23193.2; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1904 MW; CCEB69C5A202E54F CRC64;

Query Match 22.2%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db 2 KPDL 5

RESULT 7
Q9TRW1
ID Q9TRW1 PRELIMINARY; PRT; 17 AA.
AC Q9TRW1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CALDESMON-PHOSPHORYLATION site (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]_TaxID=9986;
RP SEQUENCE.
RX MEDLINE=91378498; PubMed=1898046;
RA Ikebe M., Hornick T.;
RT "Determination of the phosphorylation sites of smooth muscle caldesmon
RT by protein kinase C.";
RL Arch. Biochem. Biophys. 288:538-542(1991).
DR InterPro; IPR006018; Caldesmon_LSP.
DR Pfam; PF02029; Caldesmon; 1.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1889 MW; 77EACD3EB02F95F6 CRC64;

Query Match 22.2%; Score 4; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9
Db 8 VEKP 11

RESULT 8
Q919B0
ID Q919B0 PRELIMINARY; PRT; 17 AA.
AC Q919B0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]_TaxID=10581;
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16GCC14;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404705; AAL01367.1; -.
FT NON_TER 17
FT NON_TER 17
SQ SEQUENCE 17 AA; 1998 MW; 4471DB6BF776889B CRC64;

Query Match 22.2%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 14 DLQP 17

RESULT 9
Q9X3E9
ID Q9X3E9 PRELIMINARY; PRT; 18 AA.
AC Q9X3E9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Cytochrome b6/f complex subunit IV (fragment).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.

```

OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in *Prochlorococcus* populations flow cytometrically
RL sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMEL: AF070147; AAD20766.1; -.
FT NON TER 18
SQ SEQUENCE 18 AA; 2029 MW; EBF8A4E54FDCDE56 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db 6 KPDL 9

RESULT 10
O67971 PRELIMINARY; PRT; 18 AA.
ID O67971
AC O67971;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE B6/f complex subunit IV (Fragment).
GN PETD.
OS *Synechococcus* sp. (strain WH8103).
OC Bacteria; Cyanobacteria; Chroococcales; *Synechococcus*.
OX NCBI_TaxID=29410;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WH8103;
RX MEDLINE=98123172; PubMed=9452521;
RA Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;
RT "Rapid diversification of marine picophytoplankton with dissimilar
RT light-harvesting structures inferred from sequences of *Prochlorococcus*
RT and *Synechococcus* (Cyanobacteria)".
RL J. Mol. Evol. 46:188-201(1998).
DR EMEL: AF001492; AAC05631.1; -.
FT NON TER 18
SQ SEQUENCE 18 AA; 2098 MW; C205CA0BB21CDE4C CRC64;

Query Match 22.2%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db 6 KPDL 9

RESULT 11
Q9R4E0 PRELIMINARY; PRT; 18 AA.
ID Q9R4E0
AC Q9R4E0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Dipeptidyl aminopeptidase type I (Fragment).
OS Pseudomonas.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae.
OX NCBI_TaxID=286;
RN [1]
RP SEQUENCE.
RX MEDLINE=96200096; PubMed=8631703;
RA Ogasawara W., Ochiai K., Ando K., Yano K., Yamasaki M., Okada H.,
RA Morikawa Y.;
RT "A novel dipeptidyl aminopeptidase from *Pseudomonas* sp. strain WO24.";
RL J. Bacteriol. 178:1283-1288(1996).

SQ SEQUENCE 18 AA; 1813 MW; 369B0388C394A737 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPDV 6
Db 5 PPDV 8

RESULT 12
P82674 PRELIMINARY; PRT; 18 AA.
ID P82674
AC P82674;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mitochondrial 28S ribosomal protein S5 (MRP-S5) (Fragments).
OS *Bos taurus* (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Rutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=LIVER;
RA Koc E.C.; Burkhardt W., Blackburn K., Moseley A., Koc H.,
RA Sprenull L.L.;
RT "Identification of four proteins from the small subunit of the
RT mammalian mitochondrial ribosome using a proteomics approach.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -|- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -|- MASS SPECTROMETRY: MW=974.58; METHOD=ELECTROSPRAY; RANGE=1-8.
CC -|- SIMILARITY: BELONGS TO THE S5P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR000851; Ribosomal S5.
DR PROSITE: PS00585; RIBOSOMAL S5; PARTIAL.
KW Ribosomal protein; Mitochondrion.
FT NON TER 1
FT NON_CONS 8
FT UNSURE 17 17 OR I.
FT NON TER 18
SQ SEQUENCE 18 AA; 2127 MW; 199BC913E7E25FAF CRC64;

Query Match 22.2%; Score 4; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db 15 PDLQ 18

RESULT 13
Q9S8G8 PRELIMINARY; PRT; 18 AA.
ID Q9S8G8
AC Q9S8G8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Proline-rich protein (Fragment).
OS *Psophocarpus tetragonolobus* (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC *Psophocarpus*.
OX NCBI_TaxID=3891;
RN [1]
RP SEQUENCE.
RX MEDLINE=95277008; PubMed=7757337;
RA Esaka M., Hayakawa H.;
RT "Specific secretion of proline-rich proteins by salt-adapted winged
RT bean cells.";

RL Plant Cell Physiol. 36:441-446(1995).
SQ SEQUENCE 18 AA; 2252 MW; 4FD7D1DA18B5D94A CRC64;

Query Match 22.2%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9
DB 11 VEKP 14
|||||

RESULT 14
Q919D5 ID Q919D5 PRELIMINARY; PRT; 18 AA.
AC Q919D5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6C11;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF404692; AAL01341.1; -;
FT NON TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 14 DLQP 17
|||||

RESULT 15
Q919B3 ID Q919B3 PRELIMINARY; PRT; 18 AA.
AC Q919B3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6C11;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF404703; AAL01360.1; -;
FT NON TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 14 DLQP 17
|||||

RESULT 16
Q919B5 ID Q919B5 PRELIMINARY; PRT; 18 AA.
AC Q919B5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6C11;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF404702; AAL01362.1; -;
FT NON TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 14 DLQP 17
|||||

RESULT 17
Q919B7 ID Q919B7 PRELIMINARY; PRT; 18 AA.
AC Q919B7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6C11;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF404701; AAL01360.1; -;
FT NON TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 14 DLQP 17
|||||

RESULT 18
Q919C5 ID Q919C5 PRELIMINARY; PRT; 18 AA.
AC Q919C5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6C11;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF404703; AAL01364.1; -;
FT NON TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 14 DLQP 17
|||||

RESULT 19
Q919C5 ID Q919C5 PRELIMINARY; PRT; 18 AA.
AC Q919C5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6C11;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF404703; AAL01364.1; -;
FT NON TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 14 DLQP 17
|||||

RESULT 20
Q919C5 ID Q919C5 PRELIMINARY; PRT; 18 AA.
AC Q919C5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6C11;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF404703; AAL01364.1; -;
FT NON TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 14 DLQP 17
|||||

RESULT 21
Q919C5 ID Q919C5 PRELIMINARY; PRT; 18 AA.
AC Q919C5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6C11;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF404703; AAL01364.1; -;
FT NON TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0

```
ID Q919C5 PRELIMINARY; PRT; 18 AA.
AC Q919C5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC3;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404697; AAL01352.1; -.
FT NON TER 18
FT SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 14 DLQP 17

RESULT 19
Q919D1 ID Q919D1 PRELIMINARY; PRT; 18 AA.
AC Q919D1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC3;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404694; AAL01346.1; -.
FT NON TER 18
FT SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 14 DLQP 17

RESULT 20
Q919D3 ID Q919D3 PRELIMINARY; PRT; 18 AA.
AC Q919D3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
```

```
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC2;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404693; AAL01344.1; -.
FT NON TER 18
FT SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 14 DLQP 17

RESULT 21
Q919B9 ID Q919B9 PRELIMINARY; PRT; 18 AA.
AC Q919B9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC9;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404700; AAL01358.1; -.
FT NON TER 18
FT SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 14 DLQP 17

RESULT 22
Q919A8 ID Q919A8 PRELIMINARY; PRT; 18 AA.
AC Q919A8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC15;
```

RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RL cervical cancer isolates from Australia and New Caledonia.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF404706; AAL01369.1; -;
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
 Db 14 DLQP 17

RESULT 23

Q919C7 PRELIMINARY; PRT; 18 AA.

ID Q919C7
 AC Q919C7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE E7 protein (Fragment).
 GN E7.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16E6CC5;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RL cervical cancer isolates from Australia and New Caledonia.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF404696; AAL01350.1; -;
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
 Db 14 DLQP 17

RESULT 24

Q919C9 PRELIMINARY; PRT; 18 AA.

ID Q919C9
 AC Q919C9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE E7 protein (Fragment).
 GN E7.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16E6CC4;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RL cervical cancer isolates from Australia and New Caledonia.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF404695; AAL01348.1; -;
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
 Db 14 DLQP 17

RESULT 25

O13167 PRELIMINARY; PRT; 18 AA.

ID O13167
 AC O13167;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ribosomal protein S7 (Fragment).
 OS Xiphias gladius (Swordfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Xiphiidae; Xiphias.
 OX NCBI_TaxID=8245;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VARIOUS STRAINS;
 RA Chow S.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J26B;
 RA Chow S.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U95521; AAB58281.1; -;
 DR EMBL: U89244; AAB58379.1; -;
 DR EMBL: U95515; AAB58275.1; -;
 DR EMBL: U95516; AAB58276.1; -;
 DR EMBL: U95517; AAB58277.1; -;
 DR EMBL: U95518; AAB58278.1; -;
 DR EMBL: U95519; AAB58279.1; -;
 DR EMBL: U95520; AAB58280.1; -;
 KW Ribosomal protein.
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1978 MW; E716F226CC5BBB15 CRC64;

Query Match 22.2%; Score 4; DB 13; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EKPD 10
 Db 14 EKPD 17

RESULT 26

Q9R7I3 PRELIMINARY; PRT; 19 AA.

ID Q9R7I3
 AC Q9R7I3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE B6/f complex subunit IV (Fragment).
 GN PETD.
 OS Prochlorococcus marinus.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=1219;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MIT9107;
 RX MEDLINE=98123172; PubMed=9452521;
 RA Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;

RT "Rapid diversification of marine picophytoplankton with dissimilar
 RT light-harvesting structures inferred from sequences of Prochlorococcus
 RL and Synchococcus (Cyanobacteria).";
 RL J. Mol. Evol. 46:188-201(1998).
 DR EMBL; AF001490; AAC05627.1; -.
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 2113 MW; 1FEA1A34E54FDCDE CRC64;

Query Match 22.2%; Score 4; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
 Db 6 KPDL 9

RESULT 27

Q9S8G9 ID Q9S8G9 PRELIMINARY; PRT; 19 AA.
 AC Q9S8G9;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
 DE Proline-rich protein (Fragment).
 OS Psophocarpus tetragonolobus (Goa bean) (Asparagaceae).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 OC Psophocarpus.
 OC NCBI_TaxID=3891;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=95277008; PubMed=775737;
 RA Esaka M., Hayakawa H.;
 RT "Specific secretion of proline-rich proteins by salt-adapted winged
 RT bean cells";
 RL Plant Cell Physiol. 36:441-446(1995).
 SQ SEQUENCE 19 AA; 2118 MW; 59ED45C4F0F8779A CRC64;

Query Match 22.2%; Score 4; DB 10; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VKXP 9
 Db 7 VKXP 10

RESULT 28

O67964 ID O67964 PRELIMINARY; PRT; 20 AA.
 AC O67964;
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE B6/f complex subunit IV (Fragment).
 GN PETD.
 OS Prochlorococcus sp. (strain CCMP 1378 / MED4).
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OC NCBI_TaxID=59919;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCMP1378;
 RX MEDLINE=98123172; PubMed=9452521;
 RA Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;
 RT "Rapid diversification of marine picophytoplankton with dissimilar
 RT light-harvesting structures inferred from sequences of Prochlorococcus
 RL and Synchococcus (Cyanobacteria).";
 RL J. Mol. Evol. 46:188-201(1998).
 DR EMBL; AF001488; AAC05623.1; -.
 FT NON_TER 20

SQ SEQUENCE 20 AA; 2241 MW; C46FEA1A34E54FDC CRC64;
 Query Match 22.2%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
 Db 6 KPDL 9

RESULT 29

O9X3M3 ID O9X3M3 PRELIMINARY; PRT; 20 AA.
 AC O9X3M3;
 DT 01-NOV-1999 (TRENBLrel. 12, Created)
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
 DE Cytochrome b6/f complex subunit IV (Fragment).
 GN PETD.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OC NCBI_TaxID=1220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Urbach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 RT sorted from the Sargasso Sea and Gulf Stream";
 RL Limnol. Oceanogr. 43:1615-1630(1998).
 DR EMBL; AF070219; AAC23270.1; -.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2264 MW; C46FEA1A23D55F9C CRC64;

Query Match 22.2%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
 Db 6 KPDL 9

RESULT 30

O67966 ID O67966 PRELIMINARY; PRT; 20 AA.
 AC O67966;
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE B6/f complex subunit IV (Fragment).
 GN PETD.
 OS Prochlorococcus marinus.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OC NCBI_TaxID=1219;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NATL12;
 RX MEDLINE=98123172; PubMed=9452521;
 RA Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;
 RT "Rapid diversification of marine picophytoplankton with dissimilar
 RT light-harvesting structures inferred from sequences of Prochlorococcus
 RL and Synchococcus (Cyanobacteria).";
 RL J. Mol. Evol. 46:188-201(1998).
 DR EMBL; AF001489; AAC05625.1; -.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2259 MW; C17BEC1A34E54FDC CRC64;

Query Match 22.2%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
 Db 6 KPDL 9

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QY      8 KPD1 11
DB      ||||
        6 KPD1 9

RESULT 31
Q9R4L9
ID      Q9R4L9      PRELIMINARY;      PRT;      20 AA.
AC      Q9R4L9;
DT      01-MAY-2000 (TReMBLrel. 13, Created)
DT      01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT      01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE      P6 protein (Fragment).
OS      Streptomyces tendae.
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Streptomycineae; Streptomycetaceae; Streptomycetes.
OX      NCBI_TaxID=1932;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=95302967; PubMed=7783626;
RA      Mohrle V., Roos U., Bormann C.;
RT      "Identification of cellular proteins involved in nikkomycin production
RT      in Streptomyces tendae Tu901.";
RL      Mol. Microbiol. 15:561-571(1995).
SQ      SEQUENCE 20 AA; 2229 MW; D3E7BD4689D594FD CRC64;

Query Match      22.2%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 QPFQ 15
DB      ||||
        13 QPFQ 16

RESULT 32
Q9S8H0
ID      Q9S8H0      PRELIMINARY;      PRT;      20 AA.
AC      Q9S8H0;
DT      01-MAY-2000 (TReMBLrel. 13, Created)
DT      01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT      01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE      Proline-rich protein (Fragment).
OS      Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC      Psophocarpaceae.
OX      NCBI_TaxID=3891;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=95277008; PubMed=7757337;
RA      Esaka M., Hayakawa H.;
RT      "Specific secretion of proline-rich proteins by salt-adapted winged
RT      bean cells.";
RL      Plant Cell Physiol. 36:441-446(1995).
SQ      SEQUENCE 20 AA; 2246 MW; AEE9ED45C4F0F877 CRC64;

Query Match      22.2%; Score 4; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VEKP 9
DB      ||||
        7 VEKP 10

RESULT 33
Q91X54
ID      Q91X54      PRELIMINARY;      PRT;      20 AA.
AC      Q91X54;
DT      01-DEC-2001 (TReMBLrel. 19, Created)
DT      01-DEC-2001 (TReMBLrel. 19, Last sequence update)

QY      01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE      Unknown (Protein for IMAGE:4195625) (Fragment).
CN      1700020C11RIK.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RA      Strausberg R.;
RL      Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC012242; AAH12242.1; -
DR      MGD; MGI:1916686; 1700020C11RIK.
FT      NON TER 1
SQ      SEQUENCE 20 AA; 2278 MW; 4A7143DBC4DF384C CRC64;

Query Match      22.2%; Score 4; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VEKP 9
DB      ||||
        14 VEKP 17

RESULT 34
Q95M23
ID      Q95M23      PRELIMINARY;      PRT;      8 AA.
AC      Q95M23;
DT      01-DEC-2001 (TReMBLrel. 19, Created)
DT      01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT      01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE      Na+/K+ ATPase alpha subunit (EC 3.6.1.37) (Fragment).
GN      ATP1A1.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Pietrain;
RA      Blazkova P., Stratil A., Peelman L.J., Van Poucke M., Reiner G.,
RA      Geldermann H., Kopecky M.;
RT      "RH mapping of the porcine ATP1A1, ATP1B1, V-ATPase, IVL genes and
RT      linkage assignments of ATP1A1 and IVL to chromosome 4.";
RL      Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ344138; CAC51422.1; -.
KW      Hydrolase.
FT      NON TER 1
SQ      SEQUENCE 8 AA; 1117 MW; 604B41AB133B02D3 CRC64;

Query Match      16.7%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VEK 8
DB      ||||
        2 VEK 4

RESULT 35
Q62528
ID      Q62528      PRELIMINARY;      PRT;      8 AA.
AC      Q62528;
DT      01-JUN-1998 (TReMBLrel. 06, Created)
DT      01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT      01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE      Apolipoprotein A-II (APO-AII) (Fragment).
GN      APOA2.
OS      Mus spretus (Western wild mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RX MEDLINE=94319082; PubMed=8043949;
RA KO M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maezaki Y.,
RA Nadeau J.H.;
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";
RL Mamm. Genome 5:349-355(1994).
CC - FUNCTION: MAY STABILIZE HDL (HIGH DENSITY LIPOPROTEIN) STRUCTURE
CC BY ITS ASSOCIATION WITH LIPIDS, AND AFFECT THE HDL METABOLISM.
DR EMBL; U05692; AAB60463.1; --
DR MGD; MGI:88050; ApoA2.
DR KW Plasma; Lipid transport; HDL.
FT NON_TER 1
SQ SEQUENCE 8 AA; 827 MW; 223DDDD72DC7633B CRC64;

Query Match 16.7%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
DB 1 EXP 3

RESULT 36
ID Q9EZ14 PRELIMINARY; PRT; 9 AA.
AC Q9EZ14;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Spas (Fragment).
GN SPAS.
OS Sodalis glossinidius.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=63612;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M1;
RX MEDLINE=21117132; PubMed=11172045;
RA Dale C., Young S.A., Haydon D.T., Welburn S.C.;
RT "The insect endosymbiont Sodalis glossinidius utilizes a type III
RT secretion system for cell invasion.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1883-1888(2001).
DR EMBL; AF306650; AAG48607.1; --
FT NON_TER 9
SQ SEQUENCE 9 AA; 1035 MW; 818E633B01A33455 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
DB 6 EXP 8

RESULT 37
ID Q9R735 PRELIMINARY; PRT; 9 AA.
AC Q9R735;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FkA protein (Fragment).
GN FkA.
OS Streptomyces chrysomallus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1899;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94341259; PubMed=8062824;
RA Pahl A., Keller U.;
RT "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting
RT of two FK506-binding domains with its gene transcriptionally coupled
RT to the FKBP-12 gene.";
RL EMBL; J. 13:3472-3480(1994).
DR EMBL; Z34523; CAA84282.1; --
FT NON_TER 9
SQ SEQUENCE 9 AA; 1047 MW; 9A8BCB07633B1045 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
DB 4 EXP 6

RESULT 38
ID Q9UCS8 PRELIMINARY; PRT; 9 AA.
AC Q9UCS8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92075698; PubMed=1742316;
RA Enholm C., Boras S.E., Ienkanen H., Kirsbaum L., Metso J.,
RA Murphy B., Walker I.D.;
RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40
RT protein of human blood are different proteins which both bind to
RT apolipoprotein A-I.";
RL Blochim. Biophys. Acta 1086:255-260(1991).
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 981 MW; 7FE37775A6C7776B CRC64;

Query Match 16.7%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPD 5
DB 7 PPD 9

RESULT 39
ID Q16605 PRELIMINARY; PRT; 9 AA.
AC Q16605;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Glutathione S-transferase 2 (Fragment).
GN GSTA2 OR GST2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88330756; PubMed=3138230;
RA Chow N.W., Whang-Peng J., Kao-Shan C.S., Tam M.F., Lai H.C., Tu C.P.;
RT "Human glutathione S-transferases. The Ha multigene family encodes

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RT products of different but overlapping substrate specificities.";
 RL J. Biol. Chem. 263:12797-12800(1988).
 DR EMBL; M21867; AAA52617.1; -;
 DR EMBL; M21866; AAA35938.1; -;
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1116 MW; D168E72327633B1D CRC64;
 Query Match 16.7%; Score 3; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 EXP 9
 Db |||||
 3 EXP 5
 RESULT 40
 Q9FXLO PRELIMINARY; PRT; 9 AA.
 AC Q9FXLO;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE LIM8 protein (Fragment).
 GN LIM8.
 OS Lilium longiflorum (Trumpet lily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
 OX NCBI_TaxID=4690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Hinomoto;
 RA Uesuji H., Takase H., Hiratsuka K.;
 RT "Lilium longiflorum LIM8 gene, promoter region and partial sequence.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB050987; BAB17856.1; -;
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1021 MW; 6F8BD76685A6C2CB CRC64;
 Query Match 16.7%; Score 3; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 VQS 18
 Db |||||
 3 VQS 5
 RESULT 41
 P82429 PRELIMINARY; PRT; 9 AA.
 AC P82429;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE 44 Kda cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture.";
 RL Planta 0:0-0(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON_TER 9

SQ SEQUENCE 9 AA; 986 MW; C22CCAADG6C77776 CRC64;
 Query Match 16.7%; Score 3; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QPP 4
 Db |||||
 2 QPP 4
 RESULT 42
 Q8AYL5 PRELIMINARY; PRT; 9 AA.
 AC Q8AYL5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cytochrome P450 aromatase (Fragment).
 GN CYP19A.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
 RT "Promoter characteristics of two CYP19 genes differentially expressed
 RT in the brain and ovary of teleost fish.";
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
 DR EMBL; AF324897; AAN32618.1; -;
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1060 MW; C49E76D7272B040D CRC64;
 Query Match 16.7%; Score 3; DB 13; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 LQP 13
 Db |||||
 6 LQP 8
 RESULT 43
 Q8AUM7 PRELIMINARY; PRT; 9 AA.
 AC Q8AUM7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cytochrome P450 aromatase (Fragment).
 GN CYP19A.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
 RT "Promoter characteristics of two CYP19 genes differentially expressed
 RT in the brain and ovary of teleost fish.";
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
 DR EMBL; AF324895; AAN32616.1; -;
 DR EMBL; AF324896; AAN32617.1; -;
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;
 Query Match 16.7%; Score 3; DB 13; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEX 8
DB 8 VEX 10

RESULT 46

Q8SHA8 PRELIMINARY; PRT; 10 AA.

ID Q8SHA8
AC Q8SHA8
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE Putative membrane protein (Fragment).
GN HCM1_01C.
OS Salmonella typhi.
OG Plasmid pHCMI.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL: AL513383; CAD09867.1; -.
KW Plasmid; Complete proteome.
FT NON_TER 9
SQ SEQUENCE 9 AA; 904 MW; 5FDCD7776D86767 CRC64;

Query Match 16.7%; Score 3; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
DB 5 QPP 7

RESULT 45

Q9XBH3 PRELIMINARY; PRT; 10 AA.

ID Q9XBH3
AC Q9XBH3
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DE Celf-like protein (Fragment).
DE CELF.
GN Bacillus cereus.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 10987;
RX MEDLINE=99231848; PubMed=10217496;
RA Okstad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;
RT "genome organisation is not conserved between Bacillus cereus and
RT Bacillus subtilis.";
RL Microbiology 145:621-631(1999).
DR EMBL: AJ000394; CAB40625.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1264 MW; D3757EC3339C9D6 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 10;

QY 11 LOP 13
DB 6 LOP 8

Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEX 8
DB 8 VEX 10

RESULT 44

Q935G1 PRELIMINARY; PRT; 9 AA.

ID Q935G1
AC Q935G1
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative membrane protein (Fragment).
GN HCM1_01C.
OS Salmonella typhi.
OG Plasmid pHCMI.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL: AL513383; CAD09867.1; -.
KW Plasmid; Complete proteome.
FT NON_TER 9
SQ SEQUENCE 9 AA; 904 MW; 5FDCD7776D86767 CRC64;

Query Match 16.7%; Score 3; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
DB 5 QPP 7

RESULT 45

Q9XBH3 PRELIMINARY; PRT; 10 AA.

ID Q9XBH3
AC Q9XBH3
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DE Celf-like protein (Fragment).
DE CELF.
GN Bacillus cereus.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 10987;
RX MEDLINE=99231848; PubMed=10217496;
RA Okstad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;
RT "genome organisation is not conserved between Bacillus cereus and
RT Bacillus subtilis.";
RL Microbiology 145:621-631(1999).
DR EMBL: AJ000394; CAB40625.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1264 MW; D3757EC3339C9D6 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 10;

QY 11 LOP 13
DB 6 LOP 8

Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEX 8
DB 8 VEX 10

RESULT 44

Q935G1 PRELIMINARY; PRT; 9 AA.

ID Q935G1
AC Q935G1
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative membrane protein (Fragment).
GN HCM1_01C.
OS Salmonella typhi.
OG Plasmid pHCMI.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL: AL513383; CAD09867.1; -.
KW Plasmid; Complete proteome.
FT NON_TER 9
SQ SEQUENCE 9 AA; 904 MW; 5FDCD7776D86767 CRC64;

Query Match 16.7%; Score 3; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
DB 5 QPP 7

RESULT 45

Q9XBH3 PRELIMINARY; PRT; 10 AA.

ID Q9XBH3
AC Q9XBH3
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DE Celf-like protein (Fragment).
DE CELF.
GN Bacillus cereus.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 10987;
RX MEDLINE=99231848; PubMed=10217496;
RA Okstad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;
RT "genome organisation is not conserved between Bacillus cereus and
RT Bacillus subtilis.";
RL Microbiology 145:621-631(1999).
DR EMBL: AJ000394; CAB40625.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1264 MW; D3757EC3339C9D6 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 10;

QY 11 LOP 13
DB 6 LOP 8

Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEX 8
DB 8 VEX 10

RESULT 44

Q935G1 PRELIMINARY; PRT; 9 AA.

ID Q935G1
AC Q935G1
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative membrane protein (Fragment).
GN HCM1_01C.
OS Salmonella typhi.
OG Plasmid pHCMI.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Lars


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RESULT 48
Q47606
ID Q47606 PRELIMINARY; PRT; 11 AA.
AC Q47606;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE REase protein (Fragment).
GN REASE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63622; AAA24562.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1370 MW; 68C1FF9959CB133B CRC64;

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEK 8
Db 3 VEK 5

RESULT 49
Q47604
ID Q47604 PRELIMINARY; PRT; 11 AA.
AC Q47604;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Rease protein (Fragment).
GN REASE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63621; AAA24560.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1296 MW; 3039A71A34472AB7 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDL 11
Db 4 PDL 6

RESULT 50
O19718
ID O19718 PRELIMINARY; PRT; 11 AA.
AC O19718;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

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DE MHC class II antigen (Fragment).
CN HLA-DRB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86206008; PubMed=3458223;
RA Gregersen P.K., Shen M., Song Q.-L., Merzlyan P., Decar S., Seki T.,
RA Maccari J., Goldberg D., Murphy H., Schwenzler J., Wang C.Y.,
RA Winchester R.J., Nepom G.T., Silver J.;
RT "Molecular diversity of HLA-DR4 haplotypes.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2642-2646(1986).
DR EMBL; M15074; AAA59810.1; -.
FT NON TER 1
SQ SEQUENCE 11 AA; 1143 MW; 4E6AADA061B76D7 CRC64;

Query Match 16.7%; Score 3; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LQP 13
Db 4 LQP 6

RESULT 51
Q8RV30
ID Q8RV30 PRELIMINARY; PRT; 11 AA.
AC Q8RV30;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Methionine adenosyltransferase 1-like protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAT clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Various strains;
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
RA Morgante M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF486085; AAL85893.1; -.
DR EMBL; AF486086; AAL85894.1; -.
DR EMBL; AF486087; AAL85895.1; -.
DR EMBL; AF486088; AAL85896.1; -.
DR EMBL; AF486089; AAL85897.1; -.
DR EMBL; AF486090; AAL85898.1; -.
DR EMBL; AF486091; AAL85899.1; -.
DR EMBL; AF486092; AAL85900.1; -.
DR EMBL; AF486093; AAL85901.1; -.
DR EMBL; AF486094; AAL85902.1; -.
DR EMBL; AF486095; AAL85903.1; -.
DR EMBL; AF486096; AAL85904.1; -.
DR EMBL; AF486097; AAL85905.1; -.
DR EMBL; AF486098; AAL85906.1; -.
DR EMBL; AF486099; AAL85907.1; -.
DR EMBL; AF486100; AAL85908.1; -.
DR EMBL; AF486101; AAL85909.1; -.
DR EMBL; AF486102; AAL85910.1; -.
DR EMBL; AF486104; AAL85911.1; -.
DR EMBL; AF486105; AAL85912.1; -.
DR EMBL; AF486106; AAL85913.1; -.
DR EMBL; AF486107; AAL85914.1; -.
DR EMBL; AF486108; AAL85915.1; -.
DR EMBL; AF486109; AAL85916.1; -.
DR EMBL; AF486110; AAL85917.1; -.

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DR EMBL; AF486111; AAL85918.1; -.
DR EMBL; AF486112; AAL85919.1; -.
DR EMBL; AF486113; AAL85920.1; -.
DR EMBL; AF486114; AAL85921.1; -.
DR EMBL; AF486115; AAL85922.1; -.
DR EMBL; AF486116; AAL85923.1; -.
DR EMBL; AF486117; AAL85924.1; -.
DR EMBL; AF486118; AAL85925.1; -.
KW Transferase. 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1183 MW; 448D42ED3B05B337 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
Db |||
7 EXP 9

RESULT 52
Q8UUP1 PRELIMINARY; PRT; 11 AA.
ID Q8UUP1
AC Q8UUP1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Beta-TrCP protein (Fragment).
GN BETA-TRCP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Carnevali F.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ballarino M.;
RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus laevis";
RL Thesis (2001), Department of Genetica e Biologia Molecolare, University of Rome La Sapienza, Rome, Italy.
DR EMBL; AJ428930; CAD21927.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
Db |||
9 QPP 11

RESULT 53
Q9UC37 PRELIMINARY; PRT; 12 AA.
AC Q9UC37;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Alpha B crystallin fragment 5 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

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RX MEDLINE=92218434; PubMed=1560006;
RA Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
RT "Copurification of small heat shock protein with alpha B crystallin from human skeletal muscle.";
RL J. Biol. Chem. 267:7718-7725(1992).
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1268 MW; D37BD529CCCB1B2CD CRC64;

Query Match 16.7%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
Db |||
2 EXP 4

RESULT 54
Q8IVH0 PRELIMINARY; PRT; 12 AA.
ID Q8IVH0
AC Q8IVH0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Truncated PAX6 protein (Fragment).
GN PAX6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Neethirajan G., Krishnadas S.R., Vijayalakshmi P., Sundaresan P.;
RT "Mutation analysis in Human PAX6 gene of Aniridia.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548390; AAN86817.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1511 MW; 9E169541A67B51F1 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
Db |||
8 PDV 10

RESULT 55
P92457 PRELIMINARY; PRT; 12 AA.
ID P92457
AC P92457;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Chloroplast subunit of light-independent protochlorophyllide reductase (Fragment).
DE (Fragment).
GN CHLB GENE.
OS Euphorbia sp.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Gnetales; Gnecopsida; Ephedrales; Ephedraceae;
OC Ephedra.
OX NCBI_TaxID=41991;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263785; PubMed=9108142;
RA Karpinska B., Karpinski S., Hallgren J.E.;
RT "The chlB gene encoding a subunit of light-independent protochlorophyllide reductase is edited in chloroplast of conifers.";
RL Curr. Genet. 31:343-347(1997).
DR EMBL; X98573; CAA67182.1; -.

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Query Match      16.7%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PDV 6
      |||
Db      8 PDV 10

RESULT 60
Q88575 PRELIMINARY; PRT; 12 AA.
AC Q88575;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FA;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80883; AAA73154.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match      16.7%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PDV 6
      |||
Db      8 PDV 10

RESULT 61
Q88580 PRELIMINARY; PRT; 12 AA.
AC Q88580;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vilyuisk;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80888; AAA73159.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match      16.7%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PDV 6

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Db      8 PDV 10
      |||

RESULT 62
Q88582 PRELIMINARY; PRT; 12 AA.
AC Q88582;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TO(Vale);
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80890; AAA73161.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match      16.7%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PDV 6
      |||
Db      8 PDV 10

RESULT 63
Q88581 PRELIMINARY; PRT; 12 AA.
AC Q88581;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WW;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80889; AAA73160.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match      16.7%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PDV 6
      |||
Db      8 PDV 10

RESULT 64

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Q88576
ID Q88576 PRELIMINARY; PRT; 12 AA.
AC Q88576;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DE Myoneurin (Fragment)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment)
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MEH;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence."
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80884; AAA73155.1; -.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
DB 8 PDV 10

RESULT 65
ID Q88176 PRELIMINARY; PRT; 13 AA.
AC Q88176;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM1 OR NCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb-C; TISSUE=Liver;
RX MEDLINE=98250618; PubMed=9582442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
of a muscle-specific exon in the mouse NCAM gene."
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGI; MGI:97281; Ncam1.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13
DB 7 LQP 9

RESULT 66
ID Q8CJ33 PRELIMINARY; PRT; 13 AA.
AC Q8CJ33;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Myoneurin (Fragment)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C; TISSUE=Kidney;
RX MEDLINE=20334280; PubMed=10873615;
RA Alliel P.M., Seddiqi N., Goudou D., Cifuentes-Diaz C., Romero N.,
RA Velasco E., Rieger F., Perin J.P.;
RT "Myoneurin, a novel member of the BTR/POZ-zinc finger family highly
expressed in human muscle."
RL Biochem. Biophys. Res. Commun. 273:385-391(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C; TISSUE=Kidney;
RA Bitoun M., Perin J.P., Seddiqi N., Goudou D., Camuzat A., Mattei M.G.,
RA Rieger F., Alliel P.M.;
RT "The human and mouse myoneurin genes: Genomic organization, splice
variants, chromosomal mapping and flanking genes."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530454; AAN28707.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1445 MW; 9CB68B708CA1597E CRC64;

Query Match 16.7%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
DB 1 EXP 3

RESULT 67
ID Q67604 PRELIMINARY; PRT; 13 AA.
AC Q67604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Movement protein (Fragment).
GN BC1.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Los Mochis 1;
RA Loniello A.O., Ford R.E., Salinas R.A., Morales F.J., Maxwell D.P.;
RT "Diversity among geminiviruses associated with vegetables from Valle
del Fuerte, Sinaloa, Mexico."
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; L27273; AAA47820.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1376 MW; D471DE4D634E76C2 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
DB 7 QPP 9

RESULT 68

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Q8UJ32
ID Q8UJ32 PRELIMINARY; PRT; 13 AA.
AC Q8UJ32;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 37LRP/p40 (Fragment).
OS Picedula albicollis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=59894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B8;
RX MEDLINE=21918460; PubMed=11918793;
RA Primer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454232; AAM22911.1; -.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1674 MW; 18331625CF9559DB CRC64;

Query Match 16.7%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDL 11
DB 3 PDL 5

RESULT 69
Q55326 PRELIMINARY; PRT; 14 AA.
ID Q55326;
AC Q55326;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative ORF1 (Fragment)
OS Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR6;
RX MEDLINE=92201692; PubMed=1551590;
RA Rhie E., Stireswalt V.L., Gasparich G.E., Bryant D.A.;
RT "The psac genes of Synechococcus sp. PCC7002 and Cyanophora paradoxa:
RT cloning and sequence analysis";
RL Gene 112:123-128(1992).
DR EMBL; M86238; AAA27351.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1590 MW; 9D5226BDCB998BCA CRC64;

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13
DB 12 LQP 14

RESULT 70
Q43905 PRELIMINARY; PRT; 14 AA.
ID Q43905;
AC Q43905;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Q8UJ32
ID Q8UJ32 PRELIMINARY; PRT; 13 AA.
AC Q8UJ32;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 37LRP/p40 (Fragment).
OS Picedula albicollis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=59894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B8;
RX MEDLINE=21918460; PubMed=11918793;
RA Primer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454232; AAM22911.1; -.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1674 MW; 18331625CF9559DB CRC64;

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13
DB 12 LQP 14

RESULT 70
Q43905 PRELIMINARY; PRT; 14 AA.
ID Q43905;
AC Q43905;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Dinitrogenase reductase (Fragment).
OS Azospirillum brasilense.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Azospirillum.
OX NCBI_TaxID=192;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sp7;
RX MEDLINE=92250433; PubMed=1577701;
RA Zhang Y., Burris R.H., Roberts G.P.;
RT "Cloning, sequencing, mutagenesis, and functional characterization of
RT drat and drag genes from Azospirillum brasilense.";
RL J. Bacteriol. 174:3364-3369(1992).
DR EMBL; M87319; AAA22182.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1485 MW; D0F9B16263390219 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
DB 8 EXP 10

RESULT 71
P81715 PRELIMINARY; PRT; 14 AA.
ID P81715;
AC P81715;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Leupeptin-inactivating enzyme (EC 3.4.24.-) (LIE) (Fragment).
OS Streptomyces exfoliatus (Streptomyces hydrogenans).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1905;
RN [1]
RP SEQUENCE.
RC STRAIN=SMF13;
RX PubMed=9531495;
RA Kim I.S., Kim Y.B., Lee K.J.;
RT "Characterization of the leupeptin-inactivating enzyme from
RT Streptomyces exfoliatus SMF13 which produces leupeptin.";
RL Biochem. J. 331:539-545(1998).
CC -|- FUNCTION: A LEUCINE-SPECIFIC METALLOPROTEASE THAT PLAYS A ROLE IN
CC CONTROLLING THE AMOUNT OF LEUPEPTIN DURING COLONY DEVELOPMENT.
CC OPTIMUM PH IS 9.0 AND TEMPERATURE IS 40 DEGREES CELSIUS.
CC -|- FUNCTION: DEGRADATES LEUPEPTIN INTO THREE COMPONENTS, ACETYL-
CC LEUCINE, LEUCINE AND ARGININAL.
CC -|- CATALYTIC ACTIVITY: HAS A STRICT PREFERENCE FOR LEUCINE AT THE P1
CC SITE.
CC -|- ENZYME REGULATION: ACTIVITY IS INHIBITED BY METALLOPROTEASE
CC INHIBITORS AND ACTIVATED BY MG2+ AND CA2+.
CC -|- SUBUNIT: MONOMER.
CC -|- SUBCELLULAR LOCATION: SECRETED.
KW Hydrolase; Metalloprotease.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1373 MW; 14D627940C973260 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPD 5
DB 4 PPD 6

RESULT 72
P90342 PRELIMINARY; PRT; 14 AA.
ID P90342

AC P90342;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE ORF YER030C (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RA Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MIPS;
 RA Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95112788; PubMed=7813418;
 RA Feldmann H., Aigle M., Aljinovic G., Andre B., Baclet M.C., Barthe C.,
 RA Baur A., Becam A.M., Biteau N., Boles E., Brandt T., Brendel M.,
 RA Brueckner M., Bussereau F., Christiansen C., Contreras R., Crouzet M.,
 RA Cziepluch C., Demolis N., Delaveau T., Doignon F., Domdey H.,
 RA Duesternus S., Dubois E., Dujon B., El Bakkoury M., Entian K.D.,
 RA Feuerhahn M., Fiers W., Fobo G.M., Fritz C., Gassenhuber H.,
 RA Glansdorff N., Goffeau A., Grivell L.A., De haan M., Hein C.,
 RA Herbert C.J., Hollenberg C.P., Holmstrom K., Jacq C., Jacquet M.,
 RA Jauniaux J.C., Jonniaux J.L., Kallio T., Klesau P., Kirchrath L.,
 RA Koetter P., Korol S., Liebl S., Logghe M., Lohan A.J.E., Louis E.J.,
 RA Li Z.Y., Maat M.J., Mallet L., Mannhaupt G., Messenguy F., Miosga T.,
 RA Molenans F., Mueller S., Nasr F., Obermaier B., Perea J., Pierard A.,
 RA Piravandi E., Pohl F.M., Pohl T.M., Potier S., Proft M., Farnelle B.,
 RA Ramezani Rad M., Rieger M., Rose M., Schaeff-Gerstenschlaeger I.,
 RA Scherens B., Schwarzlose C., Skala J., Slonimski P.P., Smits P.H.M.,
 RA Souciet J.L., Steensma H.Y., Stucka R., Urestarazu A.,
 RA Van der Aart Q.J., Van Dyck L., Vassarotti A., Vetter I.,
 RA Vierendeels F., Vissers S., Wagner G., de Wergifosse P., Wolfe K.H.,
 RA Zagulski M., Zimmermann F.K., Mewes H.W., Kleine K.;
 RT "Complete DNA sequence of yeast chromosome II.";
 RL EMBO J. 13:5795-5809(1994).
 DR EMBL; Z35957; CAA85041.1; -.
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1657 MW; C6B3A4A2E8495212 CRC64;

Query Match 16.7%; Score 3; DB 3; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
 Db 12 PDV 14

RESULT 73
 Q8J1G2
 ID Q8J1G2 PRELIMINARY; PRT; 14 AA.
 AC Q8J1G2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE YPL156 (Fragment).
 GN YPL156.
 OS Ashbya gossypii (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Ashbya.
 OX NCBI_TaxID=33169;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP Alberti-Segui C., Dietrich F., Philippsen P.;
 RA "Identification of kinesin-related proteins in the filamentous fungus
 RT Ashbya gossypii."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF378570; AAN87139.1; -.
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1646 MW; 8C3A12EB808B1D15 CRC64;
 Query Match 16.7%; Score 3; DB 3; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 VQS 18
 Db 5 VQS 7

RESULT 74
 Q9P2A2
 ID Q9P2A2 PRELIMINARY; PRT; 14 AA.
 AC Q9P2A2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Truncated aldo-keto reductase (fragment).
 GN TRUNCATED AKR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=20138537; PubMed=10672042;
 RA Nishizawa M., Nakajima T., Yasuda K., Kanzaki H., Sasaguri Y.,
 RA Watanabe K., Ito S.;
 RT "Close kinship of human 20alpha-hydroxysteroid dehydrogenase gene with
 RL three aldo-keto reductase genes.";
 RL Genes Cells 5:111-125(2000).
 DR EMBL; AB037903; BAA92888.1; -.
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1632 MW; 47EB1EE28D59A8D7 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13
 Db 7 LQP 9

RESULT 75
 Q96Q50
 ID Q96Q50 PRELIMINARY; PRT; 14 AA.
 AC Q96Q50;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Mitochondrial ribosomal protein L33 (fragment).
 GN MRPL33.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21429115; PubMed=11543634;
 RA Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.,
 RA Watanabe K., Tanaka T.;
 RT "The human mitochondrial ribosomal protein genes: Mapping of 54 genes
 RL to the chromosomes and implications for human disorders.";
 RL Genomics 77:65-70(2001).
 DR EMBL; AB051623; BAB54951.1; -.
 KW Ribosomal protein.
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1744 MW; 64ED243E9AED663B CRC64;

Query Match 16.7%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEK 8
Db 6 VEK 8

Search completed: November 25, 2003, 18:25:14
Job time : 46.4223 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 58.3085 Seconds
(without alignments)
48.999 Million cell updates/sec

Title: US-09-641-801-3

Perfect score: 18

Sequence: 1 DQPPDVKEKPLQPFQVQS 18

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

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23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	22	Colostrinin derive
2	18	100.0	18	22	Colostrinin peptid
3	18	100.0	18	22	Colostrinin peptid
4	18	100.0	18	22	Colostrinin peptid
5	18	100.0	18	22	Ewe colostrinin pe
6	18	100.0	18	23	Colostrinin consti
7	18	100.0	18	23	Colostrinin consti
8	18	100.0	18	23	Neural cell regula
9	5	27.8	8	23	Ewe colostrinin pe
					Human papillomavir

10	5	27.8	10	22	AAG96833	Human complementar
11	5	27.8	15	6	AAP50841	Sequence of colony
12	5	27.8	15	9	AAP82092	HRV2-derived pepti
13	5	27.8	15	19	AAW75695	M. tuberculosis 32
14	5	27.8	15	19	AAW75696	M. tuberculosis 32
15	5	27.8	15	23	ABG67986	Human ADPI tryptic
16	5	27.8	15	23	ABG67986	Short chain dehydr
17	5	27.8	19	23	ABG60992	Dirofilaria immiti
18	5	27.8	19	23	ABG60992	D. immitis transgl
19	5	27.8	20	12	AAAR11303	Recombinant 275-29
20	5	27.8	20	12	AAAR11404	Human rhinovirus T
21	4	22.2	4	22	AAAS5927	Human leptin fragm
22	4	22.2	5	19	AAW45571	Amino-terminal pro
23	4	22.2	5	23	ABO8941	Peptide #4 used in
24	4	22.2	6	15	AAAS5954	Peptide signal seq
25	4	22.2	6	22	AAAG63056	Amino acid sequenc
26	4	22.2	6	23	AAAG6432	Vector encoded pep
27	4	22.2	6	24	ABUS6263	Peptide binding to
28	4	22.2	7	14	AAAR33159	HPV E7 protein - R
29	4	22.2	7	22	AAW44291	H11 binding site c
30	4	22.2	8	12	AAAR10631	Human Papilloma Vi
31	4	22.2	8	14	AAAR33158	HPV E7 protein - R
32	4	22.2	8	15	AAAR46821	Phytase derived pe
33	4	22.2	8	15	ABG70878	R. rhodochrous nit
34	4	22.2	9	12	AAAR10635	Human Papilloma Vi
35	4	22.2	9	14	AAAR33157	HPV E7 protein - R
36	4	22.2	9	14	AAAR33170	HPV E7 protein - R
37	4	22.2	9	14	AAAR43741	MHC Class I allele
38	4	22.2	9	14	AAAR43742	MHC Class I allele
39	4	22.2	9	15	AAAS9257	Peptide fragment (
40	4	22.2	9	15	AAAR61700	HLA-A2.1 algorithm
41	4	22.2	9	15	AAAR73799	Antigen fragment 1
42	4	22.2	9	15	AAAR73800	Antigen fragment 1
43	4	22.2	9	15	AAAR73796	Antigen fragment 1
44	4	22.2	9	16	AAAR80939	Peptide for increa
45	4	22.2	9	16	AAAR78899	HPV16 E7 11-19 cyt
46	4	22.2	9	16	AAAR78894	HPV16 E7 12-20 cyt
47	4	22.2	9	18	AAW39662	HPV16/18 E7 peptid
48	4	22.2	9	18	AAW39662	HPV16/18 E7 peptid
49	4	22.2	9	18	AAW36590	Hepatitis B virus
50	4	22.2	9	19	AAW78893	Human papillomavir
51	4	22.2	9	19	AAW54766	Peptide from HPV 1
52	4	22.2	9	19	AAW54767	Peptide from HPV 1
53	4	22.2	9	20	AAW48125	Immunogenic peptid
54	4	22.2	9	20	AAW48125	Immunogenic peptid
55	4	22.2	9	20	AAW48125	Potential T cell e
56	4	22.2	9	20	AAW28526	Beta-1 integrin ce
57	4	22.2	9	20	AAW10346	T cell epitope/MHC
58	4	22.2	9	20	AAW10511	HLA Class I motif
59	4	22.2	9	21	AAAB19059	Amino acid sequenc
60	4	22.2	9	21	AAAB33705	MHC class I associ
61	4	22.2	9	21	AAW96374	HLA-A2 binding pep
62	4	22.2	9	21	AAW96374	Telomerase peptide
63	4	22.2	9	21	AAW96658	Telomerase peptide
64	4	22.2	9	22	AAAG93801	Human papilloma vi
65	4	22.2	9	22	AAAG88547	HER2/NEU DR superm
66	4	22.2	9	22	AAAG88711	HER2/NEU DR 3a moc
67	4	22.2	9	22	AAAG88865	HER2/neu epitope B
68	4	22.2	9	22	AAAB95951	MHC class-I associ
69	4	22.2	9	22	AAAB95999	HPV 16 E7 A2 MHC-b
70	4	22.2	9	22	AAAB96001	HPV 16 E7 A2 MHC-b
71	4	22.2	9	22	AAJ03011	Hepatitis C virus
72	4	22.2	9	22	AAAB20215	HPV strain 16 E7 p
73	4	22.2	9	22	AAAB71116	Polylinker site fr
74	4	22.2	9	22	AAAB76118	Tumour associated
75	4	22.2	9	23	ABG80028	MHC class I molecu
76	4	22.2	9	23	ABG80194	MHC class I molecu
77	4	22.2	9	23	ABG69555	Human CRPI tryptic
78	4	22.2	9	23	AAW49925	Human D40 associat
79	4	22.2	9	23	AAW49948	Human D40 associat
80	4	22.2	9	23	AAU82137	Human papillomavir
81	4	22.2	9	23	AAU82137	Human papillomavir
82	4	22.2	9	23	AAU82236	Human papillomavir

83 4 22.2 9 23 AAU82237 Human papillomavir
 84 4 22.2 9 23 AAU82288 Human papillomavir
 85 4 22.2 9 23 AAU82289 Human papillomavir
 86 4 22.2 9 23 AAU82344 Human papillomavir
 87 4 22.2 9 23 AAU82344 f8 phage-displayed
 88 4 22.2 9 24 AAE13683 Human cancer-relat
 89 4 22.2 9 24 ABR04681 Human cancer-relat
 90 4 22.2 9 24 ABR05301 Human cancer-relat
 91 4 22.2 9 24 ABR05467 Human cancer-relat
 92 4 22.2 9 24 ABR05481 Human cancer-relat
 93 4 22.2 9 24 ABR20198 Human cancer-relat
 94 4 22.2 9 24 ABR20227 Human cancer-relat
 95 4 22.2 9 24 ABR20449 Human cancer-relat
 96 4 22.2 9 24 ABR20594 Human cancer-relat
 97 4 22.2 9 24 ABR20830 Human cancer-relat
 98 4 22.2 9 24 ABR20995 Human cancer-relat
 99 4 22.2 9 24 ABR21239 Human cancer-relat
 100 4 22.2 9 24 ABR21594 Human cancer-relat
 100 4 22.2 9 24 ABR21619 Human cancer-relat

ALIGNMENTS

RESULT 1
 AAB72248
 ID AAB72248 standard; peptide; 18 AA.
 AC AAB72248;
 DT 14-MAY-2001 (first entry)
 XX Colostrinin derived cytokine inducing peptide SEQ ID 3.
 DE Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX Synthetic.
 OS WO200111937-A2.
 XX 22-FEB-2001.
 XX 17-AUG-2000; 2000WO-US22818.
 XX 17-AUG-1999; 99US-0149311.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 WPI; 2001-202804/20.
 XX Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -
 XX Claim 1; Page 34; 50pp; English.
 XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response/modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.

XX SQ Sequence 18 AA;
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.2e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DQPPDVEKPDLPQFQVQS 18
 Db 1 DQPPDVEKPDLPQFQVQS 18
 RESULT 3
 AAB72534
 ID AAB72534 standard; Peptide; 18 AA.
 AC AAB72534;
 XX 09-MAY-2001 (first entry)
 XX Colostrinin peptide #3.
 XX Dermatological; oxidative stress regulator; colostrinin.
 XX Unidentified.
 XX WO200112650-A2.
 XX 22-FEB-2001.
 XX 17-AUG-2000; 2000WO-US22665.
 XX 17-AUG-1999; 99US-0149310.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Stanton GJ, Hughes TK, Boldogh I;
 WPI; 2001-218342/22.
 XX Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -
 XX Claim 6; Page 25; 48pp; English.
 XX The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 18 AA;
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.2e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DQPPDVEKPDLPQFQVQS 18
 Db 1 DQPPDVEKPDLPQFQVQS 18
 RESULT 3
 AAB72534
 ID AAB72534 standard; Peptide; 18 AA.
 AC AAB72534;
 XX 09-MAY-2001 (first entry)
 XX Colostrinin peptide #3.
 XX Dermatological; oxidative stress regulator; colostrinin.
 XX Unidentified.
 XX WO200112650-A2.
 XX 22-FEB-2001.
 XX 17-AUG-2000; 2000WO-US22665.
 XX 17-AUG-1999; 99US-0149310.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Stanton GJ, Hughes TK, Boldogh I;
 WPI; 2001-218342/22.
 XX Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -
 XX Claim 6; Page 25; 48pp; English.
 XX The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.

DE Colostrinin peptide #3.
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX
 OS Unidentified.
 XX
 PN WO200112651-A2.
 XX
 XX 22-FEB-2001.
 PD
 XX 17-AUG-2000; 2000WO-US22774.
 PF
 XX 17-AUG-1999; 99US-0149633.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Boldogh I;
 PI
 XX WPI; 2001-226545/23.
 DR
 XX Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. NO. 4.2e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DQPPDVERPDLQPFQVQS 18
 DB 1 DQPPDVERPDLQPFQVQS 18
 XX
 RESULT 4
 AAB59325
 ID AAB59325 standard; Peptide; 18 AA.
 XX
 AC AAB59325;
 XX
 DT 21-MAR-2001 (first entry)
 DE
 DE Ewe colostrinin peptide fragment B-10.
 XX
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 OS Ovis sp.
 XX
 XX WO2000075173-A2.
 PN
 PD 14-DEC-2000.
 XX
 XX 02-JUN-2000; 2000WO-GB02128.
 PF
 XX 02-JUN-1999; 99GB-0012852.
 PR
 XX (REGE-) REGEN THERAPEUTICS PLC.
 PA
 XX Georgiades JA;
 PI
 XX WPI; 2001-071058/08.
 DR
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 PS Claim 7; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 100.0%; Score 18; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. NO. 4.2e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DQPPDVERPDLQPFQVQS 18
 DB 1 DQPPDVERPDLQPFQVQS 18
 XX
 RESULT 5
 AAE20230
 ID AAE20230 standard; peptide; 18 AA.
 XX
 AC AAE20230;
 XX
 DT 18-JUN-2002 (first entry)
 DE
 DE Colostrinin constituent peptide #3.
 XX
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnery.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 18
 FT /note= "Optionally C-terminal amide"
 XX
 PN WO200213850-A1.
 XX
 PD 21-FEB-2002.
 PF
 PF 17-AUG-2000; 2000WO-US22776.
 XX
 XX 17-AUG-2000; 2000WO-US22776.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Stanton GJ, Hughes TK, Boldogh I;
 PI
 XX WPI; 2002-269151/31.
 DR
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 XX
 PS Claim 6; Page 25; 51pp; English.
 XX
 CC The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.2e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQFQVQS 18
 Db 1 DQPPDVEKPDLPQFQVQS 18

RESULT 6

AA051038
 ID AAM51038 standard; Peptide; 18 AA.

AC AAM51038;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide.

KW Colostrinin; colostrum; immunomodulator; cardiovascular;
 blood cell regulator; cytokine inducer; beta-casein; human.

OS Homo sapiens.

FH Key Location/Qualifiers
 FT Modified-site 18
 FT /note= "Optional C-terminal amidation"

PN WO200213849-A1.

PD 21-FEB-2002.

PF 17-AUG-2000; 2000WO-US22775.

PR 17-AUG-2000; 2000WO-US22775.

PA (TEXA) UNIV TEXAS SYSTEM.

PA (REGG-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue

PS Claim 1; Page 34; 54pp; English.

CC The present sequence is that of a colostrinin constituent peptide
 CC that is preferred for use as an immunological regulator and as a
 CC blood cell regulator in claimed methods of the invention. It is
 CC classified as having a beta-casein homologue precursor. Methods
 CC are claimed for: inducing a cytokine in a cell by contact with an
 CC immunological regulator, where the cell is present in a cell
 CC culture, a tissue, an organ or an organism, and the cell is
 CC mammalian, including human; modulating an immune response in a cell
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a
 CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator
 CC is administered topically or as part of a dietary supplement, and
 CC where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation
 CC by contacting blood cells with a blood cell regulator, where the
 CC blood cells are present in a cell culture or an organism, are
 CC mammalian or human, and where the blood cells are increased in
 CC number or differentiated; and a method for modulating blood cell
 CC proliferation in a patent. A claimed cytokine-inducing composition
 CC comprises a pharmaceutical carrier and an active agent such as the
 CC present peptide. Cytokines induced by this peptide in human
 CC leucocyte cultures include interferon-gamma, tumour necrosis
 CC factor-alpha, interleukin-6 and interleukin-10. It was one of the
 CC best overall inducers in almost all cytokine and blood cell
 CC proliferation experiments conducted.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.2e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQFQVQS 18

Db 1 DQPPDVEKPDLPQFQVQS 18

RESULT 7

AA014579
 ID AAO14579 standard; peptide; 18 AA.

AC AAO14579;

DT 27-MAY-2002 (first entry)

DE Neural cell regulatory colostrinin peptide 3.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

OS Unidentified.

FH Key Location/Qualifiers
 FT Modified-site 18
 FT /note= "Optional C-terminal amide"

PN WO200213851-A1.

PD 21-FEB-2002.

PF 17-AUG-2000; 2000WO-US22777.

PR 17-AUG-2000; 2000WO-US22777.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Boldogh I, Stanton JG, Hughes TK;

DR WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog

PS Claim 7; Page 21; 37pp; English.

CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich

CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.2e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVKEPDLQPFQVQS 18
 |||||
 Db 1 DQPPDVKEPDLQPFQVQS 18

RESULT 8

AA859355
 ID AAB59355 standard; Peptide; 19 AA.

AC AAB59355;

DT 21-MAR-2001 (first entry)

DE Ewe colostrinin peptide fragment derived sequence #15.

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

OS Ovis sp.

PN WO200075173-A2.

PD 14-DEC-2000.

PF 02-JUN-2000; 2000WO-GB02128.

PR 02-JUN-1999; 99GB-0012852.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Georgiades JA;

DR WPI; 2001-071058/08.

XX Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -

PS Claim 8; Page 27; 63pp; English.

XX The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrum. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.

XX Sequence 19 AA;

Query Match 100.0%; Score 18; DB 22; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.4e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVKEPDLQPFQVQS 18
 |||||
 Db 2 DQPPDVKEPDLQPFQVQS 19

RESULT 9

AAU82343

ID AAU82343 standard; Peptide; 8 AA.

AC AAU82343;

XX 09-APR-2002 (first entry)

DE Human papillomavirus (HPV) E7 antigenic peptide #229.

KW Human; human papillomavirus; HPV; E7 antigen; dermatological; virucide;
 KW cytostatic; heat shock protein; hsp; anogenital wart; plantar wart;
 KW cervical cancer; cervical dysplasia; anal cancer; anal dysplasia;
 KW recurrent respiratory papillomatosis.

XX Homo sapiens.

PN WO200200242-A2.

PD 03-JAN-2002.

PF 26-JUN-2001; 2001WO-US20240.

PR 26-JUN-2000; 2000US-214202P.

PA (STES-) STESSEN BIOTECHNOLOGIES CORP.

XX Neefe J, Goldstone S, Winnett M, Siegel M;

XX WPI; 2002-130834/17.

XX Treating human papillomavirus infection, in a subject, involves
 PT administering a fusion protein comprising a protein of HPV which is
 PT different from the type of HPV that causes the disease or condition -

PS Example; Page 27; 34pp; English.

XX The invention relates to treating a disease or condition associated with
 CC a human papillomavirus (HPV) infection, comprising administering a fusion
 CC protein of a protein of HPV, or its antigenic fragment, which is
 CC different from the type of HPV that causes the disease or condition, and
 CC a heat shock protein (hsp), or its immunostimulatory fragment. The fusion
 CC proteins are useful for treating diseases or conditions associated with
 CC HPV, such as anogenital warts, plantar warts, cervical cancer, cervical
 CC dysplasia, anal cancer, anal dysplasia, or recurrent respiratory
 CC papillomatosis. Sequences AAU82115-AAU82434 represent HPV E7 antigenic
 CC peptides of the invention.

XX Sequence 8 AA;

Query Match 27.8%; Score 5; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPDV 6
 |||||
 Db 2 QPPDV 6

RESULT 10

AAAG96833

ID AAG96833 standard; Peptide; 10 AA.

AC AAG96833;

DT 18-SEP-2001 (first entry)

DE Human complementary peptide, SEQ ID NO: 3027.

KW Human; complementary peptide; ligand; drug discovery; drug design.

OS Homo sapiens.

PN WO200142277-A2.
 PD 14-JUN-2001.
 XX
 XX 13-DEC-2000; 2000WO-GB04776.
 XX
 XX 13-DEC-1999; 99GB-0029464.
 XX
 XX (PROT-) PROTEOM LTD.
 XX
 XX Roberts GW, Heal JR;
 XX
 XX WPI; 2001-408419/43.
 XX
 XX A set of peptide ligands consisting of specific complementary peptides
 PT for proteins encoded by genes of the human genome, useful in an assay
 PT for screening and identifying of one or more novel peptides which are
 PT drug candidates or pro-drugs -
 XX
 XX Example 4; Page 477; 646pp; English.
 PS
 CC The invention relates to a set of complementary peptide ligands
 CC generated from the human genome. The complementary peptides
 CC interact with their relevant target proteins encoded in the human
 CC genome. They can be used as reagents in drug discovery and as lead
 CC ligands to facilitate drug design and development. The present
 CC sequence is a complementary peptide provided in the specification.
 XX
 XX Sequence 10 AA;
 SQ

Query Match 27.8%; Score 5; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 PDLQP 13
 Db 2 PDLQP 6

RESULT 11
 AAP50841
 ID AAP50841 standard; protein; 15 AA.
 XX
 AC AAP50841;
 XX
 XX 18-NOV-1991 (first entry)
 DT
 DE Sequence of colony stimulating factor subclass no.1 (CSF 1).
 XX
 XX Quantitative assay; clinical diagnosis; therapeutic agent;
 KW haematopoiesis; immune cell deficiency; cancer therapy.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1
 FT /label= H,S,E
 PT
 XX
 XX US4504586-A.
 XX
 XX 12-MAR-1985.
 PD
 XX
 XX 03-FEB-1983; 83US-0463516.
 PF
 XX
 XX 03-FEB-1983; 83US-0463516.
 PR
 XX
 XX (AMGE-) AMGEN.
 PA
 XX
 XX Nicolson M;
 PI
 XX WPI; 1985-080848/13.
 DR
 XX Determn. of colony stimulating factor sub-class 1 - by using

PT monoclonal antibody obtd. from cell lines ATCC HB 8207 and 8208
 XX
 PS Example; columns 9-10; 8pp; English.
 XX
 CC The inventors claim a novel murine derived hybridoma cell line which
 CC is capable of producing in a growth medium a monoclonal antibody
 CC capable of specific binding with human CSF-1 in an antigen-antibody
 CC complex. A synthetic polypeptide duplicating the sequence of AAs of
 CC residues 2 through 14 is expected to be successfully employed in
 CC immunization, cell fusion and cloning procedures as set out in the
 CC examples.
 XX
 XX Sequence 15 AA;
 SQ

Query Match 27.8%; Score 5; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 PPDVE 7
 Db 3 PPDVE 7

RESULT 12
 AAP82092
 ID AAP82092 standard; peptide; 15 AA.
 XX
 AC AAP82092;
 XX
 XX 25-MAR-2003 (updated)
 DT
 DT 26-OCT-1990 (first entry)
 XX
 XX HRV2-derived peptide corresponding to amino acids 156-170 of VP2.
 DE
 XX synthetic human rhinovirus (HRV) peptides; HRV vaccine.
 KW
 XX Human rhinovirus.
 OS
 XX EP287395-A.
 FN
 XX 19-OCT-1988.
 PD
 XX 15-APR-1988; 88EP-0303432.
 PF
 XX 16-APR-1987; 87GB-0009274.
 PR
 XX (WELL) WELLCOME FOUND LTD.
 PA
 XX Francis MJ, Clarke BE;
 PI
 XX WPI; 1988-294751/42.
 DR
 XX Vaccine against human rhinovirus -
 OS comprising synthetic peptides corresp to epitope of VP2 or
 PT equivalent amino acid residues of human rhinovirus
 FT
 XX Claim 4; Page 8; 15pp; English.
 PS
 XX Peptide can be chemically synthesised or prepd by recombinant
 CC techniques ,opt as fusion protein. One or more amino acids may be
 CC replaced by one or more amino acids which do not affect the
 CC antigenicity of the peptide. The peptide is coupled to a carrier
 CC for use in a vaccine.
 CC See also AAP82093.
 CC (Updated on 25-MAR-2003 to correct PD field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX
 XX Sequence 15 AA;
 SQ

Query Match 27.8%; Score 5; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQP 13
 |||||
 Db 9 PDLQP 13

RESULT 13
 AAW75695
 ID AAW75695 standard; peptide; 15 AA.
 XX
 AC AAW75695;
 XX
 DT 23-OCT-1998 (first entry)
 XX

XX M. tuberculosis 32A kD protein derived peptide 54 (residues 266-280).
 DE
 XX
 KW Mycobacterium tuberculosis; vaccination; extracellular product;
 KW immunodominant epitope; interleukin-12; MF59; immune response;
 KW opsonising humoral response; intracellular pathogen.
 XX

OS Synthetic.
 OS Mycobacterium tuberculosis.
 XX

PN WO9831388-A1.
 XX

PD 23-JUL-1998.
 XX

PF 15-JAN-1998; 98WO-US00942.
 XX

PR 21-JAN-1997; 97US-0786533.
 XX

PA (REGC) UNIV CALIFORNIA.
 XX

PI Harth G, Horwitz MA, Lee B;
 XX

DR WPI; 1998-413815/35.
 XX

PT Vaccines against Mycobacterium containing major extracellular
 PT proteins - used to, e.g. induce protective and therapeutic immune
 PT responses, and for detecting an immune response
 XX

PS Example 29; Page 101; 236pp; English.
 XX

CC Sequences shown in AAW75642 to AAW75698 represent synthetic peptides
 CC derived from the native 32A kD major secretory protein of M.
 CC tuberculosis. These peptides are used for identifying the immunodominant
 CC T-cell epitope of the 32A kD protein. The invention provides an agent for
 CC vaccinating mammals against Mycobacterium. The agent comprises at least
 CC one of the major abundant extracellular 110, 80, 71, 58, 45, 32A, 32B,
 CC 30, 24, 23.5, 23, 16, 14 or 12 kD proteins of M. tuberculosis, or at
 CC least 1 of their immunodominant epitopes and interleukin-12 (IL-12) or
 CC MF59 as adjuvants. The agent containing the nucleic acid encoding the
 CC extracellular products are used to raise a protective or therapeutic
 CC immune response against Mycobacterium, specifically M. tuberculosis. The
 CC immunodominant epitopes can also be used (typically in a cutaneous
 CC hypersensitivity test) to detect an immune response to vaccination.
 CC Preparation of the agent does not require selection of the most
 CC immunogenic products, so large scale production and purification are
 CC easy, resulting in a consistent, standardised formulation, having lower
 CC toxicity than killed or attenuated vaccines. The agents provide a rapid
 CC and effective response (including a strong cell-mediated component) and
 CC are safe even in immunocompromised subjects. They prevent development of
 CC an opsonising humoral response that might spread intracellular
 CC pathogens.
 XX

SQ Sequence 15 AA;
 XX

Query Match 27.8%; Score 5; DB 19; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDLQ 12
 |||||
 Db 10 KPDLQ 14

RESULT 14
 AAW75696

ID AAW75696 standard; peptide; 15 AA.
 XX

AC AAW75696;
 XX

DT 23-OCT-1998 (first entry)
 XX

XX M. tuberculosis 32A kD protein derived peptide 55 (residues 271-285).
 DE
 XX
 KW Mycobacterium tuberculosis; vaccination; extracellular product;
 KW immunodominant epitope; interleukin-12; MF59; immune response;
 KW opsonising humoral response; intracellular pathogen.
 XX

OS Synthetic.
 OS Mycobacterium tuberculosis.
 XX

PN WO9831388-A1.
 XX

PD 23-JUL-1998.
 XX

PF 15-JAN-1998; 98WO-US00942.
 XX

PR 21-JAN-1997; 97US-0786533.
 XX

PA (REGC) UNIV CALIFORNIA.
 XX

PI Harth G, Horwitz MA, Lee B;
 XX

DR WPI; 1998-413815/35.
 XX

PT Vaccines against Mycobacterium containing major extracellular
 PT proteins - used to, e.g. induce protective and therapeutic immune
 PT responses, and for detecting an immune response
 XX

PS Example 29; Page 101; 236pp; English.
 XX

CC Sequences shown in AAW75642 to AAW75698 represent synthetic peptides
 CC derived from the native 32A kD major secretory protein of M.
 CC tuberculosis. These peptides are used for identifying the immunodominant
 CC T-cell epitope of the 32A kD protein. The invention provides an agent for
 CC vaccinating mammals against Mycobacterium. The agent comprises at least
 CC one of the major abundant extracellular 110, 80, 71, 58, 45, 32A, 32B,
 CC 30, 24, 23.5, 23, 16, 14 or 12 kD proteins of M. tuberculosis, or at
 CC least 1 of their immunodominant epitopes and interleukin-12 (IL-12) or
 CC MF59 as adjuvants. The agent containing the nucleic acid encoding the
 CC extracellular products are used to raise a protective or therapeutic
 CC immune response against Mycobacterium, specifically M. tuberculosis. The
 CC immunodominant epitopes can also be used (typically in a cutaneous
 CC hypersensitivity test) to detect an immune response to vaccination.
 CC Preparation of the agent does not require selection of the most
 CC immunogenic products, so large scale production and purification are
 CC easy, resulting in a consistent, standardised formulation, having lower
 CC toxicity than killed or attenuated vaccines. The agents provide a rapid
 CC and effective response (including a strong cell-mediated component) and
 CC are safe even in immunocompromised subjects. They prevent development of
 CC an opsonising humoral response that might spread intracellular
 CC pathogens.
 XX

SQ Sequence 15 AA;
 XX

Query Match 27.8%; Score 5; DB 19; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDLQ 12
 |||||
 Db 5 KPDLQ 9

RESULT 15

ABG67986
ID ABG67986 standard; Peptide; 15 AA.
XX
AC ABG67986;
XX
XX
DT 07-OCT-2002 (first entry)
DE Human ADPI tryptic digest peptide #695.
XX
XX Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
KW Alzheimer's disease-associated feature; neuroprotective;
KW Alzheimer's disease-associated protein isoform; nootropic;
KW ADPI tryptic digest peptide.
XX
XX Homo sapiens.
OS
XX
XX WO200246767-A2.
FN
XX
XX 13-JUN-2002.
PD
XX
XX 29-NOV-2001; 2001WO-GB05289.
PF
XX
XX 08-DEC-2000; 2000US-254431P.
PR
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA
XX
XX Herath HMac, Parekh RB, Rohlf C;
PI
XX
XX WPI; 2002-508575/54.
DR
XX
XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT comprises detecting Alzheimer's disease-associated features or
PT Alzheimer's disease-associated protein isoforms in brain tissue
PT from the subject -
XX
XX Claim 7; Page 56; 427pp; English.
PS
XX
XX The present invention relates to methods and compositions for the
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in
CC a subject. The method comprises analysing a sample of brain tissue
CC from a subject by 2D electrophoresis to generate a 2D array of
CC Alzheimer's disease-associated features (ADFs), whose relative
CC abundance correlates with the presence, absence, stage or severity of
CC AD and comparing the abundance of each feature with the abundance of
CC that chosen feature in brain tissue from persons free from AD. The
CC invention also describes Alzheimer's disease-associated protein
CC isoforms (ADPIs) detectable in brain tissue. The methods and
CC compositions of the invention are useful for the screening, diagnosis
CC or prognosis of AD in a subject, for determining the stage or severity
CC of AD in a subject, for identifying a subject at risk of developing AD,
CC or for monitoring the effect of therapy administered to a subject
CC having AD. Antibodies capable of binding to ADPIs are useful for
CC treating or preventing AD, and for determining the efficacy of a given
CC treatment regime. An agent that modulates the activity of ADPI is
CC useful in the manufacture of a medicament for the treatment or
CC prevention of AD in a subject. ABG67292-ABG68038 represent human ADPI
CC tryptic digest peptides.
XX
XX Sequence 15 AA;
SQ
Query Match 27.8%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DQPPD 5
DB 5 DQPPD 9
RESULT 16
AAM47777
ID AAM47777 standard; Peptide; 15 AA.
XX

AAM47777;
XX
XX 26-FEB-2002 (first entry)
DT
XX
XX Short chain dehydrogenase 32 peptide fragment.
DE
XX
XX Short chain dehydrogenase 32; tumour; haemopathy; HIV infection;
KW immunological disease; inflammation; gene therapy; cytostatic;
KW haemostatic; virucide; immunomodulatory; antiinflammatory.
XX
XX Unidentified.
OS
XX CNI307114-A.
PN
XX
XX 08-AUG-2001.
PD
XX
XX 28-JAN-2000; 2000CN-0111584.
PF
XX
XX 28-JAN-2000; 2000CN-0111584.
PR
XX
XX (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-026893/04.
DR
XX
XX New polypeptide for treating malignant tumors and HIV infection,
PT comprises the polypeptide-short chain dehydrogenase 32 and
PT polynucleotide for coding said polypeptide -
PT
XX
XX Example 6; Page 27 (Disclosure); 33pp; Chinese.
PS
XX
XX The present invention relates to short chain dehydrogenase 32 (AAM47776).
CC The protein and its coding sequence are useful for treating various
CC diseases, such as malignant tumours, haemopathy, HIV infection,
CC immunological diseases and inflammations. The present sequence is an
CC N-terminal peptide fragment of the protein, which was used in an example
CC from the present invention.
XX
XX Sequence 15 AA;
SQ
Query Match 27.8%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PPDVE 7
DB 5 PPDVE 9
RESULT 17
ABG60992
ID ABG60992 standard; Peptide; 19 AA.
XX
XX ABG60992;
AC
XX
XX 27-AUG-2002 (first entry)
DT
XX
XX Dirofilaria immitis transglutaminase peptide #2.
DE
XX
XX Nematode; transglutaminase; nematocide; Dirofilaria immitis;
KW Brugia malayi; Onchocerca volvulus; antinematode vaccine.
XX
XX Dirofilaria immitis.
OS
XX US6383774-B1.
FN
XX
XX 07-MAY-2002.
PD
XX
XX 04-DEC-1997; 97US-0984919.
PF
XX
XX 03-DEC-1996; 96US-0781420.
PR
XX 12-JUN-1997; 97US-0874102.


```

QY      8 KPDLQ 12
      1 KPDLQ 5
      |||||
Db

RESULT 20
AAR11404
ID AAR11404 standard; Protein; 20 AA.
XX
AC AAR11404;
XX
XX 25-MAR-2003 (updated)
DT 10-JUN-1991 (first entry)
XX
XX Human rhinovirus Type 2 epitope.
XX
XX HRV2; chimaera; hepadnavirus; vaccine.
XX
OS Synthetic.
XX
XX EP421635-A.
PN
XX
XX 10-APR-1991.
PD
XX
XX 19-SEP-1990; 90EP-0310264.
PF
XX
XX 19-SEP-1989; 89GB-0021172.
PR
XX 13-AUG-1990; 90GB-0017728.
PR
XX (WELL) WELLCOME FOUND LTD.
PA (BROW) BROWN A L.
PA
XX
XX Brown AL, Clarke BE, Rowlands DJ;
PI
XX WPI; 1991-103861/15.
XX
DR N-PSDB; AAQ11228.
DR
XX
XX Particles comprising chimeric hepadnavirus core antigen protein -
PT contg. foreign aminoacid sequence comprising epitope of eg
PT hepatitis-A or -B and human immuno-deficiency virus, used as vaccine.
XX
XX Example 2; Page 7; 24pp; English.
PS
XX
XX The synthetic insert encoding this epitope was ligated
CC into the NheI restriction site of plasmid pPV-Nhe. The recombinant
CC plasmid was transformed into E.coli strain XL-1 Blue. The
CC recombinant construct was designed so as to have a diagnostic
CC internal MluI restriction site for screening the resulting clones.
CC Positive clones were cultured to high density in nutrient broth and
CC induced to express chimaeric protein comprising the HRV2 epitope by
CC addition of IPTG.
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 20 AA;

Query Match 27.8%; Score 5; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PDLPQ 13
      11 PDLPQ 15
      |||||
Db

RESULT 21
AAB59927
ID AAB59927 standard; Peptide; 4 AA.
XX
AC AAB59927;
XX
XX 06-JUN-2001 (first entry)
DT
XX

```

```

DE Human leptin fragment SEQ ID NO: 45.
XX
KW leptin; human; LSR; lipolysis stimulated receptor; obesity;
KW hypertension; anorexia; cachexia; stroke; atherosclerosis.
XX
OS Homo sapiens.
XX
XX WO200121647-A2.
PN
XX 29-MAR-2001.
PD
XX 22-SEP-2000; 2000WO-IB01470.
PF
XX 22-SEP-1999; 99US-0155506.
PR
XX (GEST ) GENSET.
PA
XX Yen F, Erickson MR, Fruebis J, Bihain B;
PI WPI; 2001-218642/22.
XX
XX New leptin polypeptide fragment and related polynucleotides, useful for
PT the prevention and treatment of obesity and obesity-related diseases
PT such as hypertension and diabetes -
XX
XX Example 10; Page 237; 247pp; English.
PS
XX
XX The present invention provides the protein and coding sequences of leptin
CC fragments which modulate the activity of lipolysis stimulated factor
CC (LSR). These sequences are useful in the treatment of obesity related
CC diseases, including obesity, anorexia, cachexia, cardiac and coronary
CC insufficiency, stroke, hypertension, atheromatous disease,
CC atherosclerosis, non-insulin dependent diabetes, hyperlipidaemia,
CC hyperuricaemia and syndrome X.
XX
SQ Sequence 4 AA;

Query Match 22.2%; Score 4; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 EKPD 10
      1 EKPD 4
      |||||
Db

RESULT 22
AAW45571
ID AAW45571 standard; peptide; 5 AA.
XX
AC AAW45571;
XX
XX 18-JUN-1998 (first entry)
DT
XX
XX Amino-terminal protecting group containing peptide 3.
DE
XX
XX Pyrococcus furiosus; aminopeptidase; thermostable; amino-deprotection;
KW sequence analysis; enzyme.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT
XX
XX WO9749819-A1.
PN
XX 31-DEC-1997.
PD
XX 19-JUN-1997; 97WO-JP02121.
PF
XX 24-JUN-1996; 96JP-0184050.
PR
XX

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PA (TAKI) TAKARA SHUZO CO LTD.
 XX Izu Y, Kato I, Miyagi M, Tanaka T, Tanigawa T;
 PI Tomono J, Tsunasawa S;
 XX WPI; 1998-077182/07.
 DR Pyrococcus furiosus DSM 3638 derived aminopeptidase - is
 PT thermostable, and used for removing amino-terminal protecting groups
 XX
 PS Disclosure; Page 49; 76pp; Japanese.
 XX This peptide has a N-terminal protecting group and can be used to
 CC determine the activity of a novel aminopeptidase enzyme derived from
 CC Pyrococcus furiosus DSM 3638. The enzyme is thermostable and removes
 CC amino-terminal protecting groups from peptides. It is effective on a
 CC range of protecting groups including acetyl, pyroglutamyl, formyl and
 CC myristoyl groups. This aminopeptidase is inhibited by amastatin and
 CC accelerated by cobalt chloride. This enzyme can be produced by culturing
 CC microbial, plant or animal cells transformants transformed with an
 CC expression vector containing the encoding nucleic acid. The enzyme can be
 CC used for efficient amino-deprotection of peptides, especially in cases
 CC where the protecting group is of uncertain or unknown structure. This is
 CC especially applicable to sequence analysis of peptides and proteins.
 XX
 SQ Sequence 5 AA;
 Query Match 22.2%; Score 4; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 DVEK 8
 Db 2 DVEK 5
 |||||
 RESULT 23
 ABB08941
 ID ABB08941 standard; peptide; 5 AA.
 XX
 AC ABB08941;
 DT 18-JUN-2002 (first entry)
 XX
 DE Peptide #4 used in a mass spectrometry method 4.
 XX
 KW Argentinated peptide; mass spectrometry; silver;
 XX sequence determination; peptide sequencing.
 OS Unidentified.
 XX
 PN CA2302877-Al.
 XX
 PD 29-SEP-2001.
 XX
 PF 29-MAR-2000; 2000CA-2302877.
 XX
 PR 29-MAR-2000; 2000CA-2302877.
 XX
 PA (UYYO-) UNIV YORK.
 XX
 PI Siu KWM, Chu IK, Lau T;
 XX
 DR WPI; 2002-106671/15.
 XX
 PT Determining peptide or protein sequence by mass spectrometry by
 PT combining oligopeptides with silver, scanning silver containing peaks
 PT in optimum collision energies and analysing doublet or triplet peak
 PT patterns -
 XX
 XX Example 5; Table 3; 46pp; English.
 XX
 CC The present sequence represents a tryptic peptide unknown to the

CC experimenter analysed using the method of the invention. The
 CC specification describes a novel method of analysing argentinated peptides
 CC using mass spectrometry by combining an oligopeptide with silver to
 CC provide an argentinated oligopeptide, submitting the sample to a mass
 CC spectrometer, scanning silver containing peaks in optimum collision
 CC energies, identifying any doublet or triplet peak pattern, and confirming
 CC with Y ions, and determining partial sequence by mass separation between
 CC two successive doublet or triplet patterns. The method of the invention
 CC is used for determining peptide or protein sequences.
 XX
 SQ Sequence 5 AA;
 Query Match 22.2%; Score 4; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 DVEK 8
 Db 2 DVEK 5
 |||||
 RESULT 24
 AAR59954
 ID AAR59954 standard; peptide; 6 AA.
 XX
 AC AAR59954;
 DT 25-MAR-2003 (updated)
 DT 14-FEB-1995 (first entry)
 XX
 DE Peptide signal sequence for treating Semliki Forest virus E1
 DE infections.
 XX
 KW Therapeutic; metabolic interactions; PSS; analogues.
 XX
 OS Synthetic.
 XX
 PN WO9416328-Al.
 XX
 PD 21-JUL-1994.
 XX
 PF 30-DEC-1993; 93WO-US12679.
 XX
 PR 30-DEC-1992; 92US-0997727.
 XX
 PA (RATH/) RATH M.
 XX
 PI Rath M;
 XX
 DR WPI; 1994-249399/30.
 XX
 XX Identifying peptide signal sequences in a protein - and use of
 PT their synthetic analogues for treating or preventing, e.g.
 PT cardiovascular and auto-immune disease, infections and cancer.
 XX
 PS Claim 24; Page 12; 28pp; English.
 XX
 CC The sequence is that of a peptide signal sequence which can be used
 CC to treat Semliki forest virus E1 viral infections.
 CC See also AAR59944-83.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 6 AA;
 Query Match 22.2%; Score 4; DB 15; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 EXPD 10
 Db 3 EXPD 6
 |||||

```

RESULT 25
AAG63056
ID AAG63056 standard; peptide; 6 AA.
XX AC
XX AAG63056;
XX DT 01-OCT-2001 (first entry)
XX DE Amino acid sequence of a Porcine parvovirus (PPV)-binding domain.
XX KW Porcine parvovirus; PPV; Quick Assay for Selecting Affinity Resins;
XX LW virus binding domain.
XX OS Unidentified.
XX PN WO200140265-A2.
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US42515.
XX PR 02-DEC-1999; 99US-0453115.
XX PA (WITE-) VI TECHNOLOGIES INC.
XX PI Hammond DJ;
XX DR WPI; 2001-475677/51.
XX PT Identifying ligands that interact with a target by Quick Assay for
XX PT Selecting Affinity Resins, involves differentiating specific or
XX PT non-specific false positive interactions from target-specific
XX PT interactions -
XX PS Claim 7; Page 28; 39pp; English.
XX CC The present sequence represents a Porcine parvovirus (PPV)-binding
XX CC domain, which binds to PPV in the presence of fibrinogen. It was
XX CC identified using the method of the invention. The method
XX CC identifies ligands that interact with a target by Quick Assay for
XX CC Selecting Affinity Resins. The method comprise differentiating false
XX CC positive interactions (either specific or non-specific) from
XX CC target-specific interaction, by distinguishing non-specific binding
XX CC ligands to agents in the screening solution from specific binding
XX CC between a ligand and target. The method is useful for identifying
XX CC ligands that interact with the target, and for multiple screenings of
XX CC the same surface-immobilized library for a number of different ligands.
XX SQ Sequence 6 AA;
Query Match 22.2%; Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 LQPF 14
Db 3 LQPF 6
RESULT 26
AAU86432
ID AAU86432 standard; Peptide; 6 AA.
XX AC
XX AAU86432;
XX DT 21-MAY-2002 (first entry)
XX DE Vector encoded peptide.
XX KW Oestrogen receptor; breast cancer; combinatorial peptide library;
XX KW receptor modulating compound.
XX OS Synthetic.

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XX WO200204956-A2.
XX 17-JAN-2002.
XX PF 11-JUL-2001; 2001WO-US21867.
XX PR 12-JUL-2000; 2000US-0614865.
XX PR 21-MAY-2001; 2001US-0860688.
XX PA (KARO-) KARO BIO USA INC.
XX PI Fowlkes DM, Barnett TR, Buehrer B;
XX WPI; 2002-154969/20.
XX PT Identifying receptor-binding peptides comprises screening combinatorial
XX PT peptide library presented in form of cells each of which coexpress one
XX PT peptide member and receptor with signal producing system for reporting
XX PT binding -
XX PS Example 501; Page 112; 175pp; English.
XX CC The invention relates to identifying a binding peptide which binds a
XX CC receptor and which is a member of a combinatorial library of peptides,
XX CC comprising screening a combinatorial peptide library presented in the
XX CC form of cells which coexpress the receptor or its ligand-binding receptor
XX CC moiety and one member of the library, together with a signal producing
XX CC system for reporting binding of the peptide to the receptor. Also
XX CC included is a method for predicting the receptor-modulating activity of a
XX CC compound which modulates the biological activity of a receptor
XX CC comprising (a) identifying peptides which bind the receptor by the
XX CC method above, (b) using a number of the peptides to predict the receptor-
XX CC modulating activity of a compound by (i) providing a panel of
XX CC identified peptides, where the members differ in their ability to bind
XX CC to the receptor depending on reference conformations the receptor is
XX CC in, where the effect of a number of reference substances known to
XX CC modulate the biological activity of the receptor on the binding of each
XX CC member of the panel is known and is characterised as a reference
XX CC fingerprint for each reference substance, (ii) screening a test substance
XX CC of unknown activity relative to the receptor to determine its effect on
XX CC the binding of each member of the panel to the receptor, thereby
XX CC obtaining a test fingerprint for the test substance, (iii) comparing the
XX CC test fingerprint to the reference fingerprints and (iv) predicting the
XX CC biological activity of the test substance based on the assumption that
XX CC its biological activity will be similar to that of reference substances
XX CC with similar fingerprints. The method is useful for identifying a binding
XX CC peptide which binds a vertebrate, mammalian, preferably human receptor,
XX CC an intracellular, nuclear, oestrogen or androgen receptor. The identified
XX CC peptides which bind to the receptor are useful for predicting the
XX CC receptor-modulating activity of a compound (e.g. ant/agonists).
XX CC The receptor-binding library members are useful in the prediction of the
XX CC ability of small organic molecules, suitable for pharmaceutical use
XX CC (e.g. in the case of oestrogen receptors, for breast cancer treatment),
XX CC to interact with the receptor. The analyte-binding molecules can also be
XX CC used for in vivo imaging. The method has several advantages over whole
XX CC animal-based assay systems in that the same technology can be applied to
XX CC a variety of different receptors, the system can be used for high
XX CC throughput screening and compound characterisation, and gives very
XX CC distinct patterns for agonists and antagonists of receptor activity using
XX CC very much less protein. The present sequence is a vector derived
XX CC peptide which is occasionally included in expressed peptides from a
XX CC combinatorial peptide library.
XX SQ Sequence 6 AA;
Query Match 22.2%; Score 4; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 DLQP 13
Db 2 DLQP 5

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RESULT 27
ABUS8263
ID ABUS8263 standard; Peptide; 6 AA.
XX AC
XX ABUS8263;
XX
DT 14-APR-2003 (first entry)
XX
DE Peptide binding to porcine parvovirus in the presence of fibrinogen #2.
XX
KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;
KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;
KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;
KW surface-immobilised library; blood composition.
XX
OS Synthetic.
XX
PN US2002155106-A1.
XX
PD 24-OCT-2002.
XX
PF 01-DEC-2000; 2000US-0727963.
XX
PR 01-DEC-2000; 2000US-0727963.
XX
PA (HAMM/) HAMMOND D J.
XX
PI Hammond DJ;
XX
DR WPI; 2003-198483/19.
XX
PT New peptide comprising a porcine parvovirus-binding, hepatitis A
PT virus-binding or prion-binding domain, useful for screening a library
PT of surface-immobilised ligands that bind to target molecules -
XX
PS Claim 7; Page 31; 35pp; English.
XX
CC The invention relates to a peptide, having a sequence of less than 20
CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis
CC A virus (HAV)-binding, or prion-binding domain. Also included are
CC a composition comprising the peptide, removing a target from a biological
CC fluid, identifying a ligand for a target or targets and identifying a
CC peptide that binds to a virus present in a blood composition. The peptide
CC is useful for identifying a ligand for a target or targets (Hepatitis A
CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine
CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,
CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a
CC peptide that binds to a virus present in a blood composition. It is used
CC to screen a library of surface-immobilised ligands that bind to target
CC molecules. The peptide allows for multiple screenings of the same
CC surface-immobilised library for a number of different ligands.
CC The present sequence is a peptide of the invention, targeting one
CC of the above listed targets.
XX
SQ Sequence 6 AA;
XX
Query Match 22.2%; Score 4; DB 24; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQPF 14
Db 3 LQPF 6

RESULT 28
AAR33159
ID AAR33159 standard; peptide; 7 AA.
XX AC
XX AAR33159;
XX

```

```

DT 25-MAR-2003 (updated)
DT 25-JUN-1993 (first entry)
XX
DE HPV E7 protein - RBG protein binding inhibitor peptide.
XX
KW Human papilloma virus; retinoblastoma gene; genital warts;
KW cervical cancer; treatment.
XX
OS Synthetic.
XX
PN EP531080-A2.
XX
PD 10-MAR-1993.
XX
PF 01-SEP-1992; 92EP-0307905.
XX
PR 04-SEP-1991; 91US-0754829.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Oliff AI, Riemen MW;
XX
DR WPI; 1993-078581/10.
XX
PT New polypeptide(s) which inhibit human papilloma virus binding to
PT RBG protein - useful for treating genital warts and cervical cancer
XX
PS Claim 7; Page 15; 15pp; English.
XX
CC The sequence is that of a peptide which inhibits binding of human
CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
CC protein. It can be used in the treatment of conditions caused by HPV,
CC esp. genital warts and cervical cancer.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 7 AA;
XX
Query Match 22.2%; Score 4; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 1 DLQP 4

RESULT 29
AAM44291
ID AAM44291 standard; Peptide; 7 AA.
XX AC AAM44291;
XX
DT 25-OCT-2001 (first entry)
XX
DE H11 binding site consensus conforming peptide (CCP) #562.
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPFC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN CA2290722-A1.
XX
PD 08-JUN-2001.
XX
PF 08-DEC-1999; 99CA-2290722.
XX
PR 08-DEC-1999; 99CA-2290722.
XX

```

PA (NOVO-) NOVOPHARM BIOTECH INC.
 XX
 PI Kaplan HA, Maili PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, MacDonald GC;
 XX
 XX
 DR WPI; 2001-425937/46.
 XX
 PT Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -
 XX
 XX
 PS Example 4; Page 103; 154pp; English.
 XX
 XX The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumors that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPCCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPCCs
 CC or a population of different SPCCs consisting of immunogenic cancer cell
 CC surface-associated SPCC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.
 XX
 SQ Sequence 7 AA;
 Query Match 22.2%; Score 4; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 11 LQPF 14
 ||||
 Db 4 LQPF 7
 RESULT 30
 AAR10631
 ID AAR10631 standard; Protein; 8 AA.
 XX
 AC AAR10631;
 XX
 XX 25-MAR-2003 (updated)
 DT 18-APR-1991 (first entry)
 XX
 XX Human Papilloma Virus-16 "(Gln27]-E7-(20-27)-AMIDE" peptide.
 DE
 XX papilloma virus; retinoblastoma gene-binding protein; genital warts;
 KW cervical cancer.
 XX
 OS Synthetic.
 XX
 XX EP412762-A.
 PN
 XX 13-FEB-1991.
 PD
 XX 06-AUG-1990; 90EP-0308652.
 PF
 XX 09-APR-1990; 90US-0506981.
 PR
 XX 07-AUG-1989; 83US-0330569.
 PR
 XX (MERI) MERCK & CO INC.
 PA (OLIF/) OLIFF A I.
 XX
 XX Oliff AI, Riemen MW;
 PI
 XX WPI; 1991-045887/07.
 DR

XX Papilloma virus and retinoblastoma gene-binding protein
 PT inhibitors - involves a specified aminoacid sequence contg. 13
 PT residues for treatment of genital warts and cervical cancer
 XX
 XX
 PS Claim 12; Page 11; 11pp; English.
 XX
 XX The peptide carries an amide group at the C-terminus. The sequence
 CC comprises residues 20 to 27 of the deduced HPV-16 E7 protein
 CC sequence (N.Salzman and P.Howley, "The Papovaviridae", Vol 2,p.379,
 CC Plenum Press, N.Y. 1987) but with Gln replacing Asp at position 27.
 CC The peptides are used as screening tools and in the prevention,
 CC therapy, prophylaxis and treatment of HPV-induced diseases. They
 CC can also be used to raise antibodies either as vaccines or to
 CC heighten the immune response to an HPV infection all ready present.
 CC See also AAR10628-R10630, AAR10632-7.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 8 AA;
 Query Match 22.2%; Score 4; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 10 DLQP 13
 ||||
 Db 1 DLQP 4
 RESULT 31
 AAR33158
 ID AAR33158 standard; peptide; 8 AA.
 XX
 AC AAR33158;
 XX
 XX 25-MAR-2003 (updated)
 DT 25-JUN-1993 (first entry)
 XX
 XX HPV E7 protein - RBG protein binding inhibitor peptide.
 DE
 XX Human papilloma virus; retinoblastoma gene; genital warts;
 KW cervical cancer; treatment.
 XX
 OS Synthetic.
 XX
 XX EP531080-A2.
 PN
 XX 10-MAR-1993.
 PD
 XX 01-SEP-1992; 92EP-0307905.
 PF
 XX 04-SEP-1991; 91US-0754829.
 PR
 XX (MERI) MERCK & CO INC.
 PA
 XX Oliff AI, Riemen MW;
 PI
 XX WPI; 1993-078581/10.
 DR
 XX New polypeptide(s) which inhibit human papilloma virus binding to
 PT RBG protein - useful for treating genital warts and cervical cancer
 XX
 PS Claim 7; Page 15; 15pp; English.
 XX
 XX The sequence is that of a peptide which inhibits binding of human
 CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
 CC protein. It can be used in the treatment of conditions caused by HPV,
 CC esp. genital warts and cervical cancer.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 8 AA;
 Query Match 22.2%; Score 4; DB 14; Length 8;
 DR

XX PS Claim 7; Page 15; 15pp; English.

XX CC The sequence is that of a peptide which inhibits binding of human

CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)

CC protein. It can be used in the treatment of conditions caused by HPV,

CC esp. genital warts and cervical cancer.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX CC

SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 14; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DIQP 13

Db 1 DIQP 4

RESULT 37

AAR43741

ID AAR43741 standard; peptide; 9 AA.

AC AAR43741;

XX

XX

DT 25-MAR-2003 (updated)

DT 19-MAY-1994 (first entry)

XX

XX MHC Class I allele HLA-A2.1 binding HPV16 E7 peptide.

XX

XX Human papilloma virus; major histocompatibility complex; prevention;

KW treatment; virus-related diseases; T cell response; cervical; human;

KW carcinoma; adenoma; screening tools; diagnostics; diagnosis.

XX

OS Synthetic.

XX

XX WO9322338-A1.

XX

PD 11-NOV-1993.

XX

XX 04-MAY-1993; 93WO-NL00093.

XX

XX 05-MAY-1992; 92EP-0201252.

PR 10-DEC-1992; 92EP-0203870.

PR 01-FEB-1993; 93EP-0200243.

PR 05-MAR-1993; 93EP-0200621.

XX

XX (UYLE-) RIJXSUNIV LEIDEN.

PA

XX

PI Kast WM, Melief CJM, Sette AD, Sidney JC;

XX

XX WPI; 1993-368718/46.

XX

XX Peptide(s) derived from human papilloma virus - which bind to a

PT human major histocompatibility complex Class I molecule, used for

PT prevention and treatment of virus-related diseases

XX

PS Claim 5; Page 51; 64pp; English.

XX

XX The sequence is that of a peptide, derived from the E7 protein of

CC human papilloma virus (HPV) (residues 11-19), which is able to bind

CC to human MHC Class I allele HLA-A2.1. It is able to induce a T cell

CC response effective against HPV, in partic. a HLA class I-restricted

CC CD8+ cytotoxic T cell response. It can be used for prevention and

CC treatment of cervical carcinoma and/or adenoma and other HPV-related

CC diseases. It can also be used as a screening tool and in diagnostic

CC applications.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 14; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DIQP 13

Db 1 DIQP 4

RESULT 39

AAR59257

ID AAR59257 standard; peptide; 9 AA.

XX

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DIQP 13

Db 4 DIQP 7

RESULT 38

AAR43742

ID AAR43742 standard; peptide; 9 AA.

XX

AC AAR43742;

XX

DT 25-MAR-2003 (updated)

DT 19-MAY-1994 (first entry)

XX

XX MHC Class I allele HLA-A2.1 binding HPV16 E7 peptide.

XX

XX Human papilloma virus; major histocompatibility complex; prevention;

KW treatment; virus-related diseases; T cell response; cervical; human;

KW carcinoma; adenoma; screening tools; diagnostics; diagnosis.

XX

OS Synthetic.

XX

XX WO9322338-A1.

XX

PD 11-NOV-1993.

XX

XX 04-MAY-1993; 93WO-NL00093.

XX

XX 05-MAY-1992; 92EP-0201252.

PR 10-DEC-1992; 92EP-0203870.

PR 01-FEB-1993; 93EP-0200243.

PR 05-MAR-1993; 93EP-0200621.

XX

XX (UYLE-) RIJXSUNIV LEIDEN.

PA

XX

PI Kast WM, Melief CJM, Sette AD, Sidney JC;

XX

XX WPI; 1993-368718/46.

XX

XX Peptide(s) derived from human papilloma virus - which bind to a

PT human major histocompatibility complex Class I molecule, used for

PT prevention and treatment of virus-related diseases

XX

PS Claim 5; Page 51; 64pp; English.

XX

XX The sequence is that of a peptide, derived from the E7 protein of

CC human papilloma virus (HPV) (residues 12-20), which is able to bind

CC to human MHC Class I allele HLA-A2.1. It is able to induce a T cell

CC response effective against HPV, in partic. a HLA class I-restricted

CC CD8+ cytotoxic T cell response. It can be used for prevention and

CC treatment of cervical carcinoma and/or adenoma and other HPV-related

CC diseases. It can also be used as a screening tool and in diagnostic

CC applications.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 14; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DIQP 13

Db 3 DIQP 6

RESULT 39

AAR59257

ID AAR59257 standard; peptide; 9 AA.

XX

AC AAR59257;
 XX
 DT 25-MAR-2003 (updated)
 DT 10-MAY-1995 (first entry)
 XX
 DE Peptide fragment (1.0229) of HPV binds HLA-A2.1.
 XX
 KW antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV;
 KW HIV1; core antigen; surface antigen; pharmaceutical composition;
 KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
 KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
 KW human leukocyte antigen.
 XX
 OS Human papilloma virus.
 XX
 PN WO9420127-A1.
 XX
 PD 15-SEP-1994.
 XX
 PF 04-MAR-1994; 94WO-US02353.
 XX
 PR 05-MAR-1993; 93US-0027146.
 PR 04-JUN-1993; 93US-0073205.
 PR 29-NOV-1993; 93US-0159184.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 PI Grey HM, Kast WM, Sette A, Sidney J;
 XX
 DR WPI; 1994-302678/37.
 XX
 PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.
 XX
 PS Example 5; Page 106; 138pp; English.
 XX
 CC AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
 CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
 CC of at least 1% as compared to a reference peptide (AAR71293). AAR59257
 CC has an IC50 of <0.003 and the sequence occurs at position 14 in the HPV
 CC E7 protein. The peptides of the invention can induce cytotoxic T
 CC lymphocytes which can react with target cells. They can be used for the
 CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,
 CC etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 9 AA;
 Query Match 22.2%; Score 4; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 10 DLQP 13
 Db 1 DLQP 4
 RESULT 40
 AAR61700
 ID AAR61700 standard; peptide; 9 AA.
 XX
 AC AAR61700;
 XX
 DT 25-MAR-2003 (updated)
 DT 12-JUN-1995 (first entry)
 XX
 DE HLA-A2.1 algorithm predicted binding peptide 33.
 XX
 KW antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV;
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;

KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
 KW diagnostic; MHC class I molecule; major histocompatibility complex;
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
 KW herpes simplex virus.
 XX
 OS Synthetic.
 XX
 PN WO9420127-A1.
 XX
 PD 15-SEP-1994.
 XX
 PF 04-MAR-1994; 94WO-US02353.
 XX
 PR 05-MAR-1993; 93US-0027146.
 PR 04-JUN-1993; 93US-0073205.
 PR 29-NOV-1993; 93US-0159184.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 PI Grey HM, Kast WM, Sette A, Sidney J;
 XX
 DR WPI; 1994-302678/37.
 XX
 PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.
 XX
 PS Disclosure; Page 70; 138pp; English.
 XX
 CC AAR61668-712 are potential peptide binders of HLA-A2.1 motif. They were
 CC predicted by using an algorithm which assigns a score for each amino
 CC acid, at each position along a peptide. A peptide is scored in the
 CC 'Grouped Ratio' algorithm as a product of the scores of each of its
 CC residues. This value can then be used to predict a population of
 CC peptides with the highest occurrence of good binders. This set of
 CC peptides was comprised of 21 peptides with high algorithm scores, and 20
 CC peptides with low algorithm scores. This peptide (source WT (sic)) had an
 CC algorithm score of 0.0017 and an A2.1 binding score of 0.0001. The
 CC correlation between binding and algorithm score was 0.69 (over all the
 CC peptides). The peptides of the invention can induce cytotoxic T
 CC lymphocytes which can react with target cells. They can be used for the
 CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,
 CC etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 9 AA;
 Query Match 22.2%; Score 4; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 KPDL 11
 Db 6 KPDL 9
 RESULT 41
 AAR73799
 ID AAR73799 standard; peptide; 9 AA.
 XX
 AC AAR73799;
 XX
 DT 25-MAR-2003 (updated)
 DT 19-JUN-1995 (first entry)
 XX
 DE Antigen fragment 115, from HPV(a) has binding affinity for HLA-2.1.
 XX
 KW antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV;
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;

KW diagnostic; MHC class I molecule; major histocompatibility complex;
KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
KW herpes simplex virus; influenza A; M1.
XX
OS Human papilloma virus strain 16(a).
XX
PN WO9420127-A1.
XX
PD 15-SEP-1994.
XX
XX 04-MAR-1994; 94WO-US02353.
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX (CYTE-) CYTEL CORP.
XX
XX Grey HM, Kast WM, Sette A, Sidney J;
XX
XX WPI; 1994-302678/37.
XX
XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX Disclosure; Page 84; 138pp; English.
XX
CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
CC motifs disclosed in the invention, these peptides were screened for
CC further motifs. Only peptides with binding affinity of at least 1%
CC (binding affinity is expressed as an IC50 value) as compared to the
CC standard peptide (AAR71293) in assays. This peptide from HPV E7
CC antigen has a binding value of 0.0130. The peptides of the invention can
CC induce cytotoxic T lymphocytes which can react with target cells. They
CC can be used for the treatment or prophylaxis of cancer, eg. prostate
CC cancer or lymphoma, etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 9 AA;
Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 DLQP 13
Db |||||
4 DLQP 7
RESULT 42
AAR73800
ID AAR73800 standard; peptide; 9 AA.
XX
XX AAR73800;
XX
XX 25-MAR-2003 (updated)
DT 19-JUN-1995 (first entry)
XX
XX Antigen fragment 116, from HPV has binding affinity for HLA-A2.1.
XX
XX antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; BBV;
KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
KW diagnostic; MHC class I molecule; major histocompatibility complex;
KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
KW herpes simplex virus; influenza A; M1.
XX
XX Human papilloma virus strain 16.

XX WO9420127-A1.
XX
XX 15-SEP-1994.
XX
XX 04-MAR-1994; 94WO-US02353.
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX (CYTE-) CYTEL CORP.
XX
XX Grey HM, Kast WM, Sette A, Sidney J;
XX
XX WPI; 1994-302678/37.
XX
XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX Disclosure; Page 84; 138pp; English.
XX
CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
CC motifs disclosed in the invention, these peptides were screened for
CC further motifs. Only peptides with binding affinity of at least 1%
CC (binding affinity is expressed as an IC50 value) as compared to the
CC standard peptide (AAR71293) in assays. This peptide from HPV E7
CC antigen has a binding value of 0.0130. The peptides of the invention can
CC induce cytotoxic T lymphocytes which can react with target cells. They
CC can be used for the treatment or prophylaxis of cancer, eg. prostate
CC cancer or lymphoma, etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 9 AA;
Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 DLQP 13
Db |||||
3 DLQP 6
RESULT 43
AAR73796
ID AAR73796 standard; peptide; 9 AA.
XX
XX AAR73796;
XX
XX 25-MAR-2003 (updated)
DT 19-JUN-1995 (first entry)
XX
XX Antigen fragment 112, from HPV has binding affinity for HLA-A2.1.
XX
XX antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; BBV;
KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
KW diagnostic; MHC class I molecule; major histocompatibility complex;
KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
KW herpes simplex virus; influenza A; M1.
XX
XX Human papilloma virus strain 16.
XX
XX WO9420127-A1.
XX
XX 15-SEP-1994.
XX
XX 04-MAR-1994; 94WO-US02353.

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XX PR 05-MAR-1993; 93US-0027146.
XX PR 04-JUN-1993; 93US-0073205.
XX PR 29-NOV-1993; 93US-0159184.
XX PA (CYTE-) CYTEL CORP.
XX PI Grey HM, Kast WM, Sette A, Sidney J;
XX WPI; 1994-302678/37.
XX DR Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
XX PT for treatment or prophylaxis of cancer, virus infection or
XX PT autoimmune diseases.
XX PS Disclosure; Page 84; 138pp; English.
XX CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
XX CC motifs disclosed in the invention, these peptides were screened for
XX CC further motifs. Only peptides with binding affinity of at least 1%
XX CC (binding affinity is expressed as an IC50 value) as compared to the
XX CC standard peptide (AAR71293) in assays. This peptide from HPV E7
XX CC antigen has a binding value of 1.4000. The peptides of the invention can
XX CC induce cytotoxic T lymphocytes which can react with target cells. They
XX CC can be used for the treatment or prophylaxis of cancer, eg. prostate
XX CC cancer or lymphoma, etc.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
Db 4 DLQP 7

RESULT 44
AAR80939
ID AAR80939 standard; peptide; 9 AA.
AC AAR80939;
XX 03-MAY-1996 (first entry)
DT Peptide for increasing HLA-A2.1 cell expression.
DE Human melanoma-associated protein; MAGE-2; tumour rejection antigen;
KW precursor; major histocompatibility complex; MHC; class 1; HLA-A2.1;
KW binding motif; cytolytic T cell; CTL; induction; peptide loading;
KW primary immune response.
XX Synthetic.
XX OS
XX PN WO9525530-A1.
XX 28-SEP-1995.
XX 21-MAR-1995; 95WO-US03535.
XX 24-MAR-1994; 94US-0217188.
XX (LUDW-) LUDWIG INST CANCER RES.
XX (UYLE-) RIJKSUNIV LEIDEN.
XX Boon-Falleur T, Kast WM, Melief CJM, Van Der Bruggen P;
XX Visseren NW;
XX WPI; 1995-344456/44.
XX New peptide(s) based on tumour rejection antigen precursor MAGE-2 -

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```

PT which bind HLA-A2 molecules to provoke cytolytic T cell prodn., used
PT partic. for treating cancers
XX Example 3; Page 37; 44pp; English.
XX Expression of HLA-A2.1 (T2) cells is increased by incubating T2
XX cells in medium containing the present peptide. T2 cells will
XX present the peptide bound to HLA-A2.1 in high amount and are good
XX antigen presenting cells. The claimed MAGE-2 peptides (see AAR80878-
XX AAR80888) can induce a similar primary immune response.
XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
Db 3 DLQP 6

RESULT 45
AAR78889
ID AAR78889 standard; peptide; 9 AA.
XX AC AAR78889;
XX 25-MAR-2003 (updated)
XX 27-MAR-1996 (first entry)
XX HPV16 E7 11-19 cytotoxic T lymphocyte epitope.
XX HPV16 E7 11-19; cytotoxic T; CTL; epitope; helper T; HTL; cell;
XX lymphocyte; antigens; treatment; disease prevention;
XX Human papillomavirus.
XX OS
XX PN WO9522317-A1.
XX 24-AUG-1995.
XX 16-FEB-1995; 95WO-US02121.
XX 16-FEB-1994; 94US-0197484.
XX (CYTE-) CYTEL CORP.
XX Vitello MA, Chesnut RW, Sette AD, Cellis E, Grey H;
XX WPI; 1995-302545/39.
XX Compsn. inducing cytotoxic T lymphocyte response to pref. viral,
XX bacterial, parasitic or tumour antigens - useful in the treatment
XX and prevention of diseases associated with the antigen e.g.
XX hepatitis B
XX Example 14; Page 72; 109pp; English.
XX A compsn. which induces a cytotoxic T lymphocyte (CTL) response to
XX a human papillomavirus (HPV) antigen (Ag) in a mammal comprises, a
XX HPV CTL Ag response inducing peptide (i.e. AAR78888-R78895) and a
XX lipid conjugated helper T cell inducing peptide. The compsn. is
XX useful in the treatment and prevention of HPV associated diseases.
XX (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13

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Db      |||||
        4 DLQP 7

RESULT 46
AAR78894
ID AAR78894 standard; peptide; 9 AA.
XX
AC AAR78894;
XX
DT 25-MAR-2003 (updated)
DT 27-MAR-1996 (first entry)
XX
DE HPV16 E7 12-20 cytotoxic T lymphocyte epitope.
XX
KW HPV16 E7 12-20; cytotoxic T; CTL; epitope; helper T; HTL; cell;
KW lymphocyte; antigens; treatment; disease prevention;
XX
OS Human papillomavirus.
XX
PN WO9522317-A1.
XX
PD 24-AUG-1995.
XX
PF 16-FEB-1995; 95WO-US02121.
XX
PR 16-FEB-1994; 94US-0197484.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Vitiello MA, Chesnut RW, Sette AD, Celis E, Grey H;
XX
DR WPI; 1995-302545/39.
XX
PT Compens. inducing cytotoxic T lymphocyte response to pref. viral,
PT bacterial, parasitic or tumour antigens - useful in the treatment
PT and prevention of diseases associated with the antigen e.g.
PT hepatitis B
XX
PS Example 14; Page 72; 109pp; English.
XX
CC A compsn. which induces a cytotoxic T lymphocyte (CTL) response to
CC a human papillomavirus (HPV) antigen (Ag) in a mammal comprises, a
CC HPV CTL Ag response inducing peptide (i.e. AAR78888-R78895) and a
CC lipid conjugated helper T cell inducing peptide. The compsn. is
CC useful in the treatment and prevention of HPV associated diseases.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db |||||
3 DLQP 6

RESULT 47
AAW39661
ID AAW39661 standard; peptide; 9 AA.
XX
AC AAW39661;
XX
DT 11-JUN-1998 (first entry)
XX
DE HPV16/18 E7 peptide (pos. 11-19).
XX
KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
KW disease; anti-tumour; anti-viral.
XX

OS Human papillomavirus.
XX
PN WO9741440-A1.
XX
PD 06-NOV-1997.
XX
PF 28-APR-1997; 97WO-NL00229.
XX
PR 23-DEC-1996; 96EP-0203670.
PR 26-APR-1996; 96EP-0201145.
PR

Human papillomavirus.
XX
PN WO9741440-A1.
XX
PD 06-NOV-1997.
XX
PF 28-APR-1997; 97WO-NL00229.
XX
PR 23-DEC-1996; 96EP-0203670.
PR 26-APR-1996; 96EP-0201145.
PR

Peptides AAW39430-W39734 are used in a novel method for the selection of
immunogenic T-cell peptide epitopes present in polypeptide antigens. The
method involves the identification of peptide sequences capable of
binding to an HLA (human leukocyte antigen) class I molecule and
measuring the binding of this epitope peptide to the HLA class I
peptide. The stability of binding of the peptide and MHC (major
histocompatibility complex) class I molecule is measured on intact human
B cells carrying the MHC molecule at their cell surfaces. The method can
be used to select peptide epitopes for generating vaccines against a
disease associated with the polypeptide, e.g. cancers or AIDS. The
peptide epitopes are especially T-cell peptide epitopes with strong
anti-tumour and anti-viral immune responses. Peptide AAW39661 is derived
from the human papillomavirus E7 protein and is capable of binding to the
human MHC Class I allele HLA-A2.1.

Query Match 22.2%; Score 4; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db |||||
4 DLQP 7

RESULT 48
AAW39662
ID AAW39662 standard; peptide; 9 AA.
XX
AC AAW39662;
XX
DT 11-JUN-1998 (first entry)
XX
DE HPV16/18 E7 peptide (pos. 12-20).
XX
KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
KW disease; anti-tumour; anti-viral.
XX
OS Human papillomavirus.
XX
PN WO9741440-A1.
XX
PD 06-NOV-1997.
XX
PF 28-APR-1997; 97WO-NL00229.
XX
PR 23-DEC-1996; 96EP-0203670.
PR 26-APR-1996; 96EP-0201145.
PR

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XX (UYLE-) RIJKSUNIV LEIDEN.
PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
XX Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;
XX WPI; 1997-549891/50.
XX Method of selecting T cell peptide epitope(s) - by measuring the
PT stability of HLA class I-peptide complexes on intact B cells
PT Example 3; Page 78; 109pp; English.
XX Peptides AAW39430-W39734 are used in a novel method for the selection of
CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The
CC method involves the identification of peptide sequences capable of
CC binding to an HLA (human leukocyte antigen) class I molecule and
CC measuring the binding of this epitope peptide to the HLA class I
CC peptide. The stability of binding of the peptide and MHC (major
CC histocompatibility complex) class I molecule is measured on intact human
CC B cells carrying the MHC molecule at their cell surfaces. The method can
CC be used to select peptide epitopes for generating vaccines against a
CC disease associated with the polypeptide, e.g. cancers or AIDS. The
CC peptide epitopes are especially T-cell peptide epitopes with strong
CC anti-tumour and anti-viral immune responses. Peptide AAW39462 is derived
CC from the human papillomavirus E7 protein and is capable of binding to the
CC human MHC Class I allele HLA-A2.1.
XX
SQ Sequence 9 AA;
Query Match 22.2%; Score 4; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 DLQP 13
Dbb ||||
3 DLQP 6
RESULT 49
AAW36590
ID AAW36590 standard; peptide; 9 AA.
XX AAW36590;
XX 25-MAR-2003 (updated)
DT 09-MAR-1998 (first entry)
XX Hepatitis B virus bulk antigen.
XX Melanoma protein; MAGE-2; tumour rejection antigen precursor; HBV:
KW binding motif; human leukocyte antigen; HLA-A2.1; cytolytic T cell;
KW CTL; induce; production; Hepatitis B virus.
XX Hepatitis B virus.
OS US5686068-A.
PN 11-NOV-1997.
PD 25-JUL-1996; 96US-0687226.
PP 25-JUL-1996; 96US-0687226.
PR 24-MAR-1994; 94US-0217188.
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYLE-) RIJKSUNIV LEIDEN.
XX Boon-Faller T, Melief CJM, Van Der Bruggen P, Van Der Burg S;
PI Visseren MW;
XX WPI; 1997-558084/51.
XX

PT Induction of cytolytic T cell production in vivo - by administering
XX MAGE-2 peptide(s)
XX Example 3; Column 9; 24pp; English.
XX This peptide sequence represents a hepatitis B virus reference peptide
CC used in determining the primary induction of the immune response against
CC MAGE-2 (a tumour rejection antigen precursor) peptides. Only peptides
CC AAW36529-39 have the ability to bind to human leukocyte antigen (HLA)
CC A2.1 molecule with high affinity and are therefore the only candidates of
CC the MAGE-2 protein to be recognised by human cytolytic T cells (CTL),
CC because CTL recognise peptides only when bound to HLA molecules.
CC Production of CTL in a subject can be induced by administering a MAGE-2
CC peptide (particularly AAW36531, AAW36533 and AAW36537) to a subject who
CC presents HLA-A2 molecules on cells. The method can be used to treat
CC subjects in need of additional CTL.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 9 AA;
SQ Query Match 22.2%; Score 4; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 DLQP 13
Dbb ||||
3 DLQP 6
RESULT 50
AAW78893
ID AAW78893 standard; peptide; 9 AA.
XX AAW78893;
XX 17-NOV-1998 (first entry)
DT Human papillomavirus 16 E7 protein fragment 11-19.
XX
XX Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
KW class II associated peptide; pathogen; gene therapy; genetic disease;
KW infection; downregulation; immune response.
XX Human papillomavirus.
OS Synthetic.
OS WO9831398-A1.
PN 23-JUL-1998.
PD 22-JAN-1998; 98WO-US01499.
PP 06-JAN-1998; 98US-0003253.
PR 22-JAN-1997; 97US-0787547.
XX (PANG-) PANGAEA PHARM INC.
XX Curley JM, Hedley ML, Langer RS, Lunsford LB;
XX WPI; 1998-427556/36.
XX New preparations of microparticles - comprising a synthetic polymer
PT matrix and nucleic acid comprising an expression vector for use in
PT gene therapy
XX Disclosure; Page 10; 101pp; English.
XX A microparticle preparation (MP) has been developed, consisting of
CC microparticles having a diameter of less than 100 nm. The MP
CC comprises: (a) a polymeric matrix (PM) consisting of one or more
CC synthetic polymers having a solubility in water of less than 1 mg/l; and
CC (b) an expression vector selected from RNA molecules (at least 50% of
CC which are closed circles) or circular plasmid DNA (at least 50% of which

CC are supercoiled). Also described is a MP of at most 20 microns in
CC diameter, comprising: (a) a PM; and (b) a NAM comprising an expression
CC control sequence operatively linked to a coding sequence, where the
CC coding sequence encodes an expression product selected from: (i) a
CC polypeptide at least 7 amino acids in length, having a sequence identical
CC to the sequence of: (i) a fragment of a naturally-occurring mammalian
CC protein; or (ii) a fragment of a naturally-occurring protein from an
CC infectious agent which infects a mammal; (2) a peptide having a length
CC and sequence which permits it to bind to an MHC class I or II molecule;
CC and (3) the polypeptide or the peptide linked to a trafficking sequence.
CC AAW69763 to AAW69765, and AAW78793 to AAW78897 are peptide fragments for
CC use in the present invention. The MPs are highly effective vehicles for
CC the delivery of polynucleotides into phagocytic cells. They can be used
CC for gene therapy, e.g. for treating genetic diseases, infections or
CC tumours or for downregulating an immune response.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
|
|
|
|
Db 4 DLQP 7

RESULT 51
AAW54766
ID AAW54766 standard; peptide; 9 AA.

XX AC AAW54766;

DT 25-SEP-1998 (first entry)

DE Peptide from HPV 16 E7 (11-19).

XX Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;
KW vaccine; treatment.

OS Synthetic.

XX PN WO9813378-A1.

XX PD 02-APR-1998.

XX PF 25-SEP-1997; 97WO-NL00536.

XX PR 26-SEP-1996; 96EP-0202701.

XX PA (UYLE-) RIJKSUNIV LEIDEN.

XX PI Drijfhout JW, Koning F;

XX DR WPI; 1998-230631/20.

XX Increasing uptake and presentation of antigen(s) - by adding mannose
PT residue(s) to antigen for increasing T cell response, useful in,
PT e.g. vaccines against viral infection(s)

XX Disclosure; Page 37; 47pp; English.

XX The peptides AAW54559-W54809 are examples of peptides to which at least
CC 1 (preferably 2) mannose can be attached to increase their uptake as
CC antigens by antigen-presenting cells. Uptake of agonist mannosylated
CC peptides will increase the T cell response, whereas uptake of antagonist
CC peptides blocks the T cell response. Blocking binding of immunogenic
CC autoantigens can be used in treatment of type I diabetes, rheumatoid
CC arthritis, graft rejection etc., also to induce T-cell non-
CC responsiveness. Vaccines containing mannosylated antigen are used to
CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths
CC and parasites.

SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
|
|
|
|
Db 4 DLQP 7

RESULT 52
AAW54767
ID AAW54767 standard; peptide; 9 AA.

XX AC AAW54767;

XX DT 25-SEP-1998 (first entry)

DE Peptide from HPV 16 E7 (12-20).

XX Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;
KW vaccine; treatment.

OS Synthetic.

XX PN WO9813378-A1.

XX PD 02-APR-1998.

XX PF 25-SEP-1997; 97WO-NL00536.

XX PR 26-SEP-1996; 96EP-0202701.

XX PA (UYLE-) RIJKSUNIV LEIDEN.

XX PI Drijfhout JW, Koning F;

XX DR WPI; 1998-230631/20.

XX Increasing uptake and presentation of antigen(s) - by adding mannose
PT residue(s) to antigen for increasing T cell response, useful in,
PT e.g. vaccines against viral infection(s)

XX Disclosure; Page 37; 47pp; English.

XX The peptides AAW54559-W54809 are examples of peptides to which at least
CC 1 (preferably 2) mannose can be attached to increase their uptake as
CC antigens by antigen-presenting cells. Uptake of agonist mannosylated
CC peptides will increase the T cell response, whereas uptake of antagonist
CC peptides blocks the T cell response. Blocking binding of immunogenic
CC autoantigens can be used in treatment of type I diabetes, rheumatoid
CC arthritis, graft rejection etc., also to induce T-cell non-
CC responsiveness. Vaccines containing mannosylated antigen are used to
CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths
CC and parasites.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
|
|
|
|
Db 3 DLQP 6

RESULT 53
AAW48125
ID AAY48125 standard; Peptide; 9 AA.

XX AC AAY48125;

```

XX 01-DEC-1999 (first entry)
XX
XX
XX Immunogenic peptide having a human leukocyte antigen binding motif #2736.
XX
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX
XX Synthetic.
XX OS Homo sapiens.
XX PN WO9945954-A1.
XX PD 16-SEP-1999.
XX PF 13-MAR-1998; 98WO-US05039.
XX PR 13-MAR-1998; 98WO-US05039.
XX PP 13-MAR-1998; 98WO-US05039.
XX PQ (EPIM-) EPIMMUNE INC.
XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -
XX
XX Claim 1; Page 137; 150pp; English.
XX
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.
XX Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)
XX e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically, and can be used to induce a cytotoxic T cell
XX response, by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polynucleotides encoding the immunogenic peptides are also useful
XX therapeutically and for immunisation as above.
XX
XX Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 20; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 KPDL 11
XX DB 1 KPDL 4
XX
XX RESULT 54
XX AAY48135
XX ID AAY48135 standard; Peptide; 9 AA.
XX AC AAY48135;
XX DT 01-DEC-1999 (first entry)

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XX Immunogenic peptide having a human leukocyte antigen binding motif #2746.
XX
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX
XX Synthetic.
XX OS Homo sapiens.
XX PN WO9945954-A1.
XX PD 16-SEP-1999.
XX PF 13-MAR-1998; 98WO-US05039.
XX PR 13-MAR-1998; 98WO-US05039.
XX PP 13-MAR-1998; 98WO-US05039.
XX PQ (EPIM-) EPIMMUNE INC.
XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -
XX
XX Claim 1; Page 138; 150pp; English.
XX
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.
XX Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)
XX e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically, and can be used to induce a cytotoxic T cell
XX response, by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polynucleotides encoding the immunogenic peptides are also useful
XX therapeutically and for immunisation as above.
XX
XX Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 20; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 KPDL 11
XX DB 6 KPDL 9
XX
XX RESULT 55
XX AAY30325
XX ID AAY30325 standard; peptide; 9 AA.
XX AC AAY30325;
XX DT 15-NOV-1999 (first entry)
XX DE Potential T cell epitope Z9 of TEK (also known as TIE2) protein.

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XX TEK protein; TIE2 protein; receptor tyrosine kinase; T cell response;
KW immune response; endothelial cell; tumor-associated vasculature;
KW coagulation; thrombosis; cancer; anticancer vaccine.
XX
XX Homo sapiens.
XX
XX WO9943801-A1.
XX
XX 02-SEP-1999.
XX
XX 26-FEB-1999; 99WO-GB00583.
XX
XX 26-FEB-1998; 98GB-0004121.
XX
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX Durrant LG, Hewett PW, Ramage JM, Spendlove I;
XX
XX WPI; 1999-540586/45.
XX
XX New peptides containing at least one epitope from Tek receptor
XX tyrosine kinase, used in vaccines against cancer
XX
XX Claim 7; Page 31; 56pp; English.
XX
XX AAY30325-35 represent T cell epitopes of the TEK protein, also known as
XX TIE2 protein. TEK is a receptor tyrosine kinase. TEK contains epitopes
XX which bind to MHC. The presentation of TEK epitopes can also stimulate
XX helper cell and/or cytotoxic T cell responses. The immune response is
XX directed against endothelial cells in the tumor-associated
XX vasculature and includes production of antibodies that bind to the
XX cells, causing coagulation and thrombosis. The immune response is
XX targeted to endothelial cells lining blood vessels of the tumor (these
XX cells overexpress Tek), so damage to even a few cells will kill many
XX tumor cells. These target cells are accessible to the immune response
XX and problems of antigenic heterogeneity, MHC loss and resistance to
XX apoptosis (associated with epithelial cells) are unlikely to occur in
XX normal endothelial cells. TEK epitopes (see AAY30320-24) are used to
XX generate antibodies, and for prevention and treatment of cancer.
XX The peptides, and recombinant DNA constructs or viral vectors that
XX express them, are useful as anticancer vaccines to target endothelial
XX cells that line blood vessels of the tumor.
XX
XX Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 20; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 VEKP 9
XX Db 3 VEKP 6
XX
XX RESULT 56
XX AAY28526
XX ID AAY28526 standard; peptide; 9 AA.
XX
XX AC AAY28526;
XX
XX 19-OCT-1999 (first entry)
XX
XX Beta-1 integrin cell adhesion modulator analogue #38.
XX
XX Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;
KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
XX
XX Synthetic.
XX
XX WO9937669-A1.
XX
XX 29-JUL-1999.
XX

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XX 21-JAN-1999; 99WO-US01236.
XX
XX 12-AUG-1998; 98US-0096212.
XX
XX 22-JAN-1998; 98US-0072119.
XX
XX 12-AUG-1998; 98US-0096211.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Brienzo A, Furcht LT, McCarthy JB;
XX
XX WPI; 1999-469112/39.
XX
XX New peptides modulating beta1 integrin subunit dependent cell
XX adhesion, useful to study cell adhesion e.g. alpha4beta1 integrin
XX dependent adhesion important in tumour cell biology
XX
XX Claim 21; Fig 14; 47pp; English.
XX
XX This sequence is a C-terminal tyrosine tagged peptide. This peptide
XX inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
XX AAY28510-Y28549 have been used to show that peptides which modulate this
XX form of cell adhesion need a C-terminal amino acid residue (Ar) which
XX has a side chain including an aromatic group, and a penultimate
XX C-terminal amino acid residue (Lip) with an alkyl side chain group, i.e.
XX a 'lipAr' motif. Studies with these peptides have also shown that
XX inhibiting peptides do not contain D-amino acids and that it is the
XX presence of the ArLip motif that conveys effective beta1 integrin
XX dependent cell adhesion inhibition. The beta-1 integrin subunit dependent
XX cell adhesion is important for cell adhesion to extracellular matrix
XX proteins, and the subunit is expressed on tumours such as melanomas.
XX Therefore these LipAr motif containing peptides may be important in the
XX treatment of cancer.
XX
XX Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 20; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 QPPD 5
XX Db 2 QPPD 5
XX
XX RESULT 57
XX AAY10346
XX ID AAY10346 standard; Peptide; 9 AA.
XX
XX AC AAY10346;
XX
XX 12-MAY-1999 (first entry)
XX
XX T cell epitope/MHC ligand SEQ ID NO:276.
XX
XX Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
KW immunisation; tumour; infectious disease; immunotherapy; cancer;
KW malignant melanoma; viral disease; hepatitis; AIDS.
XX
XX Synthetic.
XX
XX Human papillomavirus.
XX
XX WO9902183-A2.
XX
XX 21-JAN-1999.
XX
XX 10-JUL-1998; 98WO-US14289.
XX
XX 10-DEC-1997; 97US-0988320.
XX
XX 10-JUL-1997; 97CA-2209815.
XX
XX (CTL1-) CTL IMMUNOTHERAPIES CORP.
XX

```

PI Kuendig TM, Simard JJJ;
 DR WPI; 1999-120514/10.
 XX
 PT Inducing a cytotoxic T lymphocyte response - by maintaining a level
 PT of antigen in the lymphatic system of a mammal so as to provide a
 PT sustained CTL response, used to treat, e.g. AIDS
 XX
 PS Disclosure; Page 34; 1999p; English.
 XX
 CC The present invention describes a method of inducing and/or sustaining
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
 CC method comprises: (a) delivering an antigen to the mammal at a level to
 CC induce an immunological CTL response in the mammal; and (b) maintaining
 CC the level of the antigen in the mammal's lymphatic system to maintain
 CC the immunologic CTL response. The method can be used for the delivery of
 CC e.g. a differentiation antigen, a tumour-specific multilineage antigen,
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
 CC gene antigen, or a viral antigen. They can be used for the treatment of
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
 CC to the lymphatic system provides for potent CTL stimulation that takes
 CC place in the milieu of the lymphoid organ, and it sustains stimulation
 CC that is necessary to keep CTL active, cytotoxic and recirculating
 CC through the body. AAY10071 to AAY10639 represent examples of peptide
 CC antigens given in the present invention.
 XX
 SQ Sequence 9 AA;
 Query Match 22.2%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 DLQP 13
 Db ||||
 3 DLQP 6
 RESULT 58
 ID AAY10511 standard; Peptide; 9 AA.
 XX
 AC AAY10511;
 XX
 DT 12-MAY-1999 (first entry)
 XX
 DE HLA Class I motif peptide SEQ ID NO:441.
 XX
 KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
 KW immunisation; tumour; infectious disease; immunotherapy; cancer;
 KW malignant melanoma; viral disease; hepatitis; AIDS.
 XX
 OS Synthetic.
 OS Human papillomavirus.
 XX
 FN WO9902183-A2.
 XX
 PD 21-JAN-1999.
 XX
 PF 10-JUL-1998; 98WO-US14289.
 XX
 PR 10-DEC-1997; 97US-0988320.
 PR 10-JUL-1997; 97CA-2209815.
 XX
 PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
 XX
 PI Kuendig TM, Simard JJJ;
 XX
 DR WPI; 1999-120514/10.
 XX
 PT Inducing a cytotoxic T lymphocyte response - by maintaining a level
 PT of antigen in the lymphatic system of a mammal so as to provide a
 PT sustained CTL response, used to treat, e.g. AIDS

XX Disclosure; Page 44; 1999p; English.
 PS
 CC The present invention describes a method of inducing and/or sustaining
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
 CC method comprises: (a) delivering an antigen to the mammal at a level to
 CC induce an immunological CTL response in the mammal; and (b) maintaining
 CC the level of the antigen in the mammal's lymphatic system to maintain
 CC the immunologic CTL response. The method can be used for the delivery of
 CC e.g. a differentiation antigen, a tumour-specific multilineage antigen,
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
 CC gene antigen, or a viral antigen. They can be used for the treatment of
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
 CC to the lymphatic system provides for potent CTL stimulation that takes
 CC place in the milieu of the lymphoid organ, and it sustains stimulation
 CC that is necessary to keep CTL active, cytotoxic and recirculating
 CC through the body. AAY10071 to AAY10639 represent examples of peptide
 CC antigens given in the present invention.
 XX
 SQ Sequence 9 AA;
 Query Match 22.2%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 DLQP 13
 Db ||||
 3 DLQP 6
 RESULT 59
 ID AAB19059 standard; peptide; 9 AA.
 XX
 AC AAB19059;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Amino acid sequence of a betal-integrin inhibitor.
 XX
 KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;
 KW central nervous system ischemic injury; myocardial infarction;
 KW betal-integrin; angioplasty; surgical incision; injury-related trauma;
 KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 XX
 OS Synthetic.
 OS WO200056350-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US07680.
 XX
 PR 22-MAR-1999; 99US-0125634.
 PR 24-NOV-1999; 99US-0167538.
 XX
 PA (MINU) UNIV MINNESOTA
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (SENT-) SENTRON MEDICAL INC.
 XX
 PI McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
 PI Furcht LT;
 XX
 DR WPI; 2000-656062/63.
 XX
 PT Inhibition of inflammatory leukocyte mediated destruction of tissue in
 PT a patient, comprises administering a peptide inhibitor of
 PT betal-integrin, useful for treatment of e.g. cancer and osteoporosis
 XX
 PS Claim 3; Page 38; 61pp; English.
 XX
 CC AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit

CC betal-integrin which is responsible for leukocyte mediated tissue
 CC destruction. The peptides are useful for inhibiting inflammatory
 CC leukocyte mediated destruction of tissue which occurs as a result of
 CC central nervous system (CNS) ischemic injury, myocardial infarction,
 CC angioplasty, surgical incisions, injury-related trauma, and/or
 CC transplant reperfusion, exposure to heat, cold, light, electricity
 CC and/or chemicals. They are also useful for the treatment of stroke, a
 CC burn type injury, cancer, and osteoporosis.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QPPD 5
 ||||
 Db 2 QPPD 5

RESULT 60
 AAB33705
 ID AAB33705 standard; Peptide; 9 AA.
 AC AAB33705;
 XX
 DT 26-JAN-2001 (first entry)
 DE MHC class I associated immunogenic peptide SEQ ID 104.
 XX
 KW Microparticle; nucleic acid delivery; immunogenic peptide; MHC I; MHC II;
 KW major histocompatibility complex; vaginal tissue; mucosal tissue..
 XX Unidentified.
 OS
 XX WO200053161-A2.
 PN
 XX 14-SEP-2000.
 PD
 XX
 PF 10-MAR-2000; 2000WO-US06578.
 XX
 PR 11-MAR-1999; 99US-0266463.
 PR 27-MAY-1999; 99US-0321346.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Lunsford LB, Putnam D, Hedley ML;
 XX
 DR WPI; 2000-638130/61.
 XX
 PT Microparticles useful for administering a nucleic acid into the mucosal
 PT tissue preferably vaginal tissue of an animal, comprises a polymeric
 PT matrix, a lipid and a nucleic acid molecule -
 XX
 PS Disclosure; Page 16; 96pp; English.
 XX
 CC The present invention relates to microparticles which are less than 20
 CC microns in diameter, which comprise a polymeric matrix, a lipid and a
 CC nucleic acid molecule. The microparticle is specifically not
 CC encapsulated in a liposome and does not comprise a cell. The nucleotide
 CC sequence encodes an expression product that binds to major
 CC histocompatibility complex (MHC) type I or II molecules. Peptides
 CC AAB3602-B33647 represent MHC class II associated immunogenic peptides,
 CC and AAB33648-B33710 represent MHC class I associated immunogenic
 CC peptides. The peptides are examples of the expression products of the
 CC nucleotide sequences which can be included in the microparticles of the
 CC invention. Sequences AAB33711-B33716 represent alternative expression
 CC products and nuclear localisation signals also used in the invention. The
 CC microparticles are useful for administering a nucleic acid into the
 CC mucosal tissue preferably vaginal tissue of an animal.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DLQP 13
 ||||
 Db 4 DLQP 7

RESULT 61
 AAY96374
 ID AAY96374 standard; peptide; 9 AA.
 XX
 AC AAY96374;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE HLA-A2 binding peptide hTERT T765.
 XX
 KW hTERT; telomerase complex; reverse transcriptase; MHC; HLA; CTL; cancer;
 KW human leukocyte antigen; tumour-associated antigen; cytostatic; vaccine;
 KW major histocompatibility complex; cytotoxic T lymphocyte; immunotherapy.
 XX
 OS Homo sapiens.
 XX WO200025813-A1.
 PN
 XX 11-MAY-2000.
 PD
 XX
 PF 29-OCT-1999; 99WO-US25438.
 XX
 PR 29-OCT-1998; 98US-0106106.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Nadler LM, Hahn WC, Schultze JL, Vonderheide RH;
 XX
 DR WPI; 2000-365402/31.
 XX
 PT Universal tumor-associated antigens such as telomerase catalytic
 PT subunit capable of binding major histocompatibility complex molecule
 PT useful for diagnosis, prevention and treatment of cancer
 XX
 PS Disclosure; Page 75; 136pp; English.
 XX
 CC Human telomerase complex reverse transcriptase (hTERT) is expressed in
 CC more than 85 percent of human cancers. hTERT is useful as a universal
 CC tumour-associated antigen (TAA) that binds to a major histocompatibility
 CC complex molecule (MHC) hTERT peptides were analyzed for the ability to
 CC bind to HLA (human leukocyte antigen) class I molecules. Cytotoxic T
 CC lymphocytes (CTL) were then generated that kill a cell expressing hTERT
 CC or a hTERT-TAA, in a hTERT or TAA specific MHC-restricted fashion.
 CC Antigen presenting cells (APC) were also generated ex vivo for
 CC presentation of a TAA peptide or hTERT. The APC can be used to activate
 CC CTL to kill cells expressing the TAA. The TAA, hTERT peptides, APC and
 CC CTL are useful for cancer immunotherapy. Measuring the level of CTL in a
 CC sample is useful for assessing the level of immunity of a patient to a
 CC TAA or a peptide, where the sample is obtained before or after a cancer
 CC treatment is given to the patient. TAA peptides (e.g. hTERT) are also
 CC useful for diagnosis and prophylactic treatment of cancer.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DLQP 13
 ||||
 Db 4 DLQP 7

```

RESULT 62
AA986644
ID  AA986644 standard; Peptide; 9 AA.
XX
AC  AA986644;
DT  05-MAY-2000 (first entry)
XX
DE  Telomerase peptide #59.
XX
KW  Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;
KW  malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
KW  telomerase T lymphocyte.
XX
OS  Homo sapiens.
XX
PN  WO200002581-A1.
XX
PD  20-JAN-2000.
XX
PF  30-JUN-1999; 99WO-NO00220.
XX
PR  08-JUL-1998; 98NO-0003141.
XX
PA  (NHYP ) NORSK HYDRO AS.
XX
PI  Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
PI  Saeboe-Larsen S;
XX
DR  WPI; 2000-145727/13.
XX
PT  Protein or peptide fragments useful in the treatment and prophylaxis of
XX  cancer in mammals -
XX
PS  Claim 12; Page 35; 53pp; English.
XX
CC  This sequence represents a telomerase peptide of the invention, and can
CC  be used in a method for the treatment or prophylaxis of cancer. The
CC  sequences are useful in the treatment or prophylaxis of cancer.
CC  especially, breast, lung, ovarian, cervical, colorectal, prostate or
CC  pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary
CC  tract carcinomas. They are useful for generating telomerase T lymphocytes
CC  capable of recognising and destroying tumour cells in a mammal.
CC  comprising culturing T lymphocytes obtained from the mammal with the
CC  peptides. Telomerase protein is expressed only by tumour cells, hence,
CC  other body cells are not targeted or destroyed by telomerase specific T
CC  cells.
CC  Note: This sequence was indexed from WO200002581, which is the first
CC  major country equivalent to NO9803141.
XX
SQ  Sequence 9 AA;
XX
Query Match 22.2%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
Db 3 DLQP 6

RESULT 63
AA986658
ID  AA986658 standard; Peptide; 9 AA.
XX
AC  AA986658;
DT  05-MAY-2000 (first entry)
XX
DE  Telomerase peptide #73.
XX
KW  Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;
KW  malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;

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KW  telomerase T lymphocyte.
XX
OS  Homo sapiens.
XX
PN  WO200002581-A1.
XX
PD  20-JAN-2000.
XX
PF  30-JUN-1999; 99WO-NO00220.
XX
PR  08-JUL-1998; 98NO-0003141.
XX
PA  (NHYP ) NORSK HYDRO AS.
XX
PI  Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
PI  Saeboe-Larsen S;
XX
DR  WPI; 2000-145727/13.
XX
PT  Protein or peptide fragments useful in the treatment and prophylaxis of
XX  cancer in mammals -
XX
PS  Claim 12; Page 35; 53pp; English.
XX
CC  This sequence represents a telomerase peptide of the invention, and can
CC  be used in a method for the treatment or prophylaxis of cancer. The
CC  sequences are useful in the treatment or prophylaxis of cancer.
CC  especially, breast, lung, ovarian, cervical, colorectal, prostate or
CC  pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary
CC  tract carcinomas. They are useful for generating telomerase T lymphocytes
CC  capable of recognising and destroying tumour cells in a mammal.
CC  comprising culturing T lymphocytes obtained from the mammal with the
CC  peptides. Telomerase protein is expressed only by tumour cells, hence,
CC  other body cells are not targeted or destroyed by telomerase specific T
CC  cells.
CC  Note: This sequence was indexed from WO200002581, which is the first
CC  major country equivalent to NO9803141.
XX
SQ  Sequence 9 AA;
XX
Query Match 22.2%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
Db 4 DLQP 7

RESULT 64
AA993801
ID  AA993801 standard; Peptide; 9 AA.
XX
AC  AA993801;
DT  17-SEP-2001 (first entry)
XX
DE  Human papilloma virus 16 E7 peptide 1.
XX
KW  Continuous flow production; microparticle; gene therapy;
KW  antisense therapy; vaccination; treatment; autoimmune disease;
KW  immune response modulation.
XX
OS  Human wart virus.
XX
PN  WO200136583-A1.
XX
PD  25-MAY-2001.
XX
PF  17-NOV-2000; 2000WO-US31770.
XX
PR  19-NOV-1999; 99US-0443654.
XX

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PA (ZYCO-) ZYCOS INC.
XX
PI Hedley ML, Hsu Y, Tyo M;
XX
XX WPI; 2001-425203/45.
XX
XX Continuous production of microparticles containing nucleic acid for
PT e.g. gene therapy, comprises mixing a solution of polymeric material
PT and nucleic acid with a surfactant solution, removing solvent and
PT drying -
XX
XX Disclosure; Page 12; 47pp; English.
XX
XX The present sequence is that of a peptide of the invention.
CC The invention relates to a method for scalable, continuous flow
CC production of a nucleic acid containing microparticle that maintains the
CC structural integrity of the associated nucleic acid and results in a
CC microparticle having purity suitable for introduction into an animal
CC host. Microparticles prepared according to the method can be used for
CC delivery of a nucleic acid for gene therapy, antisense therapy,
CC vaccination, treatment of autoimmune disease and either specific or
CC non-specific modulation of an immune response. The microparticles may
CC also be used to deliver nucleic acid encoding a protein or peptide useful
CC in any kind of therapy. The method is economical, aseptic and scalable.
CC The method also enables control over the size of microparticles. The
CC microparticles produced are free of impurities such as organic solvents
CC and are readily dispersed in a wide range of dispersing agents.
XX
XX Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 10 DLQP 13
XX |||||
XX Db 4 DLQP 7
XX
XX
XX RESULT 65
XX AAG88547
XX ID AAG88547 standard; Peptide; 9 AA.
XX AC AAG88547;
XX DT 11-SEP-2001 (first entry)
XX DE HER2/NEU DR supermotif binding peptide core sequence #130.
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200141787-A1.
XX 14-JUN-2001.
XX PD
XX PF 11-DEC-2000; 2000WO-US33591.
XX PR 10-DEC-1999; 99US-0458299.
XX (EPIM-) EPIMMUNE INC.
XX PA Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
XX PI Keogh E;
XX WPI; 2001-374995/39.
XX
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing
PT cellular immune responses for the prevention and treatment of cancer -

XX Disclosure; Page 170; 199pp; English.
XX
XX The present invention describes isolated prepared HER2/neu epitopes (I).
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
CC culture in vitro and binds to a complex of an epitope (I), bound to a
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
CC and a second epitope and the peptide is less than 50 contiguous amino
CC acids that have 100% identity with a native peptide sequence of HER2/neu;
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising
CC (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic
CC and immunostimulant activities, and can be used in vaccines. (I), (II)
CC and (III) are useful for inducing cellular immune responses for the
CC prevention and treatment of cancer. (I) and (II) are useful for
CC monitoring or evaluating an immune response to a tumour-associated
CC antigen when incubated with a T lymphocyte sample from a patient and
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
CC based vaccines mean that immunosuppressive epitopes that may be present
CC in whole antigens may be avoided. Selected epitopes may be combined to
CC enhance immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigen is eliminated. The vaccine
CC provides the ability to direct and focus an immune response to multiple
CC selected antigens from the same pathogen. Epitope-based anti-tumour
CC vaccines provides the opportunity to combine epitopes derived from
CC multiple tumour-associated molecules addressing the problem of tumour-
CC tumour variability and reducing the likelihood of tumour escape due to
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
CC the exemplification of the present invention.
XX
XX Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 KPDL 11
XX |||||
XX Db 2 KPDL 5
XX
XX
XX RESULT 66
XX AAG88711
XX ID AAG88711 standard; Peptide; 9 AA.
XX AC AAG88711;
XX DT 11-SEP-2001 (first entry)
XX DE HER2/NEU DR 3a motif binding peptide core sequence #24.
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200141787-A1.
XX 14-JUN-2001.
XX PD
XX PF 11-DEC-2000; 2000WO-US33591.
XX PR 10-DEC-1999; 99US-0458299.
XX (EPIM-) EPIMMUNE INC.
XX PA Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
XX PI Keogh E;
XX WPI; 2001-374995/39.
XX
XX

PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing
 XX cellular immune responses for the prevention and treatment of cancer -
 PS Disclosure; Page 174; 199pp; English.
 XX
 CC The present invention describes isolated HER2/neu epitopes (I).
 CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
 CC culture in vitro and binds to a complex of an epitope (I), bound to a
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
 CC and a second epitope and the peptide is less than 50 contiguous amino
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising
 CC (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic
 CC and immunostimulant activities, and can be used in vaccines. (I), (II)
 CC and (III) are useful for inducing cellular immune responses for the
 CC prevention and treatment of cancer. (I) and (II) are useful for
 CC monitoring or evaluating an immune response to a tumour-associated
 CC antigen when incubated with a T lymphocyte sample form a patient and
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
 CC based vaccines mean that immunosuppressive epitopes that may be present
 CC in whole antigens may be avoided. Selected epitopes may be combined to
 CC enhance immunogenicity. The possible pathological side effects caused by
 CC infectious agents or whole protein antigen is eliminated. The vaccine
 CC provides the ability to direct and focus an immune response to multiple
 CC selected antigens from the same pathogen. Epitope-based anti-tumour
 CC vaccines provides the opportunity to combine epitopes derived from
 CC multiple tumour-associated molecules addressing the problem of tumour-
 CC tumour variability and reducing the likelihood of tumour escape due to
 CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
 CC the exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
 ||||
 Db 2 KPDL 5

RESULT 67
 AAG88865
 ID AAG88865 standard; Peptide; 9 AA.

XX AC AAG88865;

XX DT 11-SEP-2001 (first entry)

XX DE HER2/neu epitope B7 supermotif peptide #25.

XX KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
 XX immun response; vaccine; tumour; cancer; cytostatic; immunostimulant;
 XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

OS Homo sapiens.
 OS Synthetic.

XX PN WO200141787-A1.

XX PD 14-JUN-2001.

XX PF 11-DEC-2000; 2000WO-US33591.

XX PR 10-DEC-1999; 99US-0458299.

XX PA (EPIM-) EPIMUNE INC.

XX PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 XX Keogh E;

DR WPI; 2001-374995/39.

XX PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing
 XX cellular immune responses for the prevention and treatment of cancer -
 PS Claim 1; Page 183; 199pp; English.

XX CC The present invention describes isolated prepared HER2/neu epitopes (I).
 XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
 XX culture in vitro and binds to a complex of an epitope (I), bound to a
 XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
 XX and a second epitope and the peptide is less than 50 contiguous amino
 XX acids that have 100% identity with a native peptide sequence of HER2/neu;
 XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical
 XX excipient; (4) an isolated nucleic acid encoding a peptide comprising
 XX (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic
 XX and immunostimulant activities, and can be used in vaccines. (I), (II)
 XX and (III) are useful for inducing cellular immune responses for the
 XX prevention and treatment of cancer. (I) and (II) are useful for
 XX monitoring or evaluating an immune response to a tumour-associated
 XX antigen when incubated with a T lymphocyte sample form a patient and
 XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope
 XX based vaccines mean that immunosuppressive epitopes that may be present
 XX in whole antigens may be avoided. Selected epitopes may be combined to
 XX enhance immunogenicity. The possible pathological side effects caused by
 XX infectious agents or whole protein antigen is eliminated. The vaccine
 XX provides the ability to direct and focus an immune response to multiple
 XX selected antigens from the same pathogen. Epitope-based anti-tumour
 XX vaccines provides the opportunity to combine epitopes derived from
 XX multiple tumour-associated molecules addressing the problem of tumour-
 XX tumour variability and reducing the likelihood of tumour escape due to
 XX antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
 XX the exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
 ||||
 Db 1 KPDL 4

RESULT 68
 AAB95951
 ID AAB95951 standard; Peptide; 9 AA.

XX AC AAB95951;

XX DT 25-JUN-2001 (first entry)

XX DE MHC class-I associated HPV epitope SEQ ID 58.

XX KW Epitope; tumour antigen; antiviral; immunostimulatory; cervical cancer;
 XX human papillomavirus-associated disease; condyloma; cervical dysplasia;
 XX cervical dysplasia; major histocompatibility complex; MHC I.

OS Human papillomavirus.

XX PN WO200119408-A1.

XX PD 22-MAR-2001.

XX PF 18-SEP-2000; 2000WO-US25559.

XX PR 16-SEP-1999; 99US-0154665.

XX PR 16-SEP-1999; 99US-0398534.

XX PR 09-DEC-1999; 99US-0169846.

XX PR 09-DEC-1999; 99US-0458173.

XX PA (ZYCO-) ZYCOS INC.

XX Hedley ML, Urban RC, Chicz RM;
 XX WPI; 2001-265996/27.
 XX
 XX Novel nucleic acids encoding polypeptide polypeptides containing
 PT multiple epitopes from one or more proteins, useful for treating tumors
 PT and as vaccines against pathogenic agents -
 PT
 XX Disclosure; Page 8; 64pp; English.
 XX
 XX This invention relates to polynucleotides encoding a hybrid polypeptide
 CC comprising a signal sequence and three segments that are either
 CC contiguous or separated by a spacer amino acid or spacer peptide. The
 CC invention specifically details polynucleotides encoding a polypeptide
 CC peptide where the peptide segments are tumour antigens or a naturally
 CC occurring protein of a pathogenic agent. The polypeptide peptides exhibit
 CC antiviral and immunostimulatory activity. The polynucleotide and
 CC polypeptide peptides are useful for eliciting an immune response in a
 CC mammal. The polynucleotide and protein are useful as vaccines for
 CC treating tumours and pathogenic infections. The polynucleotide is also
 CC useful for preventing or treating human papillomavirus (HPV)-associated
 CC diseases, particularly exophytic condyloma, flat condyloma, cervical
 CC cancer, respiratory papilloma, conjunctival papilloma, genital-tract HPV
 CC infection, cervical dysplasia, high grade squamous intraepithelial
 CC lesions, and anal HPV infection. The polynucleotide and polypeptide are
 CC useful for generating or enhancing prophylactic or therapeutic immune
 CC response against pathogens, tumours or autoimmune diseases in a
 CC population of individuals having diverse MHC allotypes, as positive
 CC controls in T cell stimulation assays in vitro, and as tools to
 CC understand processing of epitopes within cells. Peptides
 CC AAB95894 - AAB96037 and AAB96044 - AAB96048 represent major
 CC histocompatibility complex I (MHC I) associated tumour and pathogen
 CC antigens. The peptides can be used as part of the polypeptide proteins of
 CC the invention. Also included are examples of the polypeptide proteins
 CC represented by AAB96050 - AAB96052, and localisation signal peptides
 CC AAB96038 - AAB96043 and AAB96049 which can be used in the construction of
 CC the polypeptide peptides.
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 XX Sequence 9 AA;
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 Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
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 QY 10 DLQP 13
 Db ||||
 4 DLQP 7
 RESULT 69
 AAB95999
 ID AAB95999 standard; Peptide; 9 AA.
 XX
 XX AAB95999;
 AC
 XX
 XX 25-JUN-2001 (first entry)
 DT
 XX HPV 16 E7 A2 MHC-binding epitope SEQ ID 101.
 DE
 XX Epitope; tumour antigen; antiviral; immunostimulatory; cervical cancer;
 KW human papillomavirus-associated disease; condyloma; cervical dysplasia;
 KW cervical dysplasia; major histocompatibility complex; MHC I.
 XX Human papillomavirus.
 OS
 XX WO200119408-A1.
 PN
 XX 22-MAR-2001.
 PD
 XX 18-SEP-2000; 2000WO-US25559.
 FF
 XX 16-SEP-1999; 99US-0154665.
 PR

PR 16-SEP-1999; 99US-0398534.
 PR 09-DEC-1999; 99US-0169846.
 PR 09-DEC-1999; 99US-0458173.
 XX
 XX (ZYCO-) ZYCOs INC.
 PA
 XX Hedley ML, Urban RC, Chicz RM;
 PI
 XX WPI; 2001-265996/27.
 DR
 XX
 XX Novel nucleic acids encoding polypeptide polypeptides containing
 PT multiple epitopes from one or more proteins, useful for treating tumors
 PT and as vaccines against pathogenic agents -
 PT
 XX Disclosure; Page 22; 64pp; English.
 PS
 XX This invention relates to polynucleotides encoding a hybrid polypeptide
 CC comprising a signal sequence and three segments that are either
 CC contiguous or separated by a spacer amino acid or spacer peptide. The
 CC invention specifically details polynucleotides encoding a polypeptide
 CC peptide where the peptide segments are tumour antigens or a naturally
 CC occurring protein of a pathogenic agent. The polypeptide peptides exhibit
 CC antiviral and immunostimulatory activity. The polynucleotide and
 CC polypeptide peptides are useful for eliciting an immune response in a
 CC mammal. The polynucleotide and protein are useful as vaccines for
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 CC diseases, particularly exophytic condyloma, flat condyloma, cervical
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 CC infection, cervical dysplasia, high grade squamous intraepithelial
 CC lesions, and anal HPV infection. The polynucleotide and polypeptide are
 CC useful for generating or enhancing prophylactic or therapeutic immune
 CC response against pathogens, tumours or autoimmune diseases in a
 CC population of individuals having diverse MHC allotypes, as positive
 CC controls in T cell stimulation assays in vitro, and as tools to
 CC understand processing of epitopes within cells. Peptides
 CC AAB95894 - AAB96037 and AAB96044 - AAB96048 represent major
 CC histocompatibility complex I (MHC I) associated tumour and pathogen
 CC antigens. The peptides can be used as part of the polypeptide proteins of
 CC the invention. Also included are examples of the polypeptide proteins
 CC represented by AAB96050 - AAB96052, and localisation signal peptides
 CC AAB96038 - AAB96043 and AAB96049 which can be used in the construction of
 CC the polypeptide peptides.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db ||||
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 RESULT 70
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 ID AAB96001 standard; Peptide; 9 AA.
 XX
 XX AAB96001;
 AC
 XX
 XX 25-JUN-2001 (first entry)
 DT
 XX HPV 16 E7 A2 MHC-binding epitope SEQ ID 103.
 DE
 XX Epitope; tumour antigen; antiviral; immunostimulatory; cervical cancer;
 KW human papillomavirus-associated disease; condyloma; cervical dysplasia;
 KW cervical dysplasia; major histocompatibility complex; MHC I.
 XX Human papillomavirus.
 OS
 XX WO200119408-A1.
 PN
 XX

PD 22-MAR-2001.
 XX 18-SEP-2000; 2000WO-US25559.
 XX 16-SEP-1999; 99US-0154665.
 XX 16-SEP-1999; 99US-0398534.
 PR 09-DEC-1999; 99US-0169846.
 PR 09-DEC-1999; 99US-0458173.
 XX (ZYCO-) ZYCOS INC.
 XX Hedley ML, Urban RC, Chicx RM;
 XX WPI; 2001-265996/27.
 XX Novel nucleic acids encoding polypeptide polypeptides containing
 PT multiple epitopes from one or more proteins, useful for treating tumors
 PT and as vaccines against pathogenic agents -
 XX Disclosure; Page 22; 64pp; English.
 XX This invention relates to polynucleotides encoding a hybrid polypeptide
 CC comprising a signal sequence and three segments that are either
 CC contiguous or separated by a spacer amino acid or spacer peptide. The
 CC invention specifically details polynucleotides encoding a polypeptide
 CC peptide where the peptide segments are tumour antigens or a naturally
 CC occurring protein of a pathogenic agent. The polypeptide peptides exhibit
 CC antiviral and immunostimulatory activity. The polynucleotide and
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 CC mammal. The polynucleotide and protein are useful as vaccines for
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 CC diseases, particularly exophytic condyloma, flat condyloma, cervical
 CC cancer, respiratory papilloma, conjunctival papilloma, genital-tract HPV
 CC infection, cervical dysplasia, high grade squamous intraepithelial
 CC lesions, and anal HPV infection. The polynucleotide and polypeptide are
 CC useful for generating or enhancing prophylactic or therapeutic immune
 CC response against pathogens, tumours or autoimmune diseases in a
 CC population of individuals having diverse MHC allotypes, as positive
 CC controls in T cell stimulation assays in vitro, and as tools to
 CC understand processing of epitopes within cells. Peptides
 CC AAB95894 - AAB96037 and AAB96044 - AAB96048 represent major
 CC histocompatibility complex I (MHC I) associated tumour and pathogen
 CC antigens. The peptides can be used as part of the polypeptide proteins of
 CC the invention. Also included are examples of the polypeptide proteins
 CC represented by AAB96050 - AAB96052, and localisation signal peptides
 CC AAB96038 - AAB96043 and AAB96049 which can be used in the construction of
 CC the polypeptide peptides.
 XX Sequence 9 AA;
 SQ Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 DLQP 13
 Db 1 DLQP 4
 RESULT 71
 ID AAJ03011
 XX AAJ03011 standard; Peptide; 9 AA.
 AC AAJ03011;
 XX 02-JUL-2001 (first entry)
 XX Hepatitis C virus epitope #3002.
 DE Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX antiviral.

OS Hepatitis C virus.
 XX WO200121189-A1.
 XX 29-MAR-2001.
 XX 19-JUL-2000; 2000WO-US19774.
 PF 19-JUL-1999; 99US-0357737.
 XX (EPIM-) EPIMMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RI, Grey HM;
 XX WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 PT Disclosure; Page 174; 214pp; English.
 PS The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX Sequence 9 AA;
 SQ Query Match 22.2%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 PDLQ 12
 Db 4 PDLQ 7
 RESULT 72
 ID AAB20215
 XX AAB20215 standard; Peptide; 9 AA.
 AC AAB20215;
 XX 14-MAY-2001 (first entry)
 DT HPV strain 16 E7 protein immunogenic peptide A2.2.
 DE Immunogenic peptide; immunogen; HPV; E7 protein; vaccine;
 KW infection; gene therapy; exophytic condyloma; flat condyloma;
 KW cervical cancer; respiratory papilloma; conjunctival papilloma;
 KW cervical dysplasia.
 XX Human papillomavirus type 16.
 OS US6183746-B1.
 XX 06-FEB-2001.
 PF 09-OCT-1998; 98US-0169425.
 XX 09-OCT-1997; 97US-0061657.
 PR (ZYCO-) ZYCOS INC.
 XX Urban RG, Chicx RM, Collins EJ, Hedley ML;
 PI WPI; 2001-190939/19.
 XX Inducing an immune response in a mammal for prophylaxis and treatment
 PT of human papilloma virus infections such as cervical cancer, comprises
 PT administering immunogenic peptides from the papilloma virus type 16 E7
 PT protein -


```

XX PS Example 1; Column 9; 23pp; English.
XX CC
XX CC The present sequence is that of immunogenic peptide A2.2 derived
XX CC from human papillomavirus type 16 (HPV16) E7 protein. It binds
XX CC with high affinity to human class I molecule HLA-A2. Immunogenic
XX CC peptides of the invention are derived from a region of the HPV16 E7
XX CC protein that includes overlapping class I HLA binding, T-cell
XX CC epitopes. Nucleic acids encoding the immunogenic peptides are
XX CC administered to a mammal, especially a human, to prevent or treat
XX CC exophytic condyloma, flat condyloma, cervical cancer, respiratory
XX CC papilloma, conjunctival papilloma, genital-tract HPV infection and
XX CC cervical dysplasia (claimed).
XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 10 DLQP 13
Db 2 DLQP 5
|||
|||

RESULT 73
AAB37116
ID AAB37116 standard; peptide; 9 AA.
AC AAB37116;
XX
XX DT 10-APR-2001 (first entry)
XX DE Tumour associated antigen Her2/neu immunogenic peptide.
XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
XX KW HLA binding peptide; immune response; glycoprotein; cytostatic;
XX KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;
XX KW human immunodeficiency virus; protozoacide; viral infection; cancer;
XX KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
XX KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
XX KW renal carcinoma; cervical carcinoma; lymphoma; malaria;
XX KW condyloma acuminatum.
XX OS Homo sapiens.
XX PN WO200100225-A1.
XX PD 04-JAN-2001.
XX PF 28-JUN-2000; 2000WO-US17842.
XX PR 29-JUN-1999; 99US-0141422.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S;
XX WPI; 2001-112389/12.
XX CC Composition comprising human leukocyte antigen binding peptide which
XX CC comprises isolated, prepared epitope useful for treating viral
XX CC infections such as acquired immunodeficiency syndrome, and cancer -
XX PS Claim 1; Page 48; 50pp; English.
XX CC The present invention describes a composition (I) which comprises at
XX CC least one human leukocyte antigen (HLA) binding peptide comprising an
XX CC isolated, prepared epitope comprising one of 547 8-11 residue amino acid
XX CC sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,
XX CC virucide, hepatotropic, antiinflammatory, anti-HIV (human
XX CC immunodeficiency virus) and protozoacide activities, which can be used
XX CC in vaccine production and is an inducer of cytotoxic T-cell response.
XX CC (I) is useful for inducing a cytotoxic T cell response against a
XX CC preselected antigen in a patient expressing a specific major
XX CC histocompatibility complex (MHC) class I allele, by contacting cytotoxic
XX CC T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to
XX CC treat and/or prevent viral infection and cancer such as prostate cancer,
XX CC hepatitis B, hepatitis C, human papilloma virus (HPV) infection,
XX CC cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal
XX CC carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
XX CC acuminatum.
XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 10 DLQP 13
Db 4 DLQP 7
|||
|||

RESULT 73
AAB37116
ID AAB37116 standard; peptide; 9 AA.
AC AAB37116;
XX
XX DT 09-APR-2001 (first entry)
XX DE Polylinker site from PUR291 for cloning HTLV-1 gp46 ATLE 495 fragment.
XX KW HTLV-1; env gene; gp46; ATLE495; beta-galactosidase; fusion protein;
XX KW serodiagnosis.
XX OS Escherichia coli.
XX PN RU2152955-C2.
XX PD 20-JUL-2000.
XX PF 15-MAY-1997; 97RU-0107950.
XX PR 15-MAY-1997; 97RU-0107950.
XX PA (AMVI-) A MED VIROLOGY RES INST.
XX PI Bobkov AF, Sankov MN, Selimova LM, Kazennova EV;
XX WPI; 2001-022430/03.
XX DR N-PSDB; AAF28703.
XX CC Fragment of gene env HTLV-1, recombinant plasmid DNA pATLE 495, strain
XX CC of Bacterium Escherichia coli HB101/pATLE 495 as producer of
XX CC polypeptide E 495.
XX PS Example 2; Column 7; 5pp; Russian.
XX CC The invention relates to a method of preparing a novel artificially
XX CC produced polypeptide consisting of the product of the HTLV-1 env
XX CC gene encoding gp46 fragment ATLE495 fused to the E. coli
XX CC beta-galactosidase. This sequence represents the peptide encoded by
XX CC the polylinker sequence from plasmid pUR291 which is downstream of
XX CC the inserted HTLV-1 gp46 ATLE 495 fragment (AAF28701). The hybrid
XX CC protein has the specific polypeptide sequence encoded by region env
XX CC of the HTLV-1 genome and can be used for the serodiagnosis of HTLV-1.
XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 10 DLQP 13
Db 2 DLQP 5
|||
|||

RESULT 74
AAB76118
ID AAB76118 standard; Peptide; 9 AA.
XX
XX AC AAB76118;
XX
XX DT 10-APR-2001 (first entry)
XX DE Tumour associated antigen Her2/neu immunogenic peptide.
XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
XX KW HLA binding peptide; immune response; glycoprotein; cytostatic;
XX KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;
XX KW human immunodeficiency virus; protozoacide; viral infection; cancer;
XX KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
XX KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
XX KW renal carcinoma; cervical carcinoma; lymphoma; malaria;
XX KW condyloma acuminatum.
XX OS Homo sapiens.
XX PN WO200100225-A1.
XX PD 04-JAN-2001.
XX PF 28-JUN-2000; 2000WO-US17842.
XX PR 29-JUN-1999; 99US-0141422.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S;
XX WPI; 2001-112389/12.
XX CC Composition comprising human leukocyte antigen binding peptide which
XX CC comprises isolated, prepared epitope useful for treating viral
XX CC infections such as acquired immunodeficiency syndrome, and cancer -
XX PS Claim 1; Page 48; 50pp; English.
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XX CC least one human leukocyte antigen (HLA) binding peptide comprising an
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XX CC sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,
XX CC virucide, hepatotropic, antiinflammatory, anti-HIV (human
XX CC immunodeficiency virus) and protozoacide activities, which can be used
XX CC in vaccine production and is an inducer of cytotoxic T-cell response.
XX CC (I) is useful for inducing a cytotoxic T cell response against a
XX CC preselected antigen in a patient expressing a specific major
XX CC histocompatibility complex (MHC) class I allele, by contacting cytotoxic
XX CC T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to
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XX CC hepatitis B, hepatitis C, human papilloma virus (HPV) infection,
XX CC cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal
XX CC carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
XX CC acuminatum.
XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

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Title: US-09-641-801-3

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Searched: 673684 seqs, 184443283 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5	27.8	8	12	US-10-365-908-98
3	5	27.8	10	11	US-09-572-404B-3027
4	5	27.8	15	12	US-10-080-608A-70
5	5	27.8	15	12	US-10-370-685-159
6	4	22.2	4	9	US-09-804-866-12
7	4	22.2	5	9	US-09-804-866-13
8	4	22.2	6	10	US-09-727-963A-17
9	4	22.2	9	9	US-09-759-960-17
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13	4	22.2	9	12	US-10-365-908-3
14	4	22.2	9	12	US-10-365-908-80
15	4	22.2	9	15	US-10-033-662-36
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					Sequence 98, Appl
					Sequence 3027, Ap
					Sequence 70, Appl
					Sequence 159, App
					Sequence 12, Appl
					Sequence 13, Appl
					Sequence 17, Appl
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					Sequence 104, App
					Sequence 6, Appli
					Sequence 3, Appli
					Sequence 80, Appl
					Sequence 36, Appl

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4	22.2	12	7	US-08-736-019-164	Sequence 164, App
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4	22.2	12	12	US-10-367-405-14	Sequence 14, Appl
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4	22.2	15	11	US-09-880-505-16	Sequence 16, Appl
4	22.2	15	11	US-09-563-222-139	Sequence 139, App
4	22.2	15	12	US-10-282-960-59	Sequence 59, Appl
4	22.2	15	14	US-10-051-643-16	Sequence 16, Appl
4	22.2	16	10	US-09-908-322-32	Sequence 32, Appl
4	22.2	16	11	US-09-783-931-32	Sequence 32, Appl
4	22.2	17	9	US-09-864-761-37550	Sequence 37550, A
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4	22.2	18	15	US-10-281-652-23	Sequence 23, Appl
4	22.2	18	15	US-10-225-567A-1996	Sequence 1996, Ap
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4	22.2	20	15	US-10-225-567A-755	Sequence 755, App
4	22.2	20	15	US-10-225-567A-1649	Sequence 1649, Ap
4	22.2	4	8	US-08-610-220A-8	Sequence 8, Appli
3	16.7	4	9	US-09-150-623-8	Sequence 8, Appli
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3	16.7	4	12	US-10-239-991-27	Sequence 27, Appl
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3	16.7	5	9	US-09-851-271A-7	Sequence 7, Appli
3	16.7	5	9	US-09-925-796-5	Sequence 5, Appli
3	16.7	5	9	US-09-941-450-5	Sequence 5, Appli
3	16.7	5	10	US-09-922-261-70	Sequence 70, Appl
3	16.7	5	10	US-09-731-558-3	Sequence 3, Appli
3	16.7	5	10	US-09-942-087A-5	Sequence 5, Appli
3	16.7	5	10	US-09-942-090-5	Sequence 5, Appli
3	16.7	5	11	US-09-995-973-7	Sequence 7, Appli
3	16.7	5	11	US-09-846-033B-211	Sequence 211, App
3	16.7	5	11	US-09-500-700-67	Sequence 67, Appl
3	16.7	5	11	US-09-930-186-2	Sequence 2, Appli
3	16.7	5	11	US-09-897-844-5	Sequence 5, Appli
3	16.7	5	11	US-09-996-484-7	Sequence 7, Appli
3	16.7	5	11	US-09-530-139-13	Sequence 13, Appl
3	16.7	5	11	US-09-989-994-2	Sequence 2, Appli
3	16.7	5	12	US-10-076-047A-239	Sequence 239, App
3	16.7	5	12	US-10-076-047A-284	Sequence 284, App
3	16.7	5	12	US-10-303-686A-48	Sequence 48, Appl
3	16.7	5	12	US-10-203-754A-1	Sequence 1, Appli

89 3 16.7 5 12 US-10-316-253-79 Sequence 79, Appl
 90 3 16.7 5 12 US-10-226-629A-3 Sequence 3, Appl
 91 3 16.7 5 12 US-10-226-629A-4 Sequence 4, Appl
 92 3 16.7 5 12 US-10-226-629A-5 Sequence 5, Appl
 93 3 16.7 5 12 US-10-226-629A-6 Sequence 6, Appl
 94 3 16.7 5 12 US-10-226-629A-7 Sequence 7, Appl
 95 3 16.7 5 12 US-10-226-629A-8 Sequence 8, Appl
 96 3 16.7 5 12 US-10-226-629A-9 Sequence 9, Appl
 97 3 16.7 5 12 US-10-226-629A-10 Sequence 10, Appl
 98 3 16.7 5 12 US-10-226-629A-11 Sequence 11, Appl
 99 3 16.7 5 12 US-10-245-415B-5 Sequence 5, Appl
 100 3 16.7 5 12 US-10-412-105-29 Sequence 29, Appl

ALIGNMENTS

RESULT 1
 US-10-281-652-3
 ; Sequence 3, Application US/10281652
 ; Publication No. US20030091606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; FILE REFERENCE: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
 ; CURRENT APPLICATION NUMBER: US/10/281,652
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: US/09/641,803
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide
 US-10-281-652-3

Query Match 100.0%; Score 18; DB 15; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4e-12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQVQS 18
 Db 1 DQPPDVEKPDLPQVQS 18

RESULT 2
 US-10-365-908-98
 ; Sequence 98, Application US/10365908
 ; Publication No. US20030170268A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neefe, John R.
 ; APPLICANT: Boux, Leslie J.
 ; APPLICANT: Winnett, Mark T.
 ; APPLICANT: Goldstone, Stephen E.
 ; APPLICANT: Siegel, Marvin
 ; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
 ; FILE REFERENCE: 12071-003001
 ; CURRENT APPLICATION NUMBER: US/10/365,908
 ; CURRENT FILING DATE: 2003-02-13
 ; PRIOR APPLICATION NUMBER: US/09/891,823
 ; PRIOR FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: US 60/214,202
 ; PRIOR FILING DATE: 2000-06-26
 ; NUMBER OF SEQ ID NOS: 140

; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 98
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Human papilloma virus
 US-10-365-908-98

Query Match 27.8%; Score 5; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

Qy 2 QPDPV 6
 Db 2 QPDPV 6

RESULT 3
 US-09-572-404B-3027
 ; Sequence 3027, Application US/09572404B
 ; Publication No. US20030078374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Proteom Ltd
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome
 ; FILE REFERENCE: Human patent
 ; CURRENT APPLICATION NUMBER: US/09/572,404B
 ; CURRENT FILING DATE: 2000-05-17
 ; NUMBER OF SEQ ID NOS: 4203
 ; SOFTWARE: Protpatent version 1.0
 ; SEQ ID NO 3027
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; OTHER INFORMATION: sequence located in GUCY2D OR GUC2D OR RETGC1 OR RETGC OR GUC1
 ; OTHER INFORMATION: CORD6 at 1069-1078 and may interact with Sequence 3028 in this
 US-09-572-404B-3027

Query Match 27.8%; Score 5; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13
 Db 2 PDLQP 6

RESULT 4
 US-10-080-608A-70
 ; Sequence 70, Application US/10080608A
 ; Publication No. US20030198956A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Makowski, Lee
 ; APPLICANT: Hyman, Paul
 ; APPLICANT: Williams, Mark
 ; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
 ; FILE REFERENCE: 8471-010-999
 ; CURRENT APPLICATION NUMBER: US/10/080,608A
 ; CURRENT FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 180
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 70
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: human rhinovirus 2
 US-10-080-608A-70

Query Match 27.8%; Score 5; DB 12; Length 15;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13
 Db 9 PDLQP 13

```

RESULT 5
US-10-370-685-159
; Sequence 159, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberger, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF.P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 159
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human rhinovirus 2
US-10-370-685-159

Query Match      27.8%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQP 13
Db 9 PDLQP 13

RESULT 6
US-09-804-866-12
; Sequence 12, Application US/09804866
; Patent No. US20020001814A1
; GENERAL INFORMATION:
; APPLICANT: Chu, Ivan K.
; APPLICANT: Lau, Tai-Chu
; TITLE OF INVENTION: Sequencing of Peptides by Mass Spectrometry
; FILE REFERENCE: 7933.208-US-U1
; CURRENT APPLICATION NUMBER: US/09/804,866
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/193,208
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Bovine ubiquitin
US-09-804-866-12

Query Match      22.2%; Score 4; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 1 DVEK 4

RESULT 7
US-09-804-866-13
; Sequence 13, Application US/09804866
; Patent No. US20020001814A1
; GENERAL INFORMATION:
; APPLICANT: Chu, Ivan K.
; APPLICANT: Lau, Tai-Chu
; TITLE OF INVENTION: Sequencing of Peptides by Mass Spectrometry
; FILE REFERENCE: 7933.208-US-U1

```

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; CURRENT APPLICATION NUMBER: US/09/804,866
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/193,208
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bovine ubiquitin
US-09-804-866-13

Query Match      22.2%; Score 4; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 2 DVEK 5

RESULT 8
US-09-727-963A-17
; Sequence 17, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence : peptide
; OTHER INFORMATION: ligand
US-09-727-963A-17

Query Match      22.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQPF 14
Db 3 LQPF 6

RESULT 9
US-09-759-960-17
; Sequence 17, Application US/09759960
; Patent No. US20010006639A1
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Praser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-759-960-17

Query Match 22.2%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
|
|
|
|
Db 4 DLQP 7

RESULT 10
US-09-829-549A-4
; Sequence 4, Application US/09829549A
; Patent No. US20020052484A1
; GENERAL INFORMATION:
; APPLICANT: The Curators of the University of Missouri
; TITLE OF INVENTION: PHAGE DISPLAY SELECTION OF ANTI FUNGAL PEPTIDES
; FILE REFERENCE: UMO 1521.1
; CURRENT APPLICATION NUMBER: US/09/829,549A
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/195,785
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(9)
; OTHER INFORMATION: Random peptide insert
US-09-829-549A-4

Query Match 22.2%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
|
|
|
|
Db 3 PDLQ 6

RESULT 11
US-09-909-460-104
; Sequence 104, Application US/09909460
; Publication No. US20020182258A1

; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; TITLE OF INVENTION: ACID
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-909-460-104

Query Match 22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
|
|
|
|
Db 4 DLQP 7

RESULT 12
US-10-350-258-6
; Sequence 6, Application US/10350258
; Publication No. US20030139345A1
; GENERAL INFORMATION:
; APPLICANT: MATTHIAS RATH
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND METHODS FOR TREATING CANCER INVASION AN
; FILE REFERENCE: 11957/23
; CURRENT APPLICATION NUMBER: US/10/350,258
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/351,317
; PRIOR FILING DATE: January 23, 2002
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-350-258-6

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPDV 6
|
|
|
|
Db 2 PPDV 5

RESULT 13
US-10-365-908-3
; Sequence 3, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19

;; PRIOR APPLICATION NUMBER: US 60/214,202
;; PRIOR FILING DATE: 2000-06-26
;; NUMBER OF SEQ ID NOS: 140
;; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-3

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
|||
DB 4 DLQP 7

RESULT 14
US-10-365-908-80
; Sequence 80, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-80

Query Match 22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPDP 5
|||
DB 2 QPDP 5

RESULT 15
US-10-033-662-36
; Sequence 36, Application US/10033662
; Publication No. US2003092197A1
; GENERAL INFORMATION:
; APPLICANT: Herman, et al.
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Card
; FILE REFERENCE: 9195-081
; CURRENT APPLICATION NUMBER: US/10/033,662
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-662-36

Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
|||
DB 1 KPDL 4

RESULT 16
US-10-128-711-66
; Sequence 66, Application US/10128711
; Publication No. US2003009634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-128-711-66

Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
|||
DB 4 DLQP 7

RESULT 17
US-10-128-711-71
; Sequence 71, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CIL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-128-711-71
Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 DLQP 13
Db 3 DLQP 6
RESULT 18
US-09-847-185-19
; Sequence 19, Application US/09847185
; Patent No. US20020076392A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CIL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/847,185
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-847-185-19
Query Match 22.2%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 DLQP 13
Db 4 DLQP 7

RESULT 19
US-09-835-853-22
; Sequence 22, Application US/09835853
; Patent No. US20020165136A1
; GENERAL INFORMATION:
; APPLICANT: BASERGA, Renato L.
; APPLICANT: RESNICOFF, Mariana
; APPLICANT: HUANG, Ziwei
; TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR LLP
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/835,853
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-847-185-19
Query Match 22.2%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 DLQP 13
Db 4 DLQP 7


```

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/704,344
; APPLICATION NUMBER:
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, Henry N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 942-8459
; TELEFAX: (202) 942-8484
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-09-835-853-22

Query Match                22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 4 DLQP 7

RESULT 20
US-10-177-390-33
; Sequence 33, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Getold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 33
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Influenza virus
US-10-177-390-33

Query Match                22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 4 DLQP 7

RESULT 21
US-10-365-908-57
; Sequence 57, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001

```

```

; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-57

Query Match                22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPD 5
Db 5 QPPD 8

RESULT 22
US-10-365-908-104
; Sequence 104, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-104

Query Match                22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPD 5
Db 1 QPPD 4

RESULT 23
US-10-062-710-228
; Sequence 228, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498

```

; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 228
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Epstein-Barr Virus
US-10-062-710-228

Query Match 22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
Db 4 DLQP 7

RESULT 24
US-10-155-922-82
; Sequence 82, Application US/10155922
; Publication No. US2003008693A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tochigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 46739200220
; CURRENT APPLICATION NUMBER: US/10/155,922
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-82

Query Match 22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEKP 9
Db 2 VEKP 5

RESULT 25
US-10-133-210-271
; Sequence 271, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay

; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Wang, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 271
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-271

Query Match 22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
Db 4 DLQP 7

RESULT 26
US-10-211-088-67
; Sequence 67, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1e1 Fusion Proteins And Assays For Molecular
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
US-10-211-088-67

Query Match 22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDL 11
Db 3 KPDL 6

RESULT 27
US-10-224-286-19
; Sequence 19, Application US/10224286
; Publication No. US20030108517A1
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISEING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50

;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: CAMPBELL & FLORES, LLP
;/ STREET: 4370 La Jolla Village Drive, Suite 700
;/ CITY: San Diego
;/ STATE: California
;/ COUNTRY: United States
;/ ZIP: 92121
;/
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patent In Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/10/224,286
;/ FILING DATE: 19-Aug-2002
;/ CLASSIFICATION: <Unknown>
;/
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/902,516
;/ FILING DATE: 29-JUL-1997
;/
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Campbell, Cathryn A.
;/ REGISTRATION NUMBER: 31,815
;/ REFERENCE/DOCKET NUMBER: P-IM 2442
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (619)535-9001
;/ TELEFAX: (619)535-8949
;/
;/ INFORMATION FOR SEQ ID NO: 19:
;/
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 10 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 19:
;/
;/ US-10-224-286-19

Query Match 22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLOP 13
Db 4 DLOP 7

RESULT 28
US-09-017-743C-122
; Sequence 122, Application US/09017743C
; Patent No. US20020177694A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; Southwood, Scott
; TITLE OF INVENTION: HIA Binding Peptides and Their
; Uses
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,743C
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298

;/ FILING DATE: 23-JAN-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Parent, Annette S.
;/ REGISTRATION NUMBER: 42,058
;/ REFERENCE/DOCKET NUMBER: 018623-008050US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 415-576-0200
;/ TELEFAX: 415-576-0300
;/ TELEX: <Unknown>
;/ INFORMATION FOR SEQ ID NO: 122:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 11 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 122:
;/
;/ US-09-017-743C-122

Query Match 22.2%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db 6 KPDL 9

RESULT 29
US-10-367-405-5
; Sequence 5, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Felix Hausch
; APPLICANT: Gary Gray
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT APPLICATION NUMBER: US/10/367,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Triticum aestivum
; US-10-367-405-5

Query Match 22.2%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQPF 14
Db 2 LQPF 5

RESULT 30
US-10-062-710-206
; Sequence 206, Application US/10062710

```

; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T Cell epitopes
US-10-062-710-206

```

```

Query Match          22.2%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 10 DLQP 13
Db 5 DLQP 8

```

```

RESULT 31
US-10-211-088-69
; Sequence 69, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular Bi
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
US-10-211-088-69

```

```

Query Match          22.2%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 8 KPDL 11
Db 4 KPDL 7

```

```

RESULT 32
US-08-736-019-164
; Sequence 164, Application US/08736019
; Publication No. US20030207799A1
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew

```

```

; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/736,019
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,833
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-736-019-164

```

```

Query Match          22.2%; Score 4; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 DVEK 8
Db 9 DVEK 12

```

```

RESULT 33
US-09-954-385-190
; Sequence 190, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzk, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-190

Query Match          22.2%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 2 DLQP 5

RESULT 34
US-10-367-405-1
; Sequence 1, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Felix Hausch
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT APPLICATION NUMBER: US/10/367,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR FILING DATE: 2002-05-14
; PRIOR FILING DATE: 2002-06-28
; PRIOR FILING DATE: 2002-10-31
; PRIOR FILING DATE: 2002-11-20
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: PYRROLIDONE CAR
; LOCATION: (1)...(1)
; OTHER INFORMATION: N terminal pyroglutamate
US-10-367-405-2

Query Match          22.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQPF 14
Db 2 LQPF 5

RESULT 35
US-10-367-405-2
; Sequence 2, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Felix Hausch
; APPLICANT: Gary Gray
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT APPLICATION NUMBER: US/10/367,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR FILING DATE: 2002-05-14
; PRIOR FILING DATE: 2002-06-28
; PRIOR FILING DATE: 2002-10-31
; PRIOR FILING DATE: 2002-11-20
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: PYRROLIDONE CAR
; LOCATION: (1)...(1)
; OTHER INFORMATION: N terminal pyroglutamate
US-10-367-405-2

Query Match          22.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQPF 14
Db 2 LQPF 5

RESULT 36
US-10-367-405-14
; Sequence 14, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Felix Hausch
; APPLICANT: Gary Gray
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT APPLICATION NUMBER: US/10/367,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR FILING DATE: 2002-05-14
; PRIOR FILING DATE: 2002-06-28
; PRIOR FILING DATE: 2002-10-31
; PRIOR FILING DATE: 2002-11-20
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-367-405-1

Query Match          22.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: triticum aestivum
US-10-367-405-14

Query Match
Best Local Similarity 22.2%; Score 4; DB 12; Length 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQPF 14
DB 2 LQPF 5

RESULT 37
US-10-075-869-37
; Sequence 37, Application US/10075869
; Publication No. US20030104622A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, Paul D.
; APPLICANT: Mi, Zhibao
; APPLICANT: Frizzell, Raymond
; APPLICANT: Glorioso, Joseph C.
; APPLICANT: Gambotto, Andrea
; TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT
; TITLE OF INVENTION: FACILITATE UPTAKE AND CYTOPLASMIC AND/OR NUCLEAR TRANSPORT
; FILE REFERENCE: AP32573-AAA 072396.0237
; CURRENT APPLICATION NUMBER: US/10/075,869
; PRIOR FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/151,980
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/188,944
; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: random peptide library
US-10-075-869-37

Query Match
Best Local Similarity 22.2%; Score 4; DB 15; Length 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 6 DLQP 9

RESULT 38
US-09-935-682-57
; Sequence 57, Application US/09935682
; Patent No. US20020059032A1
; GENERAL INFORMATION:
; APPLICANT: Societe de Conseils de Recherches et D'Applications Scientifiques
; APPLICANT: Ferrer, Camara Y.
; TITLE OF INVENTION: Rational Selection of Putative Peptides from Identified Nucleotic
; TITLE OF INVENTION: Peptide Sequences
; FILE REFERENCE: 58767.000005
; CURRENT APPLICATION NUMBER: US/09/935,682
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/257,525
; PRIOR FILING DATE: 1999-02-25

; PRIOR FILING DATE: 2002-02-24
; PRIOR APPLICATION NUMBER: PCT/FR00/00460
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-682-57

Query Match
Best Local Similarity 22.2%; Score 4; DB 9; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9
DB 7 VEKP 10

RESULT 39
US-09-880-505-16
; Sequence 16, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-880-505-16

Query Match
Best Local Similarity 22.2%; Score 4; DB 11; Length 15;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
DB 4 PDLQ 7

RESULT 40
US-09-563-222-139
; Sequence 139, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-139
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Query Match 22.2%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EKPD 10
|||||
Db 4 EKPD 7

RESULT 41

US-10-282-960-59
; Sequence 59, Application US/10282960
; Publication No. US20030143228A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Si-Yi
; APPLICANT: Zhao, You
; APPLICANT: Schroers, Roland
; TITLE OF INVENTION: Human telomerase Reverse Transcriptase as a Class-II Restricted T
; FILE REFERENCE: P02193US1
; CURRENT APPLICATION NUMBER: US/10/282,960
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/345,012
; PRIOR FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 59
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human
US-10-282-960-59

Query Match 22.2%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
|||||
Db 3 DLQP 6

RESULT 42

US-10-051-643-16
; Sequence 16, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium Vaccae
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-051-643-16

Query Match 22.2%; Score 4; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
|||||
Db 4 PDLQ 7

RESULT 43

US-09-908-322-32
; Sequence 32, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-908-322-32

Query Match 22.2%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QVQS 18
|||||
Db 6 QVQS 9

RESULT 44

US-09-783-931-32
; Sequence 32, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
; AND FRAGMENTS

```

;
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,931
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Antlex, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-783-931-32

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Query Match 22.2%; Score 4; DB 11; Length 16;

Best Local Similarity 100.0%; Pred. No. 8.4e+02; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

Oy 15 QVQS 18

Db 6 QVQS 9

RESULT 45

US-09-864-761-37550

; Sequence 37550, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeonica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-03-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37550
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010681.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
US-09-864-761-37550

```

Query Match

22.2%; Score 4; DB 9; Length 17;

Best Local Similarity 100.0%; Pred. No. 8.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 PDLQ 12

Db 8 PDLQ 11

RESULT 46

US-10-161-791-338

; Sequence 338, Application US/10161791

; Publication No. US20030186863A1

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 338:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-338

Query Match 22.2%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDVE 7
Db 1 PDVE 4

RESULT 47
US-10-161-791-341
; Sequence 341, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 341:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-341

Query Match 22.2%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDVE 7
Db 13 PDVE 16

RESULT 48
US-10-225-567A-1370
; Sequence 1370, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1370
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-225-567A-1370

Query Match 22.2%; Score 4; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db 8 PDLQ 11

RESULT 49
US-10-225-567A-1974
; Sequence 1974, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1974
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1974

Query Match      22.2%; Score 4; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PDVE 7
Db      1 PDVE 4
      |||||

RESULT 50
US-09-864-761-41948
; Sequence 41948, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US 09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-09-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00671
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41948
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
```

```
; OTHER INFORMATION: MAP TO AC002477.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
; OTHER INFORMATION: EST_HUMAN HIT: AA906517.1, EVALUATE 7.00e-04
US-09-864-761-41948

Query Match      22.2%; Score 4; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PDLQ 12
Db      14 PDLQ 17
      |||||

RESULT 51
US-10-140-372-15
; Sequence 15, Application US/10140372
; Publication No. US20030021789A1
; GENERAL INFORMATION:
; APPLICANT: XU, Yi
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: SURFACE PROTEINS FROM GRAM-POSITIVE BACTERIA
; FILE REFERENCE: P07196US01/BAS
; CURRENT APPLICATION NUMBER: US/10/140,372
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,132
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-140-372-15

Query Match      22.2%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VEKP 9
Db      6 VEKP 9
      |||||

RESULT 52
US-10-281-652-23
; Sequence 23, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 18
; TYPE: PRT
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-23

Query Match      22.2%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DVEK 8
Db      6 DVEK 9

RESULT 53
US-10-225-567A-1996
; Sequence 1996, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1996
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1996

Query Match      22.2%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PDLQ 12
Db      11 PDLQ 14

RESULT 54
US-09-814-550-6
; Sequence 6, Application US/09814550
; Patent No. US20020102641A1
; GENERAL INFORMATION:
; APPLICANT: Schiavi, Susan
; APPLICANT: Madden, Stephen
; APPLICANT: Manavalan, Parthasarathy
; APPLICANT: Levine, Michael
; APPLICANT: Jan de Beur, Suzanne
; TITLE OF INVENTION: ONCOGENIC OSTEOMALACIA-RELATED GENE 1
; FILE REFERENCE: 5014US
; CURRENT APPLICATION NUMBER: US/09/814,550
; CURRENT FILING DATE: 2001-03-22
; PRIOR FILING DATE: US 60/191,786
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/241,598
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-814-550-6
```

```

Query Match      22.2%; Score 4; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PDLQ 12
Db      3 PDLQ 6

RESULT 55
US-10-094-401-138
; Sequence 138, Application US/10094401
; Publication No. US20030069395A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Cohen, Edward H.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES
; FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US
; CURRENT APPLICATION NUMBER: US/10/094,401
; CURRENT FILING DATE: 2002-03-08
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/331,352
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/292,975
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: albumin binding peptide
US-10-094-401-138

Query Match      22.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PDLQ 12
Db      7 PDLQ 10

RESULT 56
US-10-225-567A-755
; Sequence 755, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Joseph P.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 755
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-755

Query Match      22.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PDVE 7
```

```
Db          |||||
            7 PDVE 10

RESULT 57
US-10-225-567A-1649
; Sequence 1649, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225.567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1649
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1649

Query Match      22.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DVEK 8
          |||||
Db      14 DVEK 17

RESULT 58
US-08-610-220A-8
; Sequence 8, Application US/08610220A
; Publication No. US20030099638A1
; GENERAL INFORMATION:
; APPLICANT: Troy, Carol M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
; TITLE OF INVENTION: DEATH AND USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/610,220A
; FILING DATE: MAR-04-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 48332/JPW/JML
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

Query Match      16.7%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DVE 7
          |||||
Db      1 DVE 3

RESULT 60
US-09-982-172-156
; Sequence 156, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBIO
```

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; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-156

Query Match      16.7%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 VEK 8
      |||
Db      2 VEK 4

RESULT 61
US-09-877-381-4
; Sequence 4, Application US/09877381
; Patent No. US20020146796A1
; GENERAL INFORMATION:
; APPLICANT: Richard Drake
; APPLICANT: Trenton Hinds
; APPLICANT: Cesar Compadre
; APPLICANT: Barry Hurlburt
; APPLICANT: Tammy Rechtin
; TITLE OF INVENTION: Mutated Herpes Simplex Virus Type I Thymidine
; TITLE OF INVENTION: Kinases and Uses Thereof
; FILE REFERENCE: D6128
; CURRENT APPLICATION NUMBER: US/09/877,381
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 09/338,308
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: a peptide substrate used for a colorimetric assay
US-09-877-381-4

Query Match      16.7%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 DVE 7
      |||
Db      1 DVE 3

RESULT 62
US-10-226-629A-1
; Sequence 1, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182

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; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Equine infectious anemia virus
US-10-226-629A-1

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Query Match      16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      9 PDL 11
      |||
Db      2 PDL 4

```

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RESULT 63
US-10-299-991-27
; Sequence 27, Application US/10299991
; Publication No. US20030194725A1
; GENERAL INFORMATION:
; APPLICANT: Greener et al.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AND VALIDATING POTENTIAL DRUG TARGETS
; FILE REFERENCE: PROL-P01-004
; CURRENT APPLICATION NUMBER: US/10/299,991
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/331701
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Retroviral
US-10-299-991-27

```

```

Query Match      16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      9 PDL 11
      |||
Db      2 PDL 4

```

```

RESULT 64
US-10-006-630-17
; Sequence 17, Application US/10006630
; Publication No. US20020150926A1
; GENERAL INFORMATION:
; APPLICANT: Jindal, Satish
; APPLICANT: Regnier, Fred
; APPLICANT: Evans, David
; APPLICANT: Williams, Kevin
; APPLICANT: Afeyan, No. US20020150926A1bar
; APPLICANT: Paliwal, Sandeep
; APPLICANT: Pingali, Aruna
; TITLE OF INVENTION: High Speed, automated, continuous flow,
; TITLE OF INVENTION: multi-dimensional molecular selection and analysis
; FILE REFERENCE: SYP-101DV
; CURRENT APPLICATION NUMBER: US/10/006,630
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 09/267,993
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/000,518
; PRIOR FILING DATE: 1995-06-26
; PRIOR APPLICATION NUMBER: 08/670,670
; PRIOR FILING DATE: 1996-06-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17

```

```
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif with
; OTHER INFORMATION: similarity to TVTEK
US-10-006-630-17

Query Match          16.7%; Score 3; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEK 8
   |||
Db 2 VEK 4

RESULT 65
US-10-146-221-20
; Sequence 20, Application US/10146221
; Publication No. US20020173006A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Pabo, Carl O.
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Poly Zinc Finger Proteins With Improved Linkers
; FILE REFERENCE: 019496-002510US
; CURRENT APPLICATION NUMBER: US/10/146,221
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/260,629
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: linker sequence
US-10-146-221-20

Query Match          16.7%; Score 3; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
   |||
Db 2 EXP 4

RESULT 66
US-10-097-534-42
; Sequence 42, Application US/10097534
; Publication No. US20030049607A1
; GENERAL INFORMATION:
; APPLICANT: GREENER, TSVIKA
; APPLICANT: MOSKOWITZ, HAIM
; APPLICANT: REISS, YUVAL
; APPLICANT: ALROY, IRIS
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
; TITLE OF INVENTION: MATURATION
; FILE REFERENCE: PLV-001.01
; CURRENT APPLICATION NUMBER: US/10/097,534
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,224
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/308,958
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/340,170
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 42
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: Gag protein motif
US-10-097-534-42

Query Match          16.7%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDL 11
   |||
Db 2 PDL 4

RESULT 67
US-10-198-677-56
; Sequence 56, Application US/10198677
; Publication No. US20030119023A1
; GENERAL INFORMATION:
; APPLICANT: CHOO, Yen
; APPLICANT: KLUG, Aaron
; APPLICANT: MOORE, Michael
; TITLE OF INVENTION: NUCLEIC ACID BINDING POLYPEPTIDES CHARACTERIZED BY
; TITLE OF INVENTION: FLEXIBLE LINKERS CONNECTED NUCLEIC ACID BINDING
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 8325-2011 / G11-US1
; CURRENT APPLICATION NUMBER: US/10/198,677
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: canonical linker
; OTHER INFORMATION: sequence variant
US-10-198-677-56

Query Match          16.7%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
   |||
Db 2 EXP 4

RESULT 68
US-09-779-233-29
; Sequence 29, Application US/09779233
; Patent No. US20020045158A1
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-779-233-29

Query Match          16.7%; Score 3; DB 9; Length 5;
```

Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
Db 3 EXP 5

RESULT 69
US-09-989-789-2
; Sequence 2, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Oiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide linker
US-09-989-789-2

Query Match 16.7%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
Db 3 EXP 5

RESULT 70
US-09-851-271A-7
; Sequence 7, Application US/09851271A
; Patent No. US20020064824A1
; GENERAL INFORMATION:
; APPLICANT: Gendag Limited
; TITLE OF INVENTION: Screening System
; FILE REFERENCE: 674538-2003
; CURRENT APPLICATION NUMBER: US/09/851,271A
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: PCT/GB99/03730
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: GB9824544.2
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; OTHER INFORMATION: linker
US-09-851-271A-7

Query Match 16.7%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
Db 3 EXP 5

RESULT 71
US-09-925-796-5

; Sequence 5, Application US/09925796
; Patent No. US20020081614A1
; GENERAL INFORMATION:
; APPLICANT: Case, Casey C.
; APPLICANT: Zhang, Lei
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins
; FILE REFERENCE: 019496-002000US
; CURRENT APPLICATION NUMBER: US/09/925,796
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/395,448
; PRIOR FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: 09/229,037
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-925-796-5

Query Match 16.7%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
Db 3 EXP 5

RESULT 72
US-09-941-450-5
; Sequence 5, Application US/09941450
; Patent No. US20020094529A1
; GENERAL INFORMATION:
; APPLICANT: Case, Casey C.
; APPLICANT: Urnov, Fyodor
; TITLE OF INVENTION: GENE IDENTIFICATION
; FILE REFERENCE: S7.US3 / 8325-0007.20
; CURRENT APPLICATION NUMBER: US/09/941,450
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/395,448
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-941-450-5

Query Match 16.7%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
Db 3 EXP 5

RESULT 73
US-09-922-261-70
; Sequence 70, Application US/09922261
; Patent No. US2002011471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.

```
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-261-70
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Query Match 16.7%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 4 PDV 6
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Db 3 PDV 5
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RESULT 74

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US-09-731-558-3
; Sequence 3, Application US/09731558
; Patent No. US20020146691A1
; GENERAL INFORMATION:
; APPLICANT: Case, Casey Christopher
; APPLICANT: Liu, Qiang
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
; TITLE OF INVENTION: Proteins for the Identification of Gene Function
; FILE REFERENCE: 019496-003210US
; CURRENT APPLICATION NUMBER: US/09/731,558
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US/09/456,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:flexible
; OTHER INFORMATION: polypeptide linker
US-09-731-558-3
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Query Match 16.7%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 7 EXP 9
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Db 3 EXP 5
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RESULT 75

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US-09-942-087A-5
; Sequence 5, Application US/09942087A
; Patent No. US20020160940A1
; GENERAL INFORMATION:
; APPLICANT: Case, Casey Christopher
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; APPLICANT: Wolffe, Alan
; APPLICANT: Urnov, Fyodor
; APPLICANT: Lai, Albert
; APPLICANT: Snowden, Andrew
; APPLICANT: Tan, Siyuan
; APPLICANT: Gregory, Philip
; TITLE OF INVENTION: MODULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; FILE REFERENCE: 8325-0002.21 / S2-US5
; CURRENT APPLICATION NUMBER: US/09/942,087A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/229,037
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:linker
US-09-942-087A-5
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Query Match 16.7%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 7 EXP 9
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Db 3 EXP 5
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Search completed: November 25, 2003, 20:25:28
Job time : 37.8085 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 19.6277 Seconds
(without alignments)
38.802 Million cell updates/sec

Title: US-09-641-801-3

Perfect score: 18

Sequence: 1 DQPPVEXKDLQFFQVQS 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	5	27.8	15	4	US-09-914-259-70
3	5	27.8	19	3	US-08-781-420-4
4	5	27.8	19	4	US-08-874-102-4
5	5	27.8	19	4	US-08-984-919A-4
6	5	27.8	19	4	US-09-006-595A-4
7	5	27.8	20	2	US-08-447-430A-30
8	5	27.8	20	4	US-09-342-673-30
9	4	22.2	4	3	US-08-810-720-12
10	4	22.2	5	3	US-09-202-832-6
11	4	22.2	6	5	PCT-US93-13679-11
12	4	22.2	8	1	US-07-923-724-48
13	4	22.2	8	2	US-08-609-426A-48
14	4	22.2	8	2	US-08-374-652C-38
15	4	22.2	9	1	US-08-078-176-9
16	4	22.2	9	1	US-08-078-176-10
17	4	22.2	9	1	US-08-078-175-4
18	4	22.2	9	1	US-08-217-188A-62
19	4	22.2	9	1	US-08-687-326-62
20	4	22.2	9	1	US-08-787-547-104
21	4	22.2	9	3	US-08-948-378A-17
22	4	22.2	9	3	US-08-667-725B-62
23	4	22.2	9	3	US-09-007-748-62
24	4	22.2	9	3	US-09-169-425C-17
25	4	22.2	9	4	US-08-197-484-66
26	4	22.2	9	4	US-08-197-484-71
27	4	22.2	9	4	US-09-759-960-17

28	4	22.2	9	5	PCT-US95-02121-66	Sequence 66, Appl
29	4	22.2	9	5	PCT-US95-02121-71	Sequence 71, Appl
30	4	22.2	10	2	US-08-538-387A-25	Sequence 25, Appl
31	4	22.2	10	2	US-08-538-387A-26	Sequence 26, Appl
32	4	22.2	10	2	US-08-902-516-19	Sequence 19, Appl
33	4	22.2	10	2	US-08-723-423-25	Sequence 25, Appl
34	4	22.2	10	2	US-08-723-423-26	Sequence 26, Appl
35	4	22.2	10	3	US-08-709-435-25	Sequence 25, Appl
36	4	22.2	10	3	US-08-709-435-26	Sequence 26, Appl
37	4	22.2	10	3	US-08-567-746A-25	Sequence 26, Appl
38	4	22.2	10	3	US-08-567-746A-26	Sequence 26, Appl
39	4	22.2	10	3	US-08-633-410-25	Sequence 25, Appl
40	4	22.2	10	3	US-08-633-410-26	Sequence 26, Appl
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42	4	22.2	10	3	US-08-711-426-25	Sequence 25, Appl
43	4	22.2	10	3	US-08-711-426-26	Sequence 26, Appl
44	4	22.2	10	4	US-08-669-252-25	Sequence 25, Appl
45	4	22.2	10	4	US-08-669-252-26	Sequence 26, Appl
46	4	22.2	10	4	US-09-098-122-25	Sequence 25, Appl
47	4	22.2	10	4	US-09-098-122-26	Sequence 26, Appl
48	4	22.2	10	4	US-09-847-185-19	Sequence 19, Appl
49	4	22.2	10	6	5166088-8	Patent No. 5166088
50	4	22.2	12	1	US-08-036-555B-164	Sequence 164, App
51	4	22.2	12	1	US-08-469-569-164	Sequence 164, App
52	4	22.2	12	1	US-08-249-322A-164	Sequence 164, App
53	4	22.2	12	1	US-08-469-526A-164	Sequence 164, App
54	4	22.2	12	2	US-08-734-591A-164	Sequence 164, App
55	4	22.2	12	2	US-08-469-660-164	Sequence 164, App
56	4	22.2	12	3	US-08-470-335-164	Sequence 164, App
57	4	22.2	12	3	US-08-734-664A-164	Sequence 164, App
58	4	22.2	12	3	US-08-735-021-164	Sequence 164, App
59	4	22.2	12	3	US-08-470-339-164	Sequence 164, App
60	4	22.2	12	4	US-08-467-602-164	Sequence 164, App
61	4	22.2	12	4	US-09-555-352-16	Sequence 16, Appl
62	4	22.2	12	5	PCT-US94-05083C-160	Sequence 160, App
63	4	22.2	15	2	US-08-687-956A-3	Sequence 3, Appli
64	4	22.2	15	2	US-08-997-080-16	Sequence 16, Appl
65	4	22.2	15	2	US-08-997-362-16	Sequence 16, Appl
66	4	22.2	15	3	US-08-873-970-16	Sequence 16, Appl
67	4	22.2	15	3	US-09-095-855-16	Sequence 16, Appl
68	4	22.2	15	3	US-08-705-347A-16	Sequence 16, Appl
69	4	22.2	15	4	US-09-324-542-16	Sequence 16, Appl
70	4	22.2	15	4	US-09-205-426-16	Sequence 16, Appl
71	4	22.2	15	4	US-09-200-643-16	Sequence 16, Appl
72	4	22.2	15	4	US-07-145-002B-62	Sequence 62, Appl
73	4	22.2	16	1	US-07-942-245-77	Sequence 77, Appl
74	4	22.2	16	1	US-07-942-245-92	Sequence 92, Appl
75	4	22.2	16	1	US-07-942-245-93	Sequence 93, Appl
76	4	22.2	16	1	US-08-615-942A-9	Sequence 9, Appli
77	4	22.2	16	3	US-08-750-145A-8	Sequence 8, Appli
78	4	22.2	16	3	US-08-975-698A-5	Sequence 5, Appli
79	4	22.2	16	3	US-09-361-434-2	Sequence 2, Appli
80	4	22.2	16	3	US-09-417-090-5	Sequence 5, Appli
81	4	22.2	16	3	US-08-981-392-32	Sequence 32, Appl
82	4	22.2	16	4	US-09-727-578-5	Sequence 5, Appli
83	4	22.2	16	4	US-09-635-025-2	Sequence 2, Appli
84	4	22.2	16	4	US-09-433-466-3	Sequence 3, Appli
85	4	22.2	17	1	US-08-370-567-24	Sequence 24, Appl
86	4	22.2	17	1	US-08-438-759-24	Sequence 24, Appl
87	4	22.2	17	1	US-08-729-152-46	Sequence 46, Appl
88	4	22.2	17	3	US-09-195-666A-21	Sequence 21, Appl
89	4	22.2	17	3	US-08-836-922-18	Sequence 18, Appl
90	4	22.2	17	3	US-08-602-999A-338	Sequence 338, App
91	4	22.2	17	3	US-08-602-999A-341	Sequence 341, App
92	4	22.2	17	4	US-09-635-705-21	Sequence 21, Appl
93	4	22.2	17	4	US-09-500-124-338	Sequence 338, App
94	4	22.2	17	4	US-09-500-124-341	Sequence 341, App
95	4	22.2	17	4	US-09-634-858A-21	Sequence 21, Appl
96	4	22.2	17	4	US-08-869-927C-21	Sequence 21, Appl
97	4	22.2	17	4	US-09-639-881-18	Sequence 18, Appl
98	4	22.2	17	5	PCT-US94-05684-24	Sequence 24, Appl
99	4	22.2	18	2	US-08-929-922B-11	Sequence 11, Appl
100	4	22.2	18	2		

ALIGNMENTS

RESULT 1
US-09-641-803-3
; Sequence 3, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-3

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPPDVKPDLPQFQVQS 18
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DB 1 DQPPDVKPDLPQFQVQS 18

RESULT 2
US-09-914-259-70
; Sequence 70, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human rhinovirus 2
US-09-914-259-70

Query Match 27.8%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQP 13
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DB 9 PDLQP 13

RESULT 3
US-08-781-420-4
; Sequence 4, Application US/08781420
; Patent No. 6248872

; GENERAL INFORMATION:
; APPLICANT: Chandrashekar, Ramaswamy
; APPLICANT: Mehta, Kapil
; TITLE OF INVENTION: Parasitic Nematode Transglutaminase
; TITLE OF INVENTION: Proteins, Nucleic Acid Molecules and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,420
; FILING DATE: December 3, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: HW-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-420-4

Query Match 27.8%; Score 5; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFQVQ 17
|||
DB 11 PFQVQ 15

RESULT 4
US-08-874-102-4
; Sequence 4, Application US/08874102
; Patent No. 6309644
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Kapil Mehta
; TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/874,102
FILING DATE: 12-JUN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-2-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-874-102-4

Query Match 27.8%; Score 5; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFQVQ 17
Db 11 PFQVQ 15

RESULT 5
US-08-984-919A-4
Sequence 4, Application US/08984919A
Patent No. 6383774
GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Mehta, Kapil
TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Hesk Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,919A
FILING DATE: 04-DEC-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-2-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-984-919A-4

Query Match 27.8%; Score 5; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFQVQ 17
Db 11 PFQVQ 15

RESULT 6
US-09-006-595A-4
Sequence 4, Application US/09006595A
Patent No. 6414115
GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Mehta, Kapil
TITLE OF INVENTION: Parasitic Nematode Transglutaminase
Proteins, Nucleic Acid Molecules and
Uses Thereof
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Hesk Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,595A
FILING DATE: 13-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/781,420
FILING DATE: December 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-006-595A-4

Query Match 27.8%; Score 5; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFQVQ 17
Db 11 PFQVQ 15

RESULT 7
US-08-447-430A-30
Sequence 30, Application US/08447430A
Patent No. 5916558
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Recombinant polypeptides and peptides,
TITLE OF INVENTION: nucleic acids coding for the same and use of these
TITLE OF INVENTION: polypeptides and peptides in the diagnostic of
TITLE OF INVENTION: tuberculosis.
NUMBER OF SEQUENCES: 43

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,430A
; FILING DATE:
; CLASSIFICATION: 424
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-447-430A-30

Query Match      27.8%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 KPDLQ 12
Db      1 KPDLQ 5

RESULT 8
US-09-342-673-30
; Sequence 30, Application US/09342673
; Patent No. 6531138
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant polypeptides and peptides,
; TITLE OF INVENTION: nucleic acids coding for the same and use of these
; TITLE OF INVENTION: polypeptides and peptides in the diagnostic of
; TITLE OF INVENTION: tuberculosis.
; NUMBER OF SEQUENCES: 43
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/342,673
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/447,430
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-09-342-673-30

Query Match      27.8%; Score 5; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 KPDLQ 12
Db      1 KPDLQ 5

RESULT 9
US-08-810-720-12
; Sequence 12, Application US/08810720
; Patent No. 6037527
; GENERAL INFORMATION:

```

```

; APPLICANT: Barton, Kenneth A.
; APPLICANT: Umbeck, Paul F.
; TITLE OF INVENTION: INSECTICIDAL COTTON PLANTS (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay
; STREET: One South Finckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,720
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 670513.90163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608/251-5000
; TELEFAX: 608/251-9166
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-810-720-12

Query Match      22.2%; Score 4; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DQPP 4
Db      1 DQPP 4

RESULT 10
US-09-202-832-6
; Sequence 6, Application US/09202832
; Patent No. 6194190
; GENERAL INFORMATION:
; APPLICANT: IZU, Yukiko
; APPLICANT: TANAKA, Tetsuki
; APPLICANT: MIYAGI, Masaru
; APPLICANT: TANIGAWA, Tetsuo
; APPLICANT: TOMONO, Jun
; APPLICANT: TSUNASAWA, Susumu
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: NOVEL AMINO-TERMINAL DEBLOCKING ENZYME
; FILE REFERENCE: 1422-368P
; CURRENT APPLICATION NUMBER: US/09/202,832
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa = N-acetyl-glycine
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Peptide
; US-09-202-832-6

```

Query Match 22.2%; Score 4; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DVEK 8
 Db 2 DVEK 5

RESULT 11
 PCT-US93-12679-11
 ; Sequence 11, Application PC/TUS9312679
 ; GENERAL INFORMATION:
 ; APPLICANT: Rath, Matthias
 ; TITLE OF INVENTION: SYNTHETIC OLIGOPEPTIDES ANALOGOUS TO
 ; TITLE OF INVENTION: PROTEIN SIGNAL SEQUENCES -METHODS OF IDENTIFICATION AND
 ; NUMBER OF SEQUENCES: 41
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SHELDON & MAK
 ; STREET: 401 Florence Street
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/12679
 ; FILING DATE: 30-DEC-1993
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cranfill, Raymond B
 ; REGISTRATION NUMBER: 32,845
 ; REFERENCE/DOCKET NUMBER: RATH-10016PC
 ; TELEPHONE: 415-322-5333
 ; TELEFAX: 415-322-5499
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 PCT-US93-12679-11

Query Match 22.2%; Score 4; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 EKPD 10
 Db 3 EKPD 6

RESULT 12
 US-07-923-724-48
 ; Sequence 48, Application US/07923724
 ; Patent No. 5780292
 ; GENERAL INFORMATION:
 ; APPLICANT: Nevalainen, Helena K.M.
 ; APPLICANT: Paloheimo, Marja T.
 ; APPLICANT: Miettinen-Oinonen, Arja S.K.
 ; APPLICANT: Torkkeli, Tuula K.
 ; APPLICANT: Cantrell, Michael
 ; APPLICANT: Piddington, Christopher S.
 ; APPLICANT: Rambosek, John A.
 ; APPLICANT: Turunen, Marja K.
 ; APPLICANT: Fagerstr m, Richard B.

; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
 ; TITLE OF INVENTION: in Trichoderma
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/923,724
 ; FILING DATE: 31-JUL-1992
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/496,155
 ; FILING DATE: 19-MAR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/044,077
 ; FILING DATE: 29-APR-1987
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: UK 8610600
 ; FILING DATE: 30-APR-1986
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cimbala, Michele A.
 ; REGISTRATION NUMBER: 33,851
 ; REFERENCE/DOCKET NUMBER: 1050.0240004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 48:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: both
 ; US-07-923-724-48

Query Match 22.2%; Score 4; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFQV 16
 Db 4 PFQV 7

RESULT 13
 US-08-609-426A-48
 ; Sequence 48, Application US/08609426A
 ; Patent No. 5830733
 ; GENERAL INFORMATION:
 ; APPLICANT: Nevalainen, Helena K.M.
 ; APPLICANT: Paloheimo, Marja T.
 ; APPLICANT: Miettinen-Oinonen, Arja S.K.
 ; APPLICANT: Torkkeli, Tuula K.
 ; APPLICANT: Cantrell, Michael
 ; APPLICANT: Piddington, Christopher S.
 ; APPLICANT: Rambosek, John A.
 ; APPLICANT: Turunen, Marja K.
 ; APPLICANT: Fagerstr m, Richard B.
 ; APPLICANT: Houston, Christine S.
 ; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
 ; TITLE OF INVENTION: in Trichoderma
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington

```

; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,426A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/923,724
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Grant E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 1050.0080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: both
US-08-609-426A-48

```

```

Query Match 22.2%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 13 PFQV 16
Db 4 PFQV 7

```

```

RESULT 14
US-08-374-652C-38
; Sequence 38, Application US/08374652C
; Patent No. 5834286
; GENERAL INFORMATION:
; APPLICANT: NEVALAINEN, HELENA K.M.
; APPLICANT: PALOHEIMO, MARJA T.
; APPLICANT: FAGERSTROM, RICHARD B.
; APPLICANT: MIETTINEN-OINONEN, ARJA S.
; APPLICANT: TURUNEN, MARJA K.
; APPLICANT: RAMOSEK, JOHN A.
; APPLICANT: PIDDINGTON, CHRISTOPHER S.
; APPLICANT: HOUSTON, CHRISTINE S.
; APPLICANT: CANTRELL, MICHAEL A.
; TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
; TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
; TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:

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```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,652C
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07058
; FILING DATE: 27-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/925,401
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, GRANT E.
; REGISTRATION NUMBER: 41,264
; REFERENCE/DOCKET NUMBER: 1050.071001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-374-652C-38

```

```

Query Match 22.2%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 13 PFQV 16
Db 4 PFQV 7

```

```

RESULT 15
US-08-078-176-9
; Sequence 9, Application US/08078176
; Patent No. 549784
; GENERAL INFORMATION:
; APPLICANT: BIRD, Colin R.
; APPLICANT: RAY, John A.
; APPLICANT: SCHUCH, Wolfgang W.
; TITLE OF INVENTION: PLANT DNA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/078,176
; FILING DATE: 17-JUN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9027616.3
; FILING DATE: 20-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92/11372
; FILING DATE: 19-DEC-1991

```

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US-08-078-176-10
Query Match      22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KPDL 11
      ||||
Db      6 KPDL 9

RESULT 17
US-08-078-175-4
; Sequence 4, Application US/08078175
; Patent No. 5484906
; GENERAL INFORMATION:
; APPLICANT: BIRD, Colin R.
; APPLICANT: RAY, John A.
; APPLICANT: SCHUCH, Wolfgang W.
; TITLE OF INVENTION: DNA, DNA CONSTRUCTS, CELLS AND PLANTS
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/078,175
; FILING DATE: 02-AUG-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9027616.3
; FILING DATE: 20-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/02272
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 200621/SEE36096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-078-175-4

Query Match      22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KPDL 11
      ||||
Db      6 KPDL 9

RESULT 18
US-08-217-188A-62
; Sequence 62, Application US/08217188A

```

```

; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Faller, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor Mage-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-3884
; TELEFAX: (212) 838-9200
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-217-188A-62

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
Db 3 DLQP 6

RESULT 19
US-08-687-226-62
; Sequence 62, Application US/08687225
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Faller, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: Mage-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS

```

```

; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-687-226-62

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
Db 3 DLQP 6

RESULT 20
US-08-787-547-104
; Sequence 104, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids

```



```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-104

Query Match      22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 DLQP 13
Db       4 DLQP 7

RESULT 21
US-08-948-378A-17
; Sequence 17, Application US/08948378A
; Patent No. 6013258
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
; TITLE OF INVENTION: THE HPV E7 PROTEIN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,378A
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-948-378A-17

Query Match      22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 DLQP 13
Db       4 DLQP 7

RESULT 22
US-08-667-725B-62
; Sequence 62, Application US/08667725B
; Patent No. 6063900
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor Mage-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,725B
; FILING DATE: 21 June 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6063900man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-667-725B-62

Query Match      22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 DLQP 13
Db       3 DLQP 6

RESULT 23
US-09-007-748-62
; Sequence 62, Application US/09007748
; Patent No. 6147187
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor Mage-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS

```

US-09-169-425C-17
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,748
; FILING DATE: 15 January 1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6147187man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-007-748-62

Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 10 DLQP 13
Db 3 DLQP 6

RESULT 24
US-09-169-425C-17
; Sequence 17, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chic, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,425C
; FILING DATE: 09-OCT-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,657
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-169-425C-17
Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 10 DLQP 13
Db 4 DLQP 7

RESULT 25
US-08-197-484-66
; Sequence 66, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-66

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 10 DLQP 13

```
Db          4 DLQP 7
|||||
RESULT 26
US-08-197-484-71
; Sequence 71, Application US/08197484
; Patent No. 641931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-71

Query Match          22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          10 DLQP 13
|||||
Db          3 DLQP 6

RESULT 27
US-09-759-960-17
; Sequence 17, Application US/09759960
; Patent No. 6582704
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: COLLINS, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-759-960-17

Query Match          22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          10 DLQP 13
|||||
Db          4 DLQP 7

RESULT 28
PCT-US95-02121-66
; Sequence 66, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-02121-66

Query Match 22.2%; Score 4; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 4 DLQP 7

RESULT 29
PCT-US95-02121-71
Sequence 71, Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-02121-71

Query Match 22.2%; Score 4; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 3 DLQP 6

RESULT 30
US-08-538-387A-25
Sequence 25, Application US/08538387A
Patent No. 5874214
GENERAL INFORMATION:
APPLICANT: No. 5874214a, Michael Phillip
APPLICANT: Senyei, Andrew E.
APPLICANT: David, Gary S.
TITLE OF INVENTION: REMOTELY PROGRAMMABLE
TITLE OF INVENTION: MATRICES WITH MEMORIES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/538,387A
FILING DATE: 03-OCT-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/473,660
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,196
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,504
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,486
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,147
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,662
FILING DATE: 04/25/95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6444-300G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:

; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-538-387A-25

Query Match 22.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPDL 11
|||
Db 7 KPDL 10

RESULT 31

US-08-538-387A-26
; Sequence 26, Application US/08538387A
; Patent No. 5874214
; GENERAL INFORMATION:
; APPLICANT: No. 5874214a, Michael Phillip
; APPLICANT: Senyei, Andrew E.
; APPLICANT: David, Gary S.
; TITLE OF INVENTION: REMOTELY PROGRAMMABLE
; TITLE OF INVENTION: MATRICES WITH MEMORIES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,387A
; FILING DATE: 03-OCT-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/473,660
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,196
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,504
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,486
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,147
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,662
; FILING DATE: 04/25/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6444-300G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999

; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-538-387A-26

Query Match 22.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPDL 11
|||
Db 7 KPDL 10

RESULT 32

US-08-902-516-19
; Sequence 19, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-902-516-19

Query Match 22.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 10 DLQP 13
|||
Db 4 DLQP 7

RESULT 33
US-08-723-423-25
; Sequence 25, Application US/08723423
; Patent No. 5961923
; GENERAL INFORMATION:
; APPLICANT: No. 5961923a, Michael Phillip
; APPLICANT: Parandoosh, Zahra
; APPLICANT: Senyei, Andrew E.
; APPLICANT: Xiao, Xiao-Yi
; APPLICANT: David, Gary S.
; APPLICANT: Yozo, Satoda
; APPLICANT: Zhao, Chanfeng
; APPLICANT: Potash, Hanan
; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,423
; FILING DATE: 09/30/96
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 09/06/96
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/669,252
; FILING DATE: 06/24/96
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/633,410
; FILING DATE: 06/10/96
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06145
; FILING DATE: 04/25/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/639,813
; FILING DATE: 04/02/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/567,746
; FILING DATE: 12/05/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/538,387
; FILING DATE: 10/03/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/473,660
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,196
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,504
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,486
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/480,147
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,662
; FILING DATE: 04/25/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6444-302E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-723-423-25
Query Match 22.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 KPDL 11
Db 7 KPDL 10
RESULT 34
US-08-723-423-26
; Sequence 26, Application US/08723423
; Patent No. 5961923
; GENERAL INFORMATION:
; APPLICANT: No. 5961923a, Michael Phillip
; APPLICANT: Parandoosh, Zahra
; APPLICANT: Senyei, Andrew E.
; APPLICANT: Xiao, Xiao-Yi
; APPLICANT: David, Gary S.
; APPLICANT: Yozo, Satoda
; APPLICANT: Zhao, Chanfeng
; APPLICANT: Potash, Hanan
; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,423
; FILING DATE: 09/30/96
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 09/06/96
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,504
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,486
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:

TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-709-435-25

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No.1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDL 11
Db 7 KPDL 10

RESULT 36
US-08-709-435-26
Sequence 26, Application US/08709435
Patent No. 6017496
GENERAL INFORMATION:
APPLICANT: NO. 6017496a, Michael Phillip
APPLICANT: Zahra Parandoosh
APPLICANT: Senyei, Andrew E.
APPLICANT: Xiao, Xiao-Yi
APPLICANT: David, Gary S.
APPLICANT: Yozo, Satoda
APPLICANT: Zhao, Chanfeng
APPLICANT: Potash, Hanan
TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,435
FILING DATE: 09/08/96
CLASSIFICATION: 422
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669,252
FILING DATE: 06/24/96
CLASSIFICATION: 422
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/633,410
FILING DATE: 06/10/96
CLASSIFICATION: 422
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06145
FILING DATE: 04/25/96
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/639,813
FILING DATE: 04/02/96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/567,746
FILING DATE: 12/05/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/538,387
FILING DATE: 10/03/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/473,660
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,196
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,504
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,486
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,147
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,662
FILING DATE: 04/25/95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6444-302D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-709-435-26

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No.1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDL 11
Db 7 KPDL 10

RESULT 37
US-08-567-746A-25
Sequence 25, Application US/08567746A
Patent No. 6025129
GENERAL INFORMATION:
APPLICANT: NO. 6025129a, Michael Phillip
APPLICANT: Senyei, Andrew E.
APPLICANT: Parandoosh, Zahra
APPLICANT: David, Gary S.
TITLE OF INVENTION: ASSAYS USING REMOTELY
PROGRAMMABLE MATRICES WITH MEMORIES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA

COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,746A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/473,660
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,196
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,504
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,486
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,662
FILING DATE: 04/25/95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6444-300G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-567-746A-25

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db 7 KPDL 10

RESULT 38
US-08-567-746A-26
; Sequence 26, Application US/08567746A
; Patent No. 6025129
; GENERAL INFORMATION:
; APPLICANT: No. 6025129a, Michael Phillip
; APPLICANT: Senyei, Andrew E.
; APPLICANT: Parandoosh, Zahra
; APPLICANT: David, Gary S.
; TITLE OF INVENTION: ASSAYS USING REMOTELY
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,746A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/473,660
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,196
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,504
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,486
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,662
FILING DATE: 04/25/95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6444-300G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-567-746A-26

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db 7 KPDL 10

RESULT 39
US-08-633-410-25
; Sequence 25, Application US/08633410
; Patent No. 6100026
; GENERAL INFORMATION:
; APPLICANT: No. 6100026a, Michael Phillip
; APPLICANT: Parandoosh, Zahra
; APPLICANT: David, Gary S.
; APPLICANT: Senyei, Andrew E.
; APPLICANT: Potash, Hanan
; APPLICANT: Xiao, Xiao-Yi

;; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF
;; NUMBER OF SEQUENCES: 33
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Brown, Martin, Haller & McClain
;; STREET: 1660 Union Street
;; CITY: San Diego
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92101-2926
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/633,410
;; FILING DATE: 06/10/96
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/06145
;; FILING DATE: 04/25/96
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/639,813
;; FILING DATE: 04/02/96
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/567,746
;; FILING DATE: 12/05/95
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/538,387
;; FILING DATE: 10/03/95
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/473,660
;; FILING DATE: 06/07/95
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/480,196
;; FILING DATE: 06/07/95
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/484,486
;; FILING DATE: 06/07/95
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/480,147
;; FILING DATE: 06/07/95
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/428,662
;; FILING DATE: 04/25/95
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seidman, Stephanie L
;; REGISTRATION NUMBER: 33,779
;; REFERENCE/DOCKET NUMBER: 6444-302PC
;; TELEPHONE: 619-238-0999
;; TELEFAX: 619-238-0062
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHEICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;; ORIGINAL SOURCE:
US-08-633-410-25

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 KPDL 11
Db |||||
7 KPDL 10
RESULT 40
US-08-633-410-26
; Sequence 26, Application US/08633410
; Patent No. 6100026
; GENERAL INFORMATION:
; APPLICANT: No. 6100026a, Michael Phillip
; APPLICANT: Parandosh, Zahra
; APPLICANT: David, Gary S.
; APPLICANT: Senyei, Andrew E.
; APPLICANT: Potash, Hanan
; APPLICANT: Xiao, Xiao-Yi
; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,410
; FILING DATE: 06/10/96
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06145
; FILING DATE: 04/25/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/639,813
; FILING DATE: 04/02/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/567,746
; FILING DATE: 12/05/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/538,387
; FILING DATE: 10/03/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/473,660
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,196
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,504
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,486
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,147
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,662
; FILING DATE: 04/25/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6444-302PC
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-633-410-25

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-633-410-26

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
DB 7 KPDL 10

RESULT 41
US-08-704-344-22
Sequence 22, Application US/08704344
Patent No. 6218363
GENERAL INFORMATION:
APPLICANT: BASERGA, Renato L.
APPLICANT: RESNICOFF, Mariana
APPLICANT: HUANG, Ziwei
TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR LLP
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,344
FILING DATE: 28-AUG-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, Henry N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.196
TELEPHONE: (202) 942-8459
TELEFAX: (202) 942-8484
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-704-344-22

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 4 DLQP 7

RESULT 42
US-08-711-426-25
Sequence 25, Application US/08711426
Patent No. 6284459
GENERAL INFORMATION:
APPLICANT: No. 6284459a, Michael Phillip
APPLICANT: Zahra Parandoosh
APPLICANT: Senysei, Andrew E.
APPLICANT: Xiao, Xiao-Yi
APPLICANT: David, Gary S.
APPLICANT: Yozo, Satoda
APPLICANT: Zhao, Chanfeng
TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711,426
FILING DATE:
CLASSIFICATION: 422
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669,252
FILING DATE: 06/24/96
CLASSIFICATION: 422
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06/10/96
CLASSIFICATION: 422
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06145
FILING DATE: 04/25/96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/639,813
FILING DATE: 04/02/96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/567,746
FILING DATE: 12/05/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/538,387
FILING DATE: 10/03/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/473,660
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,196
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,504
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,486
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,147
FILING DATE: 06/07/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,662
FILING DATE: 04/25/95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779

```
; REFERENCE/DOCKET NUMBER: 6444-302C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-711-426-25

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDL 11
Db 7 KPDL 10

RESULT 43
US-08-711-426-26
; Sequence 26, Application US/08711426
; Patent No. 6284459
; GENERAL INFORMATION:
; APPLICANT: No. 6284459a, Michael Phillip
; APPLICANT: Zahra Parandoosh
; APPLICANT: Senyei, Andrew E.
; APPLICANT: Xiao, Xiao-Yi
; APPLICANT: David, Gary S.
; APPLICANT: Yozo, Satoda
; APPLICANT: Zhao, Chanfeng
; APPLICANT: Potash, Hanan
; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711.426
; FILING DATE:
; CLASSIFICATION: 422
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/669,252
; FILING DATE: 06/24/96
; CLASSIFICATION: 422
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 06/10/96
; CLASSIFICATION: 422
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06145
; FILING DATE: 04/25/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/639,813
; FILING DATE: 04/02/96
; PRIOR APPLICATION DATA:

; REFERENCE/DOCKET NUMBER: 08/567,746
; FILING DATE: 12/05/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/538,387
; FILING DATE: 10/03/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/473,660
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,196
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,504
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,486
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,147
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,662
; FILING DATE: 04/25/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6444-302C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-711-426-26

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDL 11
Db 7 KPDL 10

RESULT 44
US-08-669-252-25
; Sequence 25, Application US/08669252
; Patent No. 6319668
; GENERAL INFORMATION:
; APPLICANT: No. 6319668a, Michael Phillip
; APPLICANT: Potash, Hanan
; APPLICANT: Xiao, Xiao-Yi
; APPLICANT: Parandoosh, Zahra
; APPLICANT: David, Gary S.
; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA: US/08/669,252
; FILING DATE: 06/10/96
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06145
; FILING DATE: 04/25/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/639,813
; FILING DATE: 04/02/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/567,746
; FILING DATE: 12/05/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/538,387
; FILING DATE: 10/03/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,486
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,147
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,662
; FILING DATE: 04/25/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6444-302PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-669-252-25

Query Match 22.2%, Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db 7 KPDL 10

RESULT 45
US-08-669-252-26
; Sequence 26, Application US/08669252
; Patent No. 6319668
; GENERAL INFORMATION:
; APPLICANT: No. 6319668a, Michael Phillip
; APPLICANT: Potash, Hanan
; APPLICANT: Xiao, Xiao-Yi
; APPLICANT: Parandoosh, Zahra
; APPLICANT: David, Gary S.
; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,252
; FILING DATE: 06/10/96
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06145
; FILING DATE: 04/25/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/639,813
; FILING DATE: 04/02/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/567,746
; FILING DATE: 12/05/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/538,387
; FILING DATE: 10/03/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/473,660
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,196
; FILING DATE: 06/07/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6444-302PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-669-252-26
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Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPDL 11
Db 7 KPDL 10

RESULT 46

US-09-098-122-25
; Sequence 25, Application US/09098122
; Patent No. 6372428
; GENERAL INFORMATION:
; APPLICANT: No. 6372428a, Michael Phillip
; APPLICANT: Senyei, Andrew E.
; APPLICANT: David, Gary S.
; TITLE OF INVENTION: REMOTELY PROGRAMMABLE MATRICES WITH
; TITLE OF INVENTION: MEMORIES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,122
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/473,660
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,196
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,504
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,486
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,147
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,662
; FILING DATE: 04/25/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6444-300H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-09-098-122-25

Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPDL 11
Db 7 KPDL 10

RESULT 47

US-09-098-122-26
; Sequence 26, Application US/09098122
; Patent No. 6372428
; GENERAL INFORMATION:
; APPLICANT: No. 6372428a, Michael Phillip
; APPLICANT: Senyei, Andrew E.
; APPLICANT: David, Gary S.
; TITLE OF INVENTION: REMOTELY PROGRAMMABLE MATRICES WITH
; TITLE OF INVENTION: MEMORIES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,122
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/538,387
; FILING DATE: 03-OCT-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/473,660
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,196
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,504
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,486
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,147
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,662
; FILING DATE: 04/25/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6444-300H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:

INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 US-09-098-122-26

Query Match 22.2%; Score 4; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDL 11
 Db 7 KPDL 10

RESULT 48

US-09-847-185-19
 ; Sequence 19, Application US/09847185
 ; Patent No. 6482407

GENERAL INFORMATION:

APPLICANT: Soo Hoo, William
 TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
 COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
 RESPONSE USING SAME

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: CAMPBELL & FLORES, LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/847,185

FILING DATE: 01-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/201,931

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IM 2442

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-847-185-19

Query Match 22.2%; Score 4; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
 Db 11

Db 4 DLQP 7

RESULT 49

5166058-8

; Patent No. 5166058

; APPLICANT: WANG, ELIZABETH A.; WOZNEY, JOHN M.; RPSSEN, VICKI A.

; TITLE OF INVENTION: DNA SEQUENCES ENCODING THE OSTEOINDUCTIVE

; PROTEINS

; NUMBER OF SEQUENCES: 19

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/378,537

; FILING DATE: 11-JUL-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 179,100

; FILING DATE: 08-APR-1988

; APPLICATION NUMBER: 28,285

; FILING DATE: 20-MAR-1987

; APPLICATION NUMBER: 943,332

; FILING DATE: 17-DEC-1986

; APPLICATION NUMBER: 880,776

; FILING DATE: 01-JUL-1986

; SEQ ID NO: 8:

; LENGTH: 10

5166058-8

Query Match

22.2%; Score 4; DB 6; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FQVQ 17

Db 2 FQVQ 5

RESULT 50

US-08-036-555B-164

; Sequence 164, Application US/08036555B

; Patent No. 5530109

; GENERAL INFORMATION:

APPLICANT: Goodearl, Andrew; Stroobant, Paul;

APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchionni, Mark;

APPLICANT: Chen, Maio Su; Hiles, Ian

; TITLE OF INVENTION: Glial Mitogenic Factors, Their

; TITLE OF INVENTION: Preparation and Use

; NUMBER OF SEQUENCES: 184

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/036,555B

FILING DATE: 24-MAR-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/965,173

FILING DATE: 23-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/940,389

FILING DATE: 03-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/907,138

FILING DATE: 30-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/863,703

```

; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA: U.K. 91 07566.3
; APPLICATION NUMBER: 34,266
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELEPHONE: (212) 838-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-036-555B-164

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 9 DVEK 12

RESULT 51
US-08-469-569-164
; Sequence 164, Application US/08469569
; Patent No. 5606032
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,569
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3

```

```

; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-569-164

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 9 DVEK 12

RESULT 52
US-08-249-322A-164
; Sequence 164, Application US/08249322A
; Patent No. 5716930
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,322A
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:

```



```

; NAME: Teai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 888-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-249-322A-164

Query Match          22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DVEK 8
Db      9 DVEK 12

RESULT 53
US-08-469-526A-164
; Sequence 164, Application US/08469526A
; Patent No. 5792849
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Hiles, Ian
; APPLICANT: Chen, Maio Su
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,526A
; FILING DATE: 06 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 03-JUN-1992
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200A

```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-526A-164

Query Match          22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DVEK 8
Db      9 DVEK 12

RESULT 54
US-08-734-591A-164
; Sequence 164, Application US/08734591A
; Patent No. 5854220
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Hiles, Ian
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: WordPerfect (Version 7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,591A
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,335
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 03-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; APPLICATION NUMBER: UK 91 07566.3

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; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-734-591A-164

Query Match 22.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DVEK 8
Db 9 DVEK 12

RESULT 55
US-08-469-660-164
; Sequence 164, Application US/08469660
; Patent No. 5676973
; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.; Marchionni, Mark;
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 0211-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,660
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/011,396
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/984,085
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/951,747
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/927,337
; FILING DATE: 10-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/017004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 164:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-660-164

Query Match 22.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DVEK 8
Db 9 DVEK 12

RESULT 56
US-08-470-335-164
; Sequence 164, Application US/08470335F
; Patent No. 6147190
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/00200B
; CURRENT APPLICATION NUMBER: US/08/470,335F
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.
US-08-470-335-164

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DVEK 8
Db 9 DVEK 12

RESULT 57
US-08-735-021-164
; Sequence 164, Application US/08735021B
; Patent No. 6194377
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/00200L
```

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; CURRENT APPLICATION NUMBER: US/08/735,021B
; CURRENT FILING DATE: 1996-10-22
; EARLIER APPLICATION NUMBER: 08/472,065
; EARLIER FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/965,173
; EARLIER FILING DATE: 1992-10-23
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: FRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1).....(1)
; OTHER INFORMATION: Xaa in 1 is unknown.
US-08-735-021-164

Query Match      22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DVEK 8
Db      9 DVEK 12

RESULT 58
US-08-734-664A-164
; Sequence 164, Application US/08734664A
; Patent No. 6204241
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,664A
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,322
; FILING DATE: 26-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-734-664A-164

Query Match      22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DVEK 8
Db      9 DVEK 12

RESULT 59
US-08-470-339-164
; Sequence 164, Application US/08470339C
; Patent No. 6232286
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/002008
; CURRENT APPLICATION NUMBER: US/08/470,339C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; EARLIER APPLICATION NUMBER: 91 07566.3 GB
; EARLIER FILING DATE: 1993-04-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: PRT

```

```
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.
US-08-470-339-164

Query Match      22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DVEK 8
Db      9 DVEK 12
|||||

RESULT 60
US-08-467-602-164
; Sequence 164, Application US/08467602C
; Patent No. 644642
; GENERAL INFORMATION:
; APPLICANT: Sklar, Robert
; APPLICANT: Marchionni, Mark
; APPLICANT: Gwynne, David I.
; TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND
; DISORDERS
; FILE REFERENCE: 04585/028003
; CURRENT APPLICATION NUMBER: US/08/467,602C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/209,204
; EARLIER FILING DATE: 1994-03-08
; EARLIER APPLICATION NUMBER: 08/059,022
; EARLIER FILING DATE: 1993-05-06
; NUMBER OF SEQ ID NOS: 420
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.
US-08-467-602-164

Query Match      22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DVEK 8
Db      9 DVEK 12
|||||

RESULT 61
US-09-555-352-16
; Sequence 16, Application US/09555352
; Patent No. 654479
; GENERAL INFORMATION:
; APPLICANT: Cichutek, Klaus
; APPLICANT: Mergel-Mullitzer, Heike
; TITLE OF INVENTION: PSEUDO-TYPE RETROVIRAL VECTORS WITH
; MODIFIABLE SURFACE CAPSID PROTEINS
; FILE REFERENCE: 11692-005001
; CURRENT APPLICATION NUMBER: US/09/555,352
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/DE98/03542
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: DE 197 52 855.4
; PRIOR FILING DATE: 1997-11-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 16

Query Match      22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DVEK 8
Db      9 DVEK 12
|||||

US-09-555-352-16
; ORGANISM: Murine leukemia virus
; TYPE: PRT
; LENGTH: 12
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.
US-09-555-352-16

Query Match      22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 FQVQ 17
Db      2 FQVQ 5
|||||

RESULT 62
PCT-US94-05083C-160
; Sequence 160, Application PC/TUS9405083C
; GENERAL INFORMATION:
; APPLICANT: Robert Sklar, Mark Marchionni,
; APPLICANT: David I. Gwynne
; TITLE OF INVENTION: METHODS FOR ALTERING
; TITLE OF INVENTION: MUSCLE CONDITION
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360
; MEDIUM TYPE: kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05083C
; FILING DATE: 06-MAY-94
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,204
; FILING DATE: 08-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059,022
; FILING DATE: 06-MAY-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/028W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is
; OTHER INFORMATION: unknown.
PCT-US94-05083C-160

Query Match      22.2%; Score 4; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DVEK 8
Db      9 DVEK 12
|||||
```

RESULT 63

PCT-US95-06846A-164
 ; Sequence 164, Application PC/TUS9506846A
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodearl, Andrew David; Stroobant, Paul;
 ; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
 ; APPLICANT: Chen, Maio Su; Hiles, Ian
 ; TITLE OF INVENTION: Glial Mitogenic Factors, Their
 ; PREPARATION AND USE
 ; NUMBER OF SEQUENCES: 178
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/06846A
 ; FILING DATE: 25-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/249,322
 ; FILING DATE: 26-MAY-1994
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/036,555
 ; FILING DATE: 24-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/965,173
 ; FILING DATE: 23-OCT-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/940,389
 ; FILING DATE: 03-SEP-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/907,138
 ; FILING DATE: 30-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/863,703
 ; FILING DATE: 03-APRIL-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: U.K. 91 07566.3
 ; FILING DATE: 10-APRIL-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hanson, Norman D.
 ; REGISTRATION NUMBER: 30,946
 ; REFERENCE/DOCKET NUMBER: LUD 5250.5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 638-3884
 ; INFORMATION FOR SEQ ID NO: 164:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; FEATURE:
 ; OTHER INFORMATION: Xaa in position 1 is unknown.
 PCT-US95-06846A-164

Query Match 22.2%; Score 4; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
 ||||
 Db 9 DVEK 12

RESULT 64

US-08-687-956A-3
 ; Sequence 3, Application US/08687956A
 ; Patent No. 5861157
 ; GENERAL INFORMATION:
 ; APPLICANT: BURNIE, JAMES P
 ; APPLICANT: MATTHEWS, RUTH C
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
 ; INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP
 ; STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/687,956A
 ; FILING DATE: 29-JUL-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9401689.6
 ; FILING DATE: 28-JAN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, PAUL N
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 50885/222892
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202/861-3000
 ; TELEFAX: 202/823-0944
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; HYPOTHEetical: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Streptococcus oralis
 ; US-08-687-956A-3

Query Match 22.2%; Score 4; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9
 ||||
 Db 3 VEKP 6

RESULT 65

US-08-997-080-16
 ; Sequence 16, Application US/08997080
 ; Patent No. 5968524
 ; GENERAL INFORMATION:
 ; APPLICANT: WATSON, JAMES D.
 ; APPLICANT: TAN, PAUL L.J.
 ; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
 ; RELATED DISEASES
 ; NUMBER OF SEQUENCES: 194
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Law Offices of Ann W. Speckman
 ; STREET: 2601 Elliott Avenue, Suite 4185
 ; CITY: Seattle
 ; STATE: WA

```
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-997-080-16
;
; Query Match 22.2%; Score 4; DB 2; Length 15;
; Best Local Similarity 100.0%; Pred.No. 2.5e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db 4 PDLQ 7

;
; RESULT 66
; US-08-997-362-16
; Sequence 16, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Ian, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: June 12, 1997

;
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

;
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,970
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
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```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-873-970-16

Query Match      22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PDLQ 12
Db      4 PDLQ 7

RESULT 68
US-09-095-855-16
; Sequence 16, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TREATMENT AND DIAGNOSIS OF Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095.855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-095-855-16

Query Match      22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PDLQ 12
Db      4 PDLQ 7

RESULT 69
US-08-705-347A-16
; Sequence 16, Application US/08705347A
; Patent No. 6284255
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Speckman Picard PLLC
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,347A
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206.269.0565
; TELEFAX: 206.269.0563
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-705-347A-16

Query Match      22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PDLQ 12
Db      4 PDLQ 7

RESULT 70
US-09-324-542-16
; Sequence 16, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.O.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; OF IMMUNOLOGICALLY-MEDIATED SKIN DISORDERS
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-324-542-16

Query Match          22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db 4 PDLQ 7

RESULT 71
US-09-205-426-16
; Sequence 16, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-205-426-16

Query Match          22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db 4 PDLQ 7

RESULT 72
US-09-200-643-16
; Sequence 16, Application US/09200643
; Patent No. 6410720
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002CON
; CURRENT APPLICATION NUMBER: US/09/200,643
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-200-643-16

Query Match          22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db 4 PDLQ 7

RESULT 73
US-07-145-002B-62
; Sequence 62, Application US/07145002B
; Patent No. 6482613
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; TITLE OF INVENTION: MICROBIAL PRODUCTION OF MATURE HUMAN
; TITLE OF INVENTION: LEUKOCYTE INTERFERONS
; FILE REFERENCE: 1803-0088-999
; CURRENT APPLICATION NUMBER: US/07/145,002B
; CURRENT FILING DATE: 1989-01-19
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-07-145-002B-62

Query Match          22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 5 DLQP 8

RESULT 74
US-07-942-245-77
; Sequence 77, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrie, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 77:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-77

Query Match 22.2%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 12 DVEK 15

RESULT 75
US-07-942-245-92
; Sequence 92, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-92

Query Match 22.2%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 12 DVEK 15

Search completed: November 25, 2003, 20:15:59
Job time : 21.6277 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 11.0426 Seconds
(without alignments)
104.507 Million cell updates/sec

Title: US-09-641-801-4

Perfect score: 12

Sequence: 1 LFRPLPVNVLP 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76:*

1: Pirl.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	33.3	17	2 Q20230	hypothetical 1.9K
2	4	33.3	18	2 I40062	shikimate 5-dehydr
3	4	33.3	18	2 S53125	cysteine-rich secr
4	4	33.3	20	2 S09022	carboxylesterase (
5	4	33.3	20	2 S09025	carboxylesterase (
6	4	33.3	20	2 S09023	carboxylesterase (
7	3	25.0	10	2 A44646	neurotoxin-associa
8	3	25.0	10	2 I44644	neurotoxin-associa
9	3	25.0	10	2 B56899	serum heterodimer,
10	3	25.0	10	2 S36849	Ig heavy chain V r
11	3	25.0	11	2 S69349	neuropeptide Ffami
12	3	25.0	11	2 S09024	carboxylesterase (
13	3	25.0	12	1 LFCEPE	pyrE leader peptid
14	3	25.0	12	2 S26555	T-cell receptor be
15	3	25.0	12	2 S26556	T-cell receptor be
16	3	25.0	12	2 S26554	T-cell receptor be
17	3	25.0	12	2 PA0037	insulin-like growt
18	3	25.0	12	2 A60528	inhibitory diffusi
19	3	25.0	12	2 A33520	T-cell receptor al
20	3	25.0	12	2 PH0785	aminotransferase c
21	3	25.0	12	4 PC2123	crabrolin - Europe
22	3	25.0	13	2 JZVHP1	hypothetical prote
23	3	25.0	13	2 S09395	hemolytic protein
24	3	25.0	13	2 S09018	hemolytic protein
25	3	25.0	13	2 S09018	hemolytic protein
26	3	25.0	13	2 PL0157	Ig kappa chain V-I
27	3	25.0	13	2 S47371	T-cell antigen rec
28	3	25.0	13	2 S47390	T-cell antigen rec
29	3	25.0	14	1 LFCEFS	pHEST operon leade

30	14	25.0	3	JN0390	histamine-releasin
31	14	25.0	3	S50900	chlorophyll a/b-b1
32	14	25.0	3	S27140	hypothetical prote
33	14	25.0	3	S58862	botulinum neurotox
34	14	25.0	3	S58866	botulinum neurotox
35	14	25.0	3	C33098	223K exoantigen -
36	14	25.0	3	A23996	beta-granin - rat
37	14	25.0	3	Ar0296	phenylalanyl-tRNA
38	14	25.0	3	F90931	pHEST operon leade
39	14	25.0	3	B85780	pHEST operon leade
40	14	25.0	3	AG0705	phenylalanyl-tRNA
41	15	25.0	3	LFCEP	pHE operon leader
42	15	25.0	3	E91061	hypothetical prote
43	15	25.0	3	T09463	ribosomal protein
44	15	25.0	3	PA0029	protein QA100012 -
45	15	25.0	3	FS0276	phosphoribulokinase
46	15	25.0	3	B61457	alpha-glucosidase
47	15	25.0	3	S57577	T-cell receptor V-
48	15	25.0	3	E56978	collagen alpha 2(X
49	15	25.0	3	PH0784	T-cell receptor al
50	15	25.0	3	A31902	bone acidic glycop
51	15	25.0	3	AF0832	pHE leader peptide
52	16	25.0	3	I40065	shikimate 5-dehydr
53	16	25.0	3	G49039	T-cell receptor be
54	16	25.0	3	H49039	T-cell receptor be
55	16	25.0	3	G24887	T-cell receptor be
56	16	25.0	3	A28587	T-cell receptor be
57	16	25.0	3	PH1476	T-cell receptor be
58	16	25.0	3	PH1475	T-cell receptor be
59	16	25.0	3	PH1474	T-cell receptor be
60	16	25.0	3	PH1472	T-cell receptor be
61	16	25.0	3	PH1477	T-cell receptor be
62	16	25.0	3	PH1473	T-cell receptor be
63	16	25.0	3	PH0766	T-cell receptor be
64	16	25.0	3	PH0767	T-cell receptor be
65	16	25.0	3	PH1480	T-cell receptor be
66	17	25.0	3	I65274	glutathione S-tran
67	17	25.0	3	C37520	glutathione transf
68	17	25.0	3	I49425	mitogen regulated
69	17	25.0	3	S05913	chorion class A pr
70	17	25.0	3	I49593	cystic fibrosis tr
71	17	25.0	3	I84733	gene CFTR protein
72	17	25.0	3	S66213	glucose 1-dehydrog
73	17	25.0	3	S59481	hydroxyproline-ric
74	17	25.0	3	PS0454	38K protein 3129 -
75	17	25.0	3	E22595	bombolitin V - Ame
76	17	25.0	3	E28587	T-cell receptor be
77	17	25.0	3	B31769	T-cell receptor de
78	17	25.0	3	PC2196	zymogen granule me
79	17	25.0	3	E23734	insulin-like growt
80	17	25.0	3	D53284	T-cell receptor be
81	18	25.0	3	S04229	N4-(beta-N-acetyl
82	18	25.0	3	A32220	T-cell receptor de
83	18	25.0	3	B4995	alkanal monooxygen
84	18	25.0	3	S49026	ribosomal protein
85	18	25.0	3	S23971	alpha-macroglobuli
86	18	25.0	3	S09026	carboxylesterase (
87	18	25.0	3	S57518	T cell receptor be
88	18	25.0	3	S57520	T cell receptor be
89	18	25.0	3	I54078	hypothetical PML/R
90	19	25.0	3	C56049	superoxide dismuta
91	19	25.0	3	I13046	calreticulin - rab
92	19	25.0	3	I40063	shikimate 5-dehydr
93	19	25.0	3	B33708	thionin, soluble -
94	19	25.0	3	S69153	Neb-collostatin -
95	19	25.0	3	D49404	T-cell receptor be
96	19	25.0	3	A4356	37K adherens junct
97	19	25.0	3	A41077	protein-disulfide
98	19	25.0	3	S68394	H+-transporting tw
99	20	25.0	3	S17461	flavodoxin B - Azo
100	20	25.0	3	S04961	malate dehydrogena

ALIGNMENTS

```

RESULT 1
JQ2030
hypothetical 1.9K protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus
N:Alternate names: ORF2 mini gene protein
C:Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C:Accession: JQ2030
R:Russell, R.L.O.; Rohmann, G.F.
J: Gen. Virol. 74, 1191-1195, 1993
A:Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia pseudotsug
A:Reference number: PQ6633; MUID:93286576; PMID:8389803
A:Accession: JQ2030
A:Molecule type: DNA
A:Residues: 1-17 <RUS>
A:Cross-references: DDBJ:DL33375; NID:g2222217; PIDN:BAA02640.1; PID:dl003144; PID:g2222222

Query Match      33.3%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VNVL 11
Db      5 VNVL 8

RESULT 2
I40062
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C:Species: Buchnera aphidicola
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999
C:Accession: I40062
R:Roubbakhsh, D.; Baumann, P.
Gene 155, 107-112, 1995
A:Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (endos
A:Reference number: I40061; MUID:95212914; PMID:7535281
A:Accession: I40062
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-18 <RES>
A:Cross-references: EMBL:U10496; NID:g854711; PIDN:AAA79125.1; PID:g854712
C:Genetics:
A:Gene: aroE
C:Keywords: oxidoreductase

Query Match      33.3%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 NVLP 12
Db      7 NVLP 10

RESULT 3
S53125
cysteine-rich secretory protein-3 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
C:Accession: S53125; S56161
R:Schwiderzky, U.; Haendler, B.; Schleuning, W.D.
submitted to the EMBL Data Library, March 1995
A:Description: Isolation and characterization of the androgen-dependent mouse cysteine-r
A:Reference number: S53125
A:Accession: S53125
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <SCH>
A:Cross-references: EMBL:X85321
R:Schwiderzky, U.; Haendler, B.; Schleuning, W.D.
Biochem. J. 309, 831-836, 1995

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A:Title: Isolation and characterization of the androgen-dependent mouse cysteine-rich
A:Reference number: S56161; MUID:95366959; PMID:7639699
A:Accession: S56161
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-18 <SC2>
A:Cross-references: EMBL:X85321

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Query Match      33.3%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 PFPL 5
Db      4 PFPL 7

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RESULT 4
S09022
carboxylesterase (EC 3.1.1.1) RH1, microsomal - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C:Accession: S09022
R:Hosokawa, M.; Maki, T.; Satoh, T.
Arch. Biochem. Biophys. 277, 219-227, 1990
A:Title: Characterization of molecular species of liver microsomal carboxylesterases (
A:Reference number: S09021; MUID:90179180; PMID:2310190
A:Accession: S09022
A:Molecule type: protein
A:Residues: 1-20 <HOS>
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

Query Match      33.3%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      6 PVVN 9
Db      6 PVVN 9

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RESULT 5
S09025
carboxylesterase (EC 3.1.1.1), microsomal - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C:Accession: S09025
R:Hosokawa, M.; Maki, T.; Satoh, T.
Arch. Biochem. Biophys. 277, 219-227, 1990
A:Title: Characterization of molecular species of liver microsomal carboxylesterases (
A:Reference number: S09021; MUID:90179180; PMID:2310190
A:Accession: S09025
A:Molecule type: protein
A:Residues: 1-20 <HOS>
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

Query Match      33.3%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      6 PVVN 9
Db      6 PVVN 9

```

```

RESULT 6
S09023
carboxylesterase (EC 3.1.1.1) RL2, microsomal - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C:Accession: S09023

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R;Hosokawa, M.; Maki, T.; Satoh, T.
Arch. Biochem. Biophys. 277, 219-227, 1990
A;Title: Characterization of molecular species of liver microsomal carboxylesterases of
A;Reference number: S09021; MUID:90179180; PMID:2310190
A;Accession: S09023
A;Molecule type: protein
A;Residues: 1-20 <HOS>
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase

Query Match 33.3%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PVVN 9
DB 6 PVVN 9

RESULT 7
A44646
neurotoxin-associated protein type A Hn+ 57K chain - Clostridium botulinum (fragment)
C;Species: Clostridium botulinum
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: A44646
R;Somers, E.; DasGupta, B.R.
J. Protein Chem. 10, 415-425, 1991
A;Title: Clostridium botulinum types A, B, Cl, and E produce proteins with or without he
A;Reference number: A44644; MUID:92143938; PMID:1781887
A;Contents: type A
A;Accession: A44646
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SOM>
A;Note: sequence extracted from NCBI backbone (NCBIP:83774)
A;Note: 6-Trp was also found
C;Keywords: hemagglutinin

Query Match 25.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 VLP 12
DB 7 VLP 9

RESULT 8
I44644
neurotoxin-associated protein type B Hn+ 57K chain - Clostridium botulinum (fragment)
C;Species: Clostridium botulinum
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: I44644
R;Somers, E.; DasGupta, B.R.
J. Protein Chem. 10, 415-425, 1991
A;Title: Clostridium botulinum types A, B, Cl, and E produce proteins with or without he
A;Reference number: A44644; MUID:92143938; PMID:1781887
A;Contents: type B
A;Accession: I44644
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SOM>
A;Note: sequence extracted from NCBI backbone (NCBIP:83783)
C;Keywords: hemagglutinin

Query Match 25.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 VLP 12
DB 7 VLP 9

RESULT 9
B56899
serum heterodimer, 24K chain - sandbar shark (fragment)
C;Species: Carcharhinus plumbeus (sandbar shark)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 20-Jun-2000
C;Accession: B56899
R;Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.
Comp. Biochem. Physiol. B 103, 563-568, 1992
A;Title: Purification of a novel heterodimer from shark (Carcharhinus plumbeus) serum
A;Reference number: A56899; MUID:93092592; PMID:1458832
A;Accession: B56899
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <VAZ>
C;Keywords: glycoprotein; plasma

Query Match 25.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 VVN 9
DB 7 VVN 9

RESULT 10
S36849
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
C;Accession: S36849
R;Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A;Description: In situ studies on the primary immune response to (4-hydroxy-3-nitroph
A;Reference number: S25024
A;Accession: S36849
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-10 <JAC>
A;Cross-references: EMBL:X67382; NID:G50070; PIDN:CAA47794.1; PID:e51590; PID:gl33386
C;Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 VVN 9
DB 7 VVN 9

RESULT 11
S69349
neuropeptide FFamide - great pond snail
C;Species: Lymnaea stagnalis (great pond snail)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-1999
C;Accession: S69349
R;Li, K.W.; El Filali, Z.; van Golen, F.A.; Geraerts, W.P.M.
Eur. J. Biochem. 229, 70-72, 1995
A;Title: Identification of a novel amide peptide, GLTFNNNSLFF-NH(2), involved in the
A;Reference number: S69349; MUID:95262689; PMID:7744051
A;Accession: S69349
A;Molecule type: protein
A;Residues: 1-11 <LIK>
A;Experimental source: penis complex
C;Function:
A;Description: enhances the contraction frequency and contraction amplitude of the va
A;Note: control of male reproductive behavior
C;Keywords: amidated carboxyl end; neuropeptide
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 25.0%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
|||
Db 9 LFF 11

RESULT 12

S09024
carboxylesterase (EC 3.1.1.1), microsomal - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Apr-1993
C:Accession: S09024
R:Hosokawa, M.; Maki, T.; Satoh, T.
Arch. Biochem. Biophys. 277, 219-227, 1990
A:Title: Characterization of molecular species of liver microsomal carboxylesterases of
A:Reference number: S09021; MUID:90179180; PMID:2310190
A:Accession: S09024
A:Molecule type: protein
A:Residues: 1-11 <HOS>
C:Keywords: carboxylic ester hydrolase

Query Match 25.0%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VVN 9
|||
Db 7 VVN 9

RESULT 13

LFCEPE
pvrE leader peptide - Escherichia coli
C:Species: Escherichia coli
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Mar-1993
C:Accession: A30400; A05110; Q00495
R:Poulsen, P.; Bonekamp, F.; Jensen, K.F.
EMBO J. 3, 1783-1790, 1984
A:Title: Structure of the Escherichia coli pvrE operon and control of pvrE expression by
A:Reference number: A30400; MUID:85003588; PMID:6207018
A:Accession: A30400
A:Molecule type: DNA
A:Residues: 1-12 <POU>
R:Poulsen, P.; Jensen, K.F.; Valentin-Hansen, P.; Carlsson, P.; Lundberg, L.G.
Eur. J. Biochem. 135, 223-229, 1983
A:Title: Nucleotide sequence of the Escherichia coli pvrE gene and of the DNA in front of
A:Reference number: A05110; MUID:83287414; PMID:634999
A:Accession: A05110
A:Molecule type: DNA
A:Residues: 1-12 <POU2>
C:Genetics:
A:Gene: pvrE-LP
A:Map position: 82 min
C:Superfamily: pvrE leader peptide

Query Match 25.0%; Score 3; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
|||
Db 4 LFF 6

RESULT 14

S26555
T-cell receptor beta chain (clone Cw3/1B4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S26555
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid

J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recep
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26555
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: EMBL:X68005
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/1B4
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
|||
Db 9 LFF 11

RESULT 15

S26556
T-cell receptor beta chain (clone Cw3/2C3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S26556
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.;
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recep
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26556
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: EMBL:X68006
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/2C3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
|||
Db 9 LFF 11

RESULT 16

S26554
T-cell receptor beta chain (clone Cw3/Cas7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S26554
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.;
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recep
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26554
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: EMBL:X68004
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas7
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
|||
Db 9 LFF 11

RESULT 17

PA0037
 C:Species: Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
 C:Accession: PA0037
 R:Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis
 A:Reference number: PA0001
 A:Accession: PA0037
 A:Molecule type: protein
 A:Residues: 1-12 <KAM>
 A:Experimental source: stem

Query Match 25.0%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VLP 12
 ||||
 Db 5 VLP 7

RESULT 18

A60528
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
 C:Accession: A60528
 R:Walton, P.E.; Baxter, R.C.; Burleigh, B.D.; Etherton, T.D.
 Comp. Biochem. Physiol. B 92, 561-567, 1989
 A:Title: Purification of the serum acid-stable insulin-like growth factor binding protein
 A:Reference number: A60528; MUID:89209787; PMID:2468442
 A:Accession: A60528
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <WAL>

Query Match 25.0%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PVV 8
 ||||
 Db 9 PVV 11

RESULT 19

A33520
 C:Species: Mus musculus (house mouse)
 C>Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 30-Sep-1993
 C:Accession: A33520
 R:Blat, C.; Bohlen, P.; Villaudy, J.; Chatelain, G.; Golde, A.; Harel, L.
 J. Biol. Chem. 264, 6021-6024, 1989
 A:Title: Isolation and amino-terminal sequence of a novel cellular growth inhibitor (inh)
 A:Reference number: A33520; MUID:89197888; PMID:2703477
 A:Accession: A33520
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <BLA>

Query Match 25.0%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PVV 8
 ||||
 Db 9 PVV 11

RESULT 20

PH0785
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PH0785
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A:Title: T cell receptor genes in a series of class I major histocompatibility complex allelic exclusion and antigen-specific repertoire.
 A:Reference number: PH0746; MUID:92078846; PMID:1836010
 A:Accession: PH0785
 A:Molecule type: mRNA
 A:Residues: 1-12 <CAS>
 A:Cross-references: EMBL:X60887
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVL 11
 ||||
 Db 7 NVL 9

RESULT 21

PC2123
 C:Species: synthetic
 C>Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999
 C:Accession: PC2123
 R:Miyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.
 J. Biochem. 115, 568-577, 1994
 A:Title: Construction of aminotransferase chimeras and analysis of their substrate sp
 A:Reference number: JX0315; MUID:94334304; PMID:8056774
 A:Accession: PC2123
 A:Molecule type: DNA
 A:Residues: 1-12 <MIY>
 C:Comment: This is a chimeric enzyme of Escherichia coli aspartate aminotransferase (C) and the parental enzymes catalyze the reversible amino group transfer reaction
 C:Keywords: aminotransferase

Query Match 25.0%; Score 3; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VNV 10
 ||||
 Db 2 VNV 4

RESULT 22

JZVHP1
 C:Species: Vespa crabro (European hornet)
 C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C:Accession: A01781
 R:Argiolas, A.; Pisano, J.J.
 J. Biol. Chem. 259, 10106-10111, 1984
 A:Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin
 A:Reference number: A92441; MUID:84289390; PMID:6206053
 A:Accession: A01781
 A:Molecule type: protein
 A:Residues: 1-13 <ARG>
 C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end; venom
 F:13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 25.0%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
|||
Db 1 FLP 3

RESULT 23

S09395
hypothetical protein - fruit fly (*Drosophila melanogaster*) (fragment)
C:Species: *Drosophila melanogaster*
C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C:Accession: S09395
R:Gisselmann, G.; Sewing, S.; Madsen, B.W.; Mallart, A.; Angaut-Petit, D.; Mueller-Holtkamp, J. 8, 2359-2364, 1989
A:Title: The interference of truncated with normal potassium channel subunits leads to a
A:Reference number: S09395; MUID:90005442; PMID:2551680
A:Accession: S09395
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <GIS>

Query Match 25.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPV 7
|||
Db 5 LPV 7

RESULT 24

S09018
hemolytic protein A1 - edible frog (fragment)
C:Species: *Rana esculenta* (edible frog)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: S09018
R:Simmaco, M.; De Biase, D.; Severini, C.; Aita, M.; Erspamer, G.F.; Barra, D.; Bossa, F.
Biochim. Biophys. Acta 1033, 318-323, 1990
A:Title: Purification and characterization of bioactive peptides from skin extracts of
A:Reference number: S09018; MUID:90198965; PMID:2317508
A:Accession: S09018
A:Molecule type: protein
A:Residues: 1-13 <SIM>

Query Match 25.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
|||
Db 1 FLP 3

RESULT 25

S09019
hemolytic protein B9 - edible frog (fragment)
C:Species: *Rana esculenta* (edible frog)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: S09019
R:Simmaco, M.; De Biase, D.; Severini, C.; Aita, M.; Erspamer, G.F.; Barra, D.; Bossa, F.
Biochim. Biophys. Acta 1033, 318-323, 1990
A:Title: Purification and characterization of bioactive peptides from skin extracts of
A:Reference number: S09019; MUID:90198965; PMID:2317508
A:Accession: S09019
A:Molecule type: protein
A:Residues: 1-13 <SIM>

Query Match 25.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6

Db |||
1 FLP 3

RESULT 26

PL0157
IG kappa chain V-II region (anti-myelin-associated glycoprotein, PEC) - human (fragment)
C:Species: *Homo sapiens* (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Feb-1997
C:Accession: PL0157; C61458
R:Broutet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-
A:Reference number: A61458; MUID:90039128; PMID:2478651
A:Accession: PL0157
A:Molecule type: protein
A:Residues: 1-13 <BRO>
A:Accession: C61458
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BR2>

A:Comment: This protein is one of monoclonal IgM reactive with myelin-associated gly-
C:Keywords: glycoprotein; heterotetramer; immunoglobulin

Query Match 25.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPV 7
|||
Db 11 LPV 13

RESULT 27

S47371
T-cell antigen receptor VJ junction beta chain - human
C:Species: *Homo sapiens* (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47371
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by
A:Reference number: S47355
A:Accession: S47371
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35696; MUID:9527483; PIDN:CAA84765.1; PID:9527484
C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
|||
Db 11 LFF 13

RESULT 28

S47390
T-cell antigen receptor VJ junction beta chain - human
C:Species: *Homo sapiens* (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47390
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by
A:Reference number: S47355
A:Accession: S47390
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>

A;Cross-references: EMBL:Z35703; NID:g527499; PIDN:CAA84772.1; PID:g527500
C;Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
|||
Db 11 LFF 13

RESULT 29

LFCFS

pheST operon leader peptide - Escherichia coli (strain K-12)
N;Alternate names: phenylalanyl-tRNA synthetase operon leader peptide
C;Species: Escherichia coli
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 01-Mar-2002
C;Accession: S11551; I53984; C64930; S06908
R;Fayat, G.; Mayaux, J.F.; Sacerdot, C.; Fromant, M.; Grunberg-Manago, M.;
J. Mol. Biol. 171, 239-261, 1993
A;Title: Escherichia coli phenylalanyl-tRNA synthetase operon region. Evidence for an at
A;Reference number: A30391; MUID:84090239; PMID:6317865
A;Accession: S11551
A;Molecule type: DNA
A;Residues: 1-14 <FR>
A;Cross-references: EMBL:V00291; NID:g43065; PIDN:CAA23563.1; PID:g43069
R;Mayaux, J.
Gene 30, 137-146, 1984
A;Title: IS4 transposition in the attenuator region of the Escherichia coli pheS, T oper
A;Reference number: I53984; MUID:85077605; PMID:6096210
A;Accession: I53984
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-14 <RES>
A;Cross-references: GB:M13251; NID:gl47182; PIDN:AAA24333.1; PID:gl47185
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C64930
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-14 <BLAT>
A;Cross-references: GB:AE000266; GB:U00096; NID:gl787997; PIDN:AACT4785.1; PID:gl788008;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: pheM
A;Map position: 37 min
C;Function:
C;Superfamily: pheST leader peptide

Query Match 25.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFF 4
|||
Db 8 PFF 10

RESULT 30

JN0390

histamine-releasing peptide II - oriental hornet
N;Alternate names: venom protein HR-2
C;Species: Vespa orientalis (oriental hornet)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 23-Aug-1997
C;Accession: JN0390; S10919
R;Miroshnikov, A.I.; Snezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Gus
Blaorg. Khim. 7, 1467-1477, 1981
A;Title: Structure and properties of histamine releasing peptides from the venom of Vesp

A;Reference number: JN0389

A;Accession: JN0390

A;Molecule type: protein

A;Residues: 1-14 <MIR>

R;Tuichibaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
Biochemistry (N.Y.) 53, 183-190, 1988

A;Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis.

A;Reference number: S06445

A;Accession: S10919

A;Molecule type: protein

A;Residues: 1-14 <GUI>

C;Superfamily: crabrolin

C;Keywords: amidated carboxyl end; venom

F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 25.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6

|||

Db 1 FLP 3

RESULT 31

S50900

chlorophyll a/b-binding protein lhcb5 - spinach (fragment)

N;Alternate names: light-harvesting complex LHCIIc protein

C;Species: Spinacia oleracea (spinach)

C;Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999

C;Accession: S50900

R;Walters, R.G.; Ruban, A.V.; Horton, P.

Eur. J. Biochem. 226, 1063-1069, 1994

A;Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyc

A;Reference number: S50900; MUID:95112835; PMID:7813461

A;Accession: S50900

A;Molecule type: protein

A;Residues: 1-14 <WAL>

C;Superfamily: chlorophyll a/b-binding protein

C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photos

Query Match 25.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6

|||

Db 2 FLP 4

RESULT 32

S27140

hypothetical protein 1 estrogen receptor 5'-region - human

C;Species: Homo sapiens (man)

C;Date: 05-Mar-1994 #sequence_revision 12-May-1995 #text_change 18-Aug-2000

C;Accession: S27140

R;Keaveney, M.; Klug, J.; Gannon, F.

DNA Seq. 2, 347-358, 1992

A;Title: Sequence analysis of the 5' flanking region of the human estrogen receptor g

A;Reference number: S27140; MUID:93075998; PMID:1476547

A;Accession: S27140

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-14 <KEA>

A;Cross-references: EMBL:X62462; NID:g31201; PIDN:CAA44319.1; PID:g31202

C;Superfamily: unassigned leader peptides

Query Match 25.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6

|||

Db 6 FLP 8

RESULT 33

S58862
botulinum neurotoxin type A and B hemagglutinin component II - Clostridium botulinum (strain N; Alternate names: HA-II protein
C; Species: Clostridium botulinum
C; Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 15-Oct-1999
C; Accession: S58862; S58858
R; East, A.K.; Stacey, J.M.; Collins, M.D.
Syst. Appl. Microbiol. 17, 306-312, 1994
A; Title: Cloning and sequencing of a hemagglutinin component of the botulinum neurotoxin
A; Reference number: S58855
A; Accession: S58862
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-14 <EAS>
A; Cross-references: EMBL:X79104; NID:g870937; PIDN:CAA55719.1; PID:g870941
A; Experimental source: strain NCTC 7272
A; Accession: S58858
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-14 <EA2>
A; Cross-references: EMBL:X79103; NID:g870932; PIDN:CAA55715.1; PID:g870936
A; Experimental source: strain Eklund 17B
C; Keywords: hemagglutinin; neurotoxin

Query Match 25.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 7 FLP 9

RESULT 34

S58866
botulinum neurotoxin type B hemagglutinin component II - Clostridium botulinum (NCTC 7272; Alternate names: protein HA-II
C; Species: Clostridium botulinum
A; Variety: NCTC 7273
C; Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Oct-1999
C; Accession: S58866
R; East, A.K.; Stacey, J.M.; Collins, M.D.
Syst. Appl. Microbiol. 17, 306-312, 1994
A; Title: Cloning and sequencing of a hemagglutinin component of the botulinum neurotoxin
A; Reference number: S58855
A; Accession: S58866
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-14 <EAS>
A; Cross-references: EMBL:X79102; NID:g870942; PIDN:CAA55711.1; PID:g870946
A; Experimental source: NCTC 7273
C; Keywords: hemagglutinin; neurotoxin

Query Match 25.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 7 FLP 9

RESULT 35

C33098
223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C; Species: Plasmodium falciparum
C; Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C; Accession: C33098
R; Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A; Reference number: A33098
A; Accession: C33098
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-14 <NIC>

Query Match 25.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VLP 12
Db 1 VLP 3

RESULT 36

A23996
beta-granin - rat (fragment)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Jun-1993
C; Accession: A23996
R; Hutton, J.C.; Hansen, F.; Peshavaria, M.
FEBS Lett. 185, 336-340, 1985
A; Title: Beta-granins: 21 kDa co-secreted peptides of the insulin granule closely related to beta-granin
A; Reference number: A23996; MUID:85285598; PMID:3896848
A; Accession: A23996
A; Molecule type: protein
A; Residues: 1-14 <HUT>

Query Match 25.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPV 7
Db 1 LPV 3

RESULT 37

AF0296
phenylalanyl-tRNA synthetase operon leader peptide [imported] - Yersinia pestis (strain C; Species: Yersinia pestis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C; Accession: AF0296
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.; deno-Tarrega, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barral Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
A; Accession: AF0296
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-14 <KUP>
A; Cross-references: GB:AL590842; PIDN:CAC91234.1; PID:gi5980423; GSPDB:GN00175
C; Genetics:
A; Gene: pheM

Query Match 25.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4
Db 8 FFF 10

RESULT 38

F90931
phest operon leader peptide - Escherichia coli (strain O157:H7, substrain RIMD 050995; C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Nov-2001

C;Accession: F90931
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: F90931
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-14 <HAY>
 A;Cross-references: GB:BA000007; PIDN:BA035845.1; PID:g13361889; GSPDB:GN00154
 A;Experimental source: strain O157:H7, substrain RMD 050952
 C;Genetics:
 A;Gene: ECs2422

Query Match 25.0%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FFF 4
 ||||
 Db 8 FFF 10

RESULT 39
 B85780
 pheST operon leader peptide - *Escherichia coli* (strain O157:H7, substrain EDL933)
 C;Species: *Escherichia coli*
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
 C;Accession: B85780
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: B85780
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-14 <STO>
 A;Cross-references: GB:AE005174; MID:g13515726; PIDN:AAG56702.1; GSPDB:GN00145; UWGP:227
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: pheM

Query Match 25.0%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FFF 4
 ||||
 Db 8 FFF 10

RESULT 40
 AG0705
 phenylalanyl-tRNA synthetase operon leader peptide [imported] - *Salmonella enterica* subsp.
 C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
 A;Note: this species has also been called *Salmonella typhi*
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AG0705
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AG0705
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-14 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD02016.1; PID:g16502854; GSPDB:GN00176
 C;Genetics:

A;Gene: STV1774

Query Match 25.0%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4
 ||||
 Db 8 FFF 10

RESULT 41

LFECE
 phe operon leader peptide - *Escherichia coli* (strain K-12)
 N;Alternate names: attenuator peptide
 C;Species: *Escherichia coli*

C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 01-Mar-2002
 C;Accession: A03593; B36494; A65038
 R;Zurawski, G.; Brown, K.; Killingly, D.; Yanofsky, C.
 Proc. Natl. Acad. Sci. U.S.A. 75, 4271-4275, 1978
 A;Title: Nucleotide sequence of the leader region of the phenylalanine operon of *Esch*
 A;Reference number: A03593; MUID:79033820; PMID:360214
 A;Accession: A03593
 A;Molecule type: DNA
 A;Residues: 1-15 <ZUR>

A;Cross-references: GB:V00314; GB:J01658; MID:g42378; PIDN:CAA23600.1; PID:g42379
 R;Gavini, N.; Davidson, B.E.
 J. Biol. Chem. 265, 21532-21535, 1990
 A;Title: pheA mutants of *Escherichia coli* have a defective pheA attenuator.

A;Reference number: A36494; MUID:91072346; PMID:2254312
 A;Accession: B36494
 A;Molecule type: DNA

A;Residues: 1-15 <GNV>

A;Cross-references: GB:M58024; GB:J05694; MID:g147178; PIDN:AAA62783.1; PID:g147180
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of *Escherichia coli* K-12.

A;Reference number: A6720; MUID:97426617; PMID:9278503

A;Accession: A65038

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-15 <BLAT>

A;Cross-references: GB:AE000346; GB:U00096; MID:g2367141; PIDN:AAC75647.1; PID:g17889

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: pheL; pheA

A;Map position: 56 min

C;Superfamily: pheA leader peptide

Query Match 25.0%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4
 ||||
 Db 6 FFF 8

RESULT 42

E91061

hypothetical protein ECs3461 [imported] - *Escherichia coli* (strain O157:H7, substrain

C;Species: *Escherichia coli*

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

A;Accession: E91061

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and g
 A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: E91061

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-15 <HAY>

A;Cross-references: GB:BA000007; PIDN:BAE36884.1; PID:G13362932; GSPDB:GN00154

A;Experimental source: strain O157:H7, substrain RIMD 050952

C;Genetics:

A;Gene: ECs3461

Query Match

25.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4

|||

Db 6 FFF 8

RESULT 43

T09463

ribosomal protein S14 - brown alga (*Pyraliella littoralis*) mitochondrion (fragment)

C;Species: mitochondrion *Pyraliella littoralis*

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999

C;Accession: T09463

R;Rousvoal, S.; Oudot, M.; Fontaine, J.; Kloareg, B.; Goer, S.L.

J. Mol. Biol. 277, 1047-1057, 1998

A;Title: Witnessing the evolution of transcription in mitochondria: The mitochondrial ge

A;Reference number: Z16681; MUID:98239704; PMID:9571021

A;Accession: T09463

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-15 <ROU>

A;Cross-references: EMBL:AF034976; NID:G32431103; PID:G32431104

A;Experimental source: strain Roscoff

C;Genetics:

A;Gene: rps14

A;Genome: mitochondrion

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match

25.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12

|||

Db 6 VLP 8

RESULT 44

PA0029

Protein QA100012 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997

C;Accession: PA0029

R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimensions

A;Reference number: PA0001

A;Accession: PA0029

A;Molecule type: protein

A;Residues: 1-15 <KAM>

A;Experimental source: callus

Query Match

25.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVN 9

|||

Db 10 VVN 12

RESULT 45

PS0276

phosphoribulokinase (EC 2.7.1.19) - rice (strain Nihonbare) (fragment)

C;Species: *Oryza sativa* (rice)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995

A;Accession: PS0276

R;Tsugita, A.

submitted to JIPID, April 1993

A;Reference number: PS0206

A;Accession: PS0276

A;Molecule type: protein

A;Residues: 1-15 <TSU>

A;Experimental source: leaf, chlorophyll, stem

C;Keywords: phosphotransferase

Query Match

25.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8

|||

Db 5 PVV 7

RESULT 46

B61457

alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)

C;Species: Tetrahymena pyriformis

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999

C;Accession: B61457

R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.

J. Protozool. 36, 562-567, 1989

A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purifica

A;Reference number: A61457; MUID:90095988; PMID:2689637

A;Accession: B61457

A;Molecule type: protein

A;Residues: 1-15 <BAN>

C;Genetics:

A;Genetic code: SGC5

C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; m

Query Match

25.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12

|||

Db 1 VLP 3

RESULT 47

S57577

T cell receptor V-J junctional alpha chain region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999

C;Accession: S57577

R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.

submitted to the EMBL Data Library, June 1995

A;Description: T cell receptor repertoire for a viral epitope in humans is diversifie

A;Reference number: S57494

A;Accession: S57577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-15 <BUR>

A;Cross-references: EMBL:Z49945; NID:G887492; PIDN:CAA90216.1; PID:G887493

C;Keywords: T-cell receptor

Query Match

25.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3

|||

Db 12 LFF 14

RESULT 48

E56978
collagen alpha 2(XI) chain - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995
C:Accession: E56978
R:Wu, J.J.; Eyre, D.R.
J. Biol. Chem. 270, 18865-18870, 1995
A:Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Ins
A:Reference number: A56978; MUID:95370194; PMID:7642541
A:Accession: E56978
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <WR>
A>Note: the residue designated 'X' is modified lysine cross-linked to 1(XI) Lys-23 in FS

Query Match 25.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8
|||
DB 11 PVV 13

RESULT 49
PH0784
T-cell receptor alpha chain (F1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0784
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0784
A:Molecule type: mRNA
A:Residues: 1-15 <AS>
A:Cross-references: EMBL:X60885
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11
|||
DB 10 NVL 12

RESULT 50
A31902
bone acidic glycoprotein-75 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 31-Dec-1993
C:Accession: A31902
R:Gorski, J.P.; Shimizu, K.
J. Biol. Chem. 263, 15938-15945, 1988
A:Title: Isolation of new phosphorylated glycoprotein from mineralized phase of bone tha
A:Reference number: A31902; MUID:89034045; PMID:2846530
A:Accession: A31902
A:Molecule type: protein
A:Residues: 1-15 <GOR>
A>Note: 14-Glu and 15-Glu were also found
C:Keywords: glycoprotein

Query Match 25.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPV 7
|||

DB 1 LPV 3

RESULT 51
AF0832
pne leader peptide [imported] - Salmonella enterica subsp. enterica serovar Typhi (str
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A>Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AF0832
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra
S.; Moulie, S.; O'Gea, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica ser
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF0832
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05845.1; PID:g16503820; GSPDB:GN00176
C:Genetics:
A:Gene: STY2853a

Query Match 25.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFF 4
|||
DB 6 PFF 8

RESULT 52
I40065
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C:Species: Buchnera aphidicola
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999
C:Accession: I40065
R:Roubaksh, D.; Baumann, P.
Gene 155, 107-112, 1995
A:Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (end
A:Reference number: I40061; MUID:95212914; PMID:7535281
A:Accession: I40065
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: EMBL:U10499; NID:g854717; PIDN:AAA79128.1; PID:g854718
C:Genetics:
A:Gene: aroE
C:Keywords: oxidoreductase

Query Match 25.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
|||
DB 3 LFF 5

RESULT 53
G49039
T-cell receptor beta chain V-D-J-C region (V beta 4, J beta 2.2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: G49039
R:Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis usi
A:Reference number: A49039; MUID:92164737; PMID:1311263
A:Accession: G49039

A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-16 <ROS>
 A>Note: sequence extracted from NCBI backbone (NCBIP:90719)
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
 Db 13 LFF 15

RESULT 54

H49039
 T-cell receptor beta chain V-D-J-C region (V beta 5, J beta 1.4) - human (fragment)

C:Species: Homo sapiens (man)
 C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
 C:Accession: H49039
 R:Rosenberg, W.M.; Moss, P.A.; Bell, J.I.

A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using Eur. J. Immunol. 22, 541-549, 1992
 A:Reference number: A49039; MUID:92164737; PMID:1311263

A:Accession: H49039
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-16 <ROS>
 A>Note: sequence extracted from NCBI backbone (NCBIP:90720)
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
 Db 13 LFF 15

RESULT 55

G24687
 T-cell receptor beta-1 chain J-B1.4 segment - human (fragment)

C:Species: Homo sapiens (man)
 C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
 C:Accession: G24687

R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
 A:Title: Organization and sequences of the diversity, joining, and constant region genes
 A:Reference number: A94081; MUID:86094276; PMID:3866244

A:Accession: G24687
 A:Molecule type: DNA
 A:Residues: 1-16 <TOY>

A:Cross-references: GB:M14158; NID:G338844; PIDN:AAA60671.1; PID:G553683
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
 Db 5 LFF 7

RESULT 56

A28587
 T-cell receptor beta-2 chain J-B2.2 segment - human (fragment)

C:Species: Homo sapiens (man)
 C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
 C:Accession: A28587
 R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
 A:Title: Organization and sequences of the diversity, joining, and constant region genes
 A:Reference number: A94081; MUID:86094276; PMID:3866244
 A:Accession: A28587

A:Molecule type: DNA

A:Residues: 1-16 <TOY>
 A:Cross-references: GB:M14159; NID:G338852; PIDN:AAA60676.1; PID:G553687
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
 Db 5 LFF 7

RESULT 57

PH1476
 T-cell receptor beta chain (clone 223/14) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C:Accession: PH1476
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; J. Exp. Med. 177, 811-820, 1993

A:Title: T cell receptor selection by and recognition of two class I major histocompatibility complex (MHC) class I molecules
 A:Reference number: PH1430; MUID:93171821; PMID:8436911

A:Accession: PH1476
 A:Molecule type: mRNA
 A:Residues: 1-16 <CAS>
 A:Experimental source: cytolytic T-lymphocyte
 C:Superfamily: immunoglobulin homology
 C:Keywords: receptor; T-cell

Query Match 25.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
 Db 13 LFF 15

RESULT 58

PH1475
 T-cell receptor beta chain (clone 223/S) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C:Accession: PH1475
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; J. Exp. Med. 177, 811-820, 1993

A:Title: T cell receptor selection by and recognition of two class I major histocompatibility complex (MHC) class I molecules
 A:Reference number: PH1430; MUID:93171821; PMID:8436911

A:Accession: PH1475
 A:Molecule type: mRNA
 A:Residues: 1-16 <CAS>
 A:Experimental source: cytolytic T-lymphocyte
 C:Superfamily: immunoglobulin homology
 C:Keywords: receptor; T-cell

Query Match 25.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
 Db 13 LFF 15

RESULT 59

PH1474
 T-cell receptor beta chain (clone A2/25) - mouse (fragment)

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C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1474
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1474
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Experimental source: cytolytic T-lymphocyte
A;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell

Query Match      25.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LFF 3
      |||
Db      13 LFF 15

RESULT 60
PH1472
T-cell receptor beta chain (clone A24/12.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1472
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1472
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Experimental source: cytolytic T-lymphocyte
A;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell

Query Match      25.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LFF 3
      |||
Db      13 LFF 15

RESULT 61
PH1477
T-cell receptor beta chain (clone A3/H2R5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1477
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1477
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Experimental source: cytolytic T-lymphocyte
A;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell

Query Match      25.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LFF 3
      |||
Db      13 LFF 15

RESULT 62
PH1473
T-cell receptor beta chain (clone A3/IIIC5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1473
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.;
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompa
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1473
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Experimental source: cytolytic T-lymphocyte
A;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell

Query Match      25.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LFF 3
      |||
Db      13 LFF 15

RESULT 63
PH0766
T-cell receptor beta chain (J3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0766
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility comple
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0766
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Cross-references: EMBL:X60860; NID:g52745; PIDN:CAA43250.1; PID:g52746
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match      25.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LFF 3
      |||
Db      13 LFF 15

RESULT 64
PH0767
T-cell receptor beta chain (J5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0767
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility comple
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0767
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Cross-references: EMBL:X60861; NID:g52752; PIDN:CAA43251.1; PID:g52753
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

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Query Match 25.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
Db 13 LFF 15

RESULT 65

PH1480
T-cell receptor beta chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 27-Oct-1995
C:Accession: PH1480; PH1478
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
J. Exp. Med. 177; 811-820, 1993
A>Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1480
A:Molecule type: mRNA
A:Residues: 1-16 <CAS1>
A:Experimental source: cytolytic T-lymphocyte, clone A3/C80b
A:Accession: PH1478
A:Molecule type: mRNA
A:Residues: 1-16 <CAS2>
A:Experimental source: cytolytic T-lymphocyte, clone A24/PBF5
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 25.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
Db 13 LFF 15

RESULT 66

I65274
glutathione S-transferase Ya subunit (put.) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Jun-1999
C:Accession: I65274
R:Roehkopf, G.S.; Telakowski-Hopkins, C.A.; Stotish, R.L.; Pickett, C.B.
Biochemistry 25; 993-1002, 1986
A>Title: Multiplicity of glutathione S-transferase genes in the rat and association with
A:Reference number: I52395; MUID:86187772; PMID:2421763
A:Accession: I65274
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-17 <RES>
A:Cross-references: GB:M12894; NID:g204504; PIDN:AAA1289.1; PID:g204505
C:Superfamily: glutathione transferase

Query Match 25.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPV 7
Db 1 LPV 3

RESULT 67

C37520
glutathione transferase (EC 2.5.1.18) MII - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 30-Sep-1993
C:Accession: C37520; N24735
R:Mannervik, B.; Alin, P.; Gurchenberg, C.; Jansson, H.; Tahir, M.K.; Warholm, M.; Jor
Proc. Natl. Acad. Sci. U.S.A. 82; 7202-7206, 1985

A>Title: Identification of three classes of cytosolic glutathione transferase common
A:Reference number: A24735; MUID:86042634; PMID:3864155
A:Accession: C37520
A:Molecule type: protein
A:Residues: 1-17 <MAN>
C:Superfamily: glutathione transferase
C:Keywords: transferase

Query Match 25.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PVV 8
Db 9 PVV 11

RESULT 68

I49425
mitogen regulated protein - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: I49425
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Madeau,
Mamm. Genome 5; 349-355, 1994
A>Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49425
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-17 <RES>
A:Cross-references: EMBL:U05748; NID:g497088; PIDN:AAB60483.1; PID:g497089
C:Superfamily: prolactin

Query Match 25.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVL 11
Db 5 NVL 7

RESULT 69

S05913
chorion class A protein L2 precursor - silkworm (fragment)
C:Species: Bombyx mori (silkworm)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
C:Accession: S05913
R:Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.
J. Mol. Biol. 209; 1-19, 1989
A>Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridi
A:Reference number: S05913; MUID:90040707; PMID:2810362
A:Accession: S05913
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-17 <SPO>
A:Cross-references: EMBL:X15558; NID:g5771; PIDN:CAA33567.1; PID:g5772
A>Note: this sequence was submitted to the EMBL Data Library, Jun-1989
C:Genetics:
A:Map position: 2
C:Superfamily: chorion class A protein pc292

Query Match 25.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFL 5
Db 6 FFL 8

RESULT 70

I49593
cystic fibrosis transmembrane conductance regulator - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C:Accession: I49593
R:Denamur, E.; Chehab, F.F.
Hum. Mol. Genet. 3, 1089-1094, 1994
A:Title: Analysis of the mouse and rat CFTR promoter regions.
A:Reference number: I49593; MUID:95072572; PMID:7526924
A:Accession: I49593
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-17 <RES>
A:Cross-references: GB:L04873; NID:G414726; PIDN:AAA73562.1; PID:G553892
C:Gene: CFTR
C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette

Query Match 25.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
|||
Db 15 LFF 17

RESULT 71
I84733
Gene CFTR protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: I84733
R:Denamur, E.; Chehab, F.F.
Hum. Mol. Genet. 3, 1089-1094, 1994
A:Title: Analysis of the mouse and rat CFTR promoter regions.
A:Reference number: I49593; MUID:95072572; PMID:7526924
A:Accession: I84733
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-17 <RES>
A:Cross-references: GB:L26098; NID:G425185; PIDN:AAA73561.1; PID:G915270
C:Gene: CFTR
C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette

Query Match 25.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
|||
Db 15 LFF 17

RESULT 72
S66213
Glucose 1-dehydrogenase (EC 1.1.1.47) - Haloferax mediterranei (fragment)
C:Species: Haloferax mediterranei
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 30-Oct-1998
C:Accession: S66213
R:Bonete, M.J.; Pire, C.; Llorca, F.I.; Camacho, M.L.
FEBS Lett. 383, 227-229, 1996
A:Title: Glucose dehydrogenase from the halophilic Archaeon Haloferax mediterranei: enzymology and molecular biology
A:Reference number: S66213; MUID:96198607; PMID:8925901
A:Accession: S66213
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <BON>
C:Keywords: oxidoreductase

Query Match 25.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;

QY 1 LFF 3
|||
Db 15 LFF 17

RESULT 73
S59481
hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)
C:Species: Phaseolus vulgaris (kidney bean)
C>Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998
C:Accession: S59481
R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A:Title: Specificity in the immobilisation of cell wall proteins in response to different pH values
A:Reference number: S59481; MUID:96011753; PMID:7548825
A:Accession: S59481
A:Molecule type: protein
A:Residues: 1-17 <WOJ>
C:Keywords: glycoprotein; hydroxyproline
F:6,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 25.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8
|||
Db 13 PVV 15

RESULT 74
PS0454
38K protein 3129 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C:Accession: PS0454
R:Tsugita, A.
submitted to JFIPD, April 1993
A:Reference number: PS0206
A:Accession: PS0454
A:Molecule type: protein
A:Residues: 1-17 <TSU>
A:Experimental source: leaf, chloroplast, stem
A>Note: molecular weight 38K, pI 5.9

Query Match 25.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVN 9
|||
Db 9 VVN 11

RESULT 75
E22595
Bombolitin V - American common bumblebee
C:Species: Bombus pennsylvanicus (American common bumblebee)
C>Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 08-Dec-1995
C:Accession: E22595
R:Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 260, 1437-1444, 1985
A:Title: Bombolitin, a new class of mast cell degranulating peptides from the venom of the bumblebee
A:Reference number: A92504; MUID:85105003; PMID:2578459
A:Accession: E22595
A:Molecule type: protein
A:Residues: 1-17 <ARG>
C:Keywords: amidated carboxyl end; hemolysis; venom
F:17/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 25.0%; Score 3; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVL 11
 |||
Db 2 NVL 4

Search completed: November 25, 2003, 18:28:16
Job time : 12.0426 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 5.80851 Seconds
(without alignments)
97.154 Million cell updates/sec

Title: US-09-641-801-4

Perfect score: 12

Sequence: 1 LFFFLPVNVLP 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	41.7	17	1	UP36 UPEMJ
2	4	33.3	14	1	UC15 MAIZE
3	3	25.0	5	1	PAP2 PARMA
4	3	25.0	12	1	GRAR RANRU
5	3	25.0	12	1	TM2A METMA
6	3	25.0	12	1	UN39 CLOPA
7	3	25.0	12	1	XZPT_ECOLI
8	3	25.0	13	1	CRBL_VESAN
9	3	25.0	13	1	CRBL_VESCR
10	3	25.0	13	1	CRBL_VESLE
11	3	25.0	13	1	CRBL_VESMA
12	3	25.0	13	1	CRBL_VESTR
13	3	25.0	13	1	CRBL_VESXA
14	3	25.0	13	1	FIBB_RABIT
15	3	25.0	13	1	FIBB_RANES
16	3	25.0	13	1	HPB1 RANES
17	3	25.0	13	1	PEDI HYDAT
18	3	25.0	13	1	TEMA RANTE
19	3	25.0	13	1	TEME RANTE
20	3	25.0	13	1	TEMP RANTE
21	3	25.0	13	1	YPNP PHOLU
22	3	25.0	14	1	ADFA TENMO
23	3	25.0	14	1	CRBL_VESOR
24	3	25.0	14	1	LPE2_ECOLI
25	3	25.0	14	1	PHI_FUSE
26	3	25.0	15	1	CDN4 LITCE
27	3	25.0	15	1	CKX WHEAT
28	3	25.0	15	1	ESTB SCHGA
29	3	25.0	15	1	LPP_ECOLI
30	3	25.0	15	1	PH3_PRUSE
31	3	25.0	15	1	UC08 MAIZE
32	3	25.0	15	1	UP01 METAN
33	3	25.0	16	1	PH2_PRUSE

RESULT 1

ALIGNMENTS

34	3	25.0	17	1	BOL5_MEGPE
35	3	25.0	17	1	TPIS_PINPS
36	3	25.0	18	1	AZM_OCTVU
37	3	25.0	18	1	ALL2_CYPDO
38	3	25.0	18	1	LUXB_KRYAS
39	3	25.0	19	1	COOT_SARBU
40	3	25.0	19	1	MTFH_TRIMR
41	3	25.0	19	1	PSBW_SYNVU
42	3	25.0	19	1	UP25_UPEIN
43	3	25.0	19	1	UP27_UPEMJ
44	3	25.0	19	1	UP28_UPEMJ
45	3	25.0	20	1	CISY_STRHY
46	3	25.0	20	1	COGI_PARM
47	3	25.0	20	1	EFTU_MYCSI
48	3	25.0	20	1	FLA_VIBAL
49	3	25.0	20	1	FRE3_LITIN
50	3	25.0	20	1	MDH_KIBAR
51	3	25.0	20	1	MIF_PIG
52	3	25.0	20	1	TENB_ACTTE
53	2	16.7	4	1	FFKA_ATEFL
54	2	16.7	4	1	FLRF_HIRME
55	2	16.7	4	1	FLRN_ATEFL
56	2	16.7	5	1	PRCT_PERAM
57	2	16.7	5	1	RE11_LITRU
58	2	16.7	5	1	RE21_LITRU
59	2	16.7	5	1	RE31_LITRU
60	2	16.7	5	1	RE32_LITRU
61	2	16.7	5	1	UC22_MAIZE
62	2	16.7	6	1	ACPH_RABIT
63	2	16.7	6	1	PARP_MONEX
64	2	16.7	6	1	TRPI_PSEPU
65	2	16.7	7	1	PARI_HELTI
66	2	16.7	7	1	PARI_MACRS
67	2	16.7	7	1	PARI_PROCL
68	2	16.7	7	1	PAP2_PROCL
69	2	16.7	7	1	PPH2_LYCES
70	2	16.7	7	1	UN06_PINPS
71	2	16.7	8	1	AKHG_GRYBI
72	2	16.7	8	1	AKH_LIABA
73	2	16.7	8	1	ALL6_CYPDO
74	2	16.7	8	1	CADI_ENTFA
75	2	16.7	8	1	CLP_THICU
76	2	16.7	8	1	COW2_CONPU
77	2	16.7	8	1	CPDI_ENTFA
78	2	16.7	8	1	FARI_PANRE
79	2	16.7	8	1	FARI_PENMO
80	2	16.7	8	1	FAR2_MACRS
81	2	16.7	8	1	FAR3_HOMAM
82	2	16.7	8	1	FAR3_HOMAM
83	2	16.7	8	1	FUSS_FUSSO
84	2	16.7	8	1	HTFI_PERAM
85	2	16.7	8	1	NPB_BOVIN
86	2	16.7	8	1	NS3_MYCTU
87	2	16.7	8	1	PLP_BRANA
88	2	16.7	8	1	UPAL_HUMAN
89	2	16.7	9	1	BS43_SERPL
90	2	16.7	9	1	FAR2_PANRE
91	2	16.7	9	1	FAR3_MACRS
92	2	16.7	9	1	FAR6_MACRS
93	2	16.7	9	1	FAR8_MACRS
94	2	16.7	9	1	FARP_CALSI
95	2	16.7	9	1	FIBB_EKIPA
96	2	16.7	9	1	FIBB_MACFU
97	2	16.7	9	1	FIBB_PAPAN
98	2	16.7	9	1	FIBB_PAPHA
99	2	16.7	9	1	FIBB_THEGE
100	2	16.7	9	1	MOSF_CLYJA

P07496 megabombus
P81666 pinus pinas
P30800 octopus vul
P82153 cydia pomon
P18300 kryptophana
Q09148 sarcophaga
P81530 trichuris m
P12313 synechococc
P82031 uperoleia i
P82039 uperoleia m
P82040 uperoleia m
P20903 streptomyce
P20731 paralithode
P81407 mycoplasma
P83150 vibrio algi
P56249 litoria inf
P19978 kibdelospor
P80928 sus scrofa
P30834 actinia ten
P58705 anthopleura
P42561 hirudo medi
P58707 anthopleura
P01373 periplaneta
P82070 litoria rub
P82071 litoria rub
P82072 litoria rub
P80628 zea mays (m
P25154 cryctolagus
P41966 moniezia ex
P36414 pseudomonas
P41871 helisoma tr
P83274 macrobrachi
P38499 procamburus
P38498 procamburus
P83379 lycopersico
P81675 pinus pinas
P14086 gryllus bim
P25418 libellula a
P82157 cydia pomon
P13268 enterococcu
P80488 thiobacillu
P58785 conus purpu
P13269 enterococcu
P41872 panagrellus
P83316 penaeus mon
P83275 macrobrachi
P41486 homarus ame
P41487 homarus ame
P81010 fusarium so
P04548 periplaneta
P15507 bos taurus
P81152 mycobacteri
P81707 brassica na
P30087 homo sapien
P83375 serratia pl
P41873 panagrellus
P83276 macrobrachi
P83279 macrobrachi
P83281 macrobrachi
P38495 callinectes
P19346 erythrocebu
P19345 macaca fusc
P19344 papio anubi
P19343 papio hamad
P19342 theropithec
P19853 clypeaster

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UP36 UPEMJ
ID UP36 UPEMJ STANDARD; PRT; 17 AA.
AC P82043;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 3.6.
OS Uperoleia mjobergii (Australian toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104954;
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "New antibiotic uperin peptides from the dorsal glands of the
RL Aust. J. Chem. 49:1325-1331(1996).
CC -!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1826; METHOD=FAB.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 17
FT SEQUENCE 17 AA; 1778 MW; 784DBBB46263CA3D CRC64;
SQ SEQUENCE 17 AA; 1778 MW; 784DBBB46263CA3D CRC64;

Query Match 41.7%; Score 5; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVNVL 11
DB 9 VVNVL 13
|||||

RESULT 2
UC15 MAIZE STANDARD; PRT; 14 AA.
AC P80621;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 245)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huot J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.8, ITS MW IS: 35.7 kDa.
DR Maize-2DPAGE; P80621; COLEOPTILE.
DR MaizeDB; 123947; -.
FT NON_TER 1
FT NON_TER 14
FT SEQUENCE 14 AA; 1396 MW; C68949275F404CD2 CRC64;

Query Match 33.3%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8
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DB 5 LPVV 8

RESULT 3
PAP2 PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleiidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mores sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON_TER 5
FT SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4
DB 2 FFF 4
|||||

RESULT 4
GRAR RANRU STANDARD; PRT; 12 AA.
AC P40754;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Granuliberin-R.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=78062810; PubMed=589733;
RA Nakajima T., Yasuhara T.;
RT "A new mast cell degranulating peptide, granuliberin-R, in the frog
RT (Rana rugosa) skin.";
RL Chem. Pharm. Bull. 25:2464-2465(1977).
RN [2]
RP SYNTHESIS.
RX MEDLINE=78189201; PubMed=657408;
RA Nakajima T., Yasuhara T., Hirai Y., Kitada C., Fujino M., Takeyama M.,
RA Koyama K., Yajima H.;
RT "Synthesis of the dodecapeptide amide corresponding to the entire
RT amino acid sequence of granuliberin-R, a new frog skin peptide from
RT Rana rugosa.";

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OS	OC	Query Match	Score 3	DB 1	Length 12
Clostridium pasteurianum.		Best Local Similarity	100.0%	Pred. No. 1.4e+03	
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.		Matches	3	Conservative	0
		Mismatches	0	Indels	0
		Gaps	0		0

QY 1 LFP 3
Db 4 LFP 6

RESULT 8
CRBL_VESAN STANDARD; PRT; 13 AA.
AC P17233;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespid chemotactic peptide A (VESCP-A).
OS Vespa analis (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7449;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
RA Fujino M.;
RL (In) Munekata E. (eds.);
RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation,
RL Osaka (1984).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1386 MW; C85554365DF9233D CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
Db 1 FLP 3

RESULT 10
CRBL_VESLE STANDARD; PRT; 13 AA.
AC P17235;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespid chemotactic peptide L (VESCP-L).
OS Vespa lewisii (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7452;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RL (In) Izumiya N. (eds.);
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,
RL Osaka (1985).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1384 MW; C850402B8819233D CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
Db 1 FLP 3

RESULT 11
CRBL_VESMA STANDARD; PRT; 13 AA.
AC P17232;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespid chemotactic peptide M (VESCP-M).
OS Vespa mandarinia (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7446;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
RA Fujino M.;
RL (In) Munekata E. (eds.);
RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation,
RL Osaka (1984).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.

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FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1384 MW; 265040289DF92338 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
DB 1 FLP 3

RESULT 12
CRLB_VESXA STANDARD; PRT; 13 AA.
ID CRLB_VESXA STANDARD; PRT; 13 AA.
AC P17234;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespid chemotactic peptide T (VESP-T).
OS Vespa tropica (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7450;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Nakajima T., Erspaer V.;
RL (In) Sakakibara S. (eds.);
RL Peptide chemistry 1982, pp.213-218, Protein Research Foundation,
RL Osaka (1983).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD RES 13
SQ SEQUENCE 13 AA; 1354 MW; 220140365DFE5338 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
DB 1 FLP 3

RESULT 13
CRLB_VESXA STANDARD; PRT; 13 AA.
ID CRLB_VESXA STANDARD; PRT; 13 AA.
AC P17234;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespid chemotactic peptide X (VESP-X).
OS Vespa xanthoptera (Japanese hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7448;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RL (In) Izumiya N. (eds.);
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,
RL Osaka (1985).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD RES 13
SQ SEQUENCE 13 AA; 1368 MW; C85040365DF9233D CRC64;

FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1368 MW; C85040365DF9233D CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
DB 1 FLP 3

RESULT 14
FIBB_RABIT STANDARD; PRT; 13 AA.
ID FIBB_RABIT STANDARD; PRT; 13 AA.
AC P14478;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro: IPR002181; Fibrinogen C.
DR PROSITE: PS00514; FIBRINAG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 13 FIBRINOPEPTIDE B.
FT MOD RES 4 4 SULFATION.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1493 MW; 9417F3B76337CB1A CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
DB 8 VLP 10

RESULT 15
HPA1_RANES STANDARD; PRT; 13 AA.
ID HPA1_RANES STANDARD; PRT; 13 AA.
AC P32415;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hemolytic protein A1 (Fragment).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90198965; PubMed=2317508;
RA Simmaco M., de Biase D., Severini C., Alta M., Erspaer G.F.,
RA Barra D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta.";
```

RL Biochim. Biophys. Acta 1033:318-323(1990).
 CC -!- FUNCTION: Shows hemolytic activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; S09018.
 KW Amphibian defense peptide; Amidation; Hemolysis.
 FT MOD_RES 13 13 AMIDATION.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1390 MW; C6BA768B9DFE587D CRC64;
 Query Match 25.0%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 FLP 6
 Db 1 FLP 3

RESULT 16
 HPB9 RANES
 ID HPB9 RANES STANDARD; PRT; 13 AA.
 AC P32416;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hemolytic protein B9 (Fragment).
 OS Rana esculenta (Edible frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8401;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90198965; PubMed=2317508;
 RA Siammaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
 RA Barra D., Bossa F.;
 RT "Purification and characterization of bioactive peptides from skin
 RT extracts of Rana esculenta.";
 RL Biochim. Biophys. Acta 1033:318-323(1990).
 CC -!- FUNCTION: Shows hemolytic activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; S09019.
 KW Amphibian defense peptide; Amidation; Hemolysis.
 FT MOD_RES 13 13 AMIDATION.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;
 Query Match 25.0%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 FLP 6
 Db 1 FLP 3

RESULT 17
 PEDI_HYDAT
 ID PEDI_HYDAT STANDARD; PRT; 13 AA.
 AC P80578;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Pedin.
 OS Hydra attenuata (Hydra) (Hydra vulgaris).
 CC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;
 CC Hydridae; Hydra.
 OX NCBI_TaxID=6087;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=96232307; PubMed=8674432;

RA Hoffmeister S.A.H.;
 RT "Isolation and characterization of two new morphogenetically active
 RT peptides from Hydra vulgaris.";
 RL Development 122:1941-1948(1996).
 CC -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT
 CC DEVELOPMENT.
 CC Morphogen.
 KW SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;
 Query Match 25.0%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 10 VLP 12
 Db 7 VLP 9

RESULT 18
 TEMA_RANTE
 ID TEMA_RANTE STANDARD; PRT; 13 AA.
 AC P56917;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Temporin A.
 OS Rana temporaria (European common frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8407;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Siammaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 RT temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive
 CC bacteria.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the brevinin family.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT MOD_RES 13 13 AMIDATION.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1398 MW; 2653612B99EBCD408 CRC64;
 Query Match 25.0%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 FLP 6
 Db 1 FLP 3

RESULT 19
 TEMA_RANTE
 ID TEMA_RANTE STANDARD; PRT; 13 AA.
 AC P56920;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Temporin E.
 OS Rana temporaria (European common frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8407;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97175050; PubMed=9022710;

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RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Baria D.;
RA "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 13
SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
DB 1 VLP 3

RESULT 20
TEMP_RANTE STANDARD; PRT; 13 AA.
AC P56921;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin F.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=9175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Baria D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
CC GRAM-POSITIVE BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 13
SQ SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
DB 1 FLP 3

RESULT 21
YFNP_PHOJU STANDARD; PRT; 13 AA.
AC P41122;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in pnp 3' region (ORF3) (Fragment).
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.

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OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K122;
RX MEDLINE=94266731; PubMed=8206856;
RA Clarke D.J., Dowds B.C.A.;
RT "The gene coding for polynucleotide phosphorylase in Photorhabdus sp.
RT strain K122 is induced at low temperatures.";
RL J. Bacteriol. 176:3775-3784(1994).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X76069; CA53672.1; -.
KW Hypothetical protein.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1634 MW; 64774A4F6267A364 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFL 5
DB 3 PFL 5

RESULT 22
ADFA_TENMO STANDARD; PRT; 14 AA.
AC P82965;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Antidiuretic factor A (ADFA) (ADF) (Antidiuretic hormone A) (ADHA).
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC TISSUE=Head;
RX MEDLINE=21642653; PubMed=11756661;
RA Eigenheer R.A., Nicolson S.W., Schegg K.M., Hull J.J., Schooley D.A.;
RT "Identification of a potent antidiuretic factor acting on beetle
RT Malpighian tubules.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:84-89(2002).
CC -!- FUNCTION: Strong inhibitor of fluid secretion by the Malpighian
CC tubules. Uses cGMP as a second messenger and inhibits fluid
CC production by decreasing cAMP concentration.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1541.58; METHOD=MALDI.
CC -!- SIMILARITY: STRONG, TO THE C-TERMINAL OF T.MOLITOR CUTICULAR
CC PROTEIN LFCP29.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005184; P:neuropeptide hormone activity; NAS.
DR GO; GO:0007218; P:neuropeptide signaling pathway; NAS.
KW Neuropeptide; Hormone.
SQ SEQUENCE 14 AA; 1543 MW; F49C91A3F16E43D1 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVN 9
DB 1 VVN 3

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RESULT 23

CRBL_VESOR STANDARD; PRT; 14 AA.
 AC FL236;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Histamine releasing peptide II (HR-II).
 OS Vespa orientalis (Oriental hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7447;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
 RA Rozynov B.V., Gushchin I.S.;
 RT "Structure and properties of histamine releasing peptides from the
 RT venom of Vespa orientalis hornet."
 RL Bioorg. Khim. 7:1467-1477(1981).
 CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
 CC of neutrophils.
 CC PIR; JN0390; JN0390.
 KW Mast cell degranulation; Chemotaxis; Amidation.
 FT MOD RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA; 1524 NW; 22015B4A6CEDFD38 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6

Db 1 FLP 3

RESULT 24

LPF2_ECOLI STANDARD; PRT; 14 AA.
 AC P06985;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Phenylalanyl-tRNA synthetase operon leader peptide (PheST attenuator
 DE peptide).
 GN PHM OR PHTL OR B1715 OR C5495 OR Z2744 OR ECS2422 OR STY1774 OR T1217
 GN OR SF1516.
 OS Escherichia coli,
 OS Escherichia coli O6,
 OS Escherichia coli O157:H7,
 OS Salmonella typhi, and
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562, 217992, 83334, 601, 623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E. coli;
 RX MEDLINE=85210878; PubMed=3158742;
 RA Springer M., Mayaux J.-P., Fayat G., Plunbridge J.A., Graffe M.,
 RA Blanquet S., Grunberg-Manago M.;
 RT "Attenuation control of the Escherichia coli phenylalanyl-tRNA
 RT synthetase operon."
 RL J. Mol. Biol. 181:467-478(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E. coli;
 RX MEDLINE=84030239; PubMed=6317865;
 RA Fayat G., Mayaux J.-P., Sacerdot C., Fromant M., Springer M.,
 RA Grunberg-Manago M., Blanquet S.;

"Escherichia coli phenylalanyl-tRNA synthetase operon region.
 Evidence for an attenuation mechanism. Identification of the gene for
 the ribosomal protein L20."
 J. Mol. Biol. 171:239-261(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E. coli;
 RX MEDLINE=88163794; PubMed=3126825;
 RA Springer M., Graffe M., Mayaux J.-P., Dardel F., Fayat G.,
 RA Blanquet S., Grunberg-Manago M.;
 RT "Open reading frames in the control regions of the phenylalanyl-tRNA
 RT synthetase operon of E. coli."
 RL Biochimie 69:1065-1070(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E. coli; STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E. coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 RT of uropathogenic Escherichia coli."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E. coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Apodaca J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
 RL Nature 409:529-533(2001).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E. coli; STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Toke T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12."
 RL DNA Res. 8:11-22(2001).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S. typhi; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18."
 RL Nature 413:848-852(2001).
 RN [9]

RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative Genomics of Salmonella enterica serovar Typhi strains Ty2
RT and C718.";
RL J. Bacteriol. 185:2330-2337(2003).
RN [10]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang X., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN -----
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DR EMBL; M10423; AAA23961.1; -;
DR EMBL; V00291; CAA23563.1; -;
DR EMBL; M13251; AAA24333.1; -;
DR EMBL; AB000266; AAC74785.1; -;
DR EMBL; AB016761; AN80571.1; -;
DR EMBL; AB005394; AAG56702.1; -;
DR EMBL; AF002558; BAB35845.1; -;
DR EMBL; AL627271; CAD02016.1; -;
DR EMBL; AB016838; AAC68872.1; -;
DR EMBL; AB015174; AAN43106.1; -;
DR PIR; B85780; B85780.
DR PIR; F90931; F90931.
DR PIR; S11551; LFECPFS.
DR EcoGene; EGI1272; phem.
KW Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1762 MW; 7031C48E006F0D4 CRC64;
Query Match 25.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FFF 4
Db 8 FFF 10

RESULT 25
PHI_PRUSE
ID PHI_PRUSE STANDARD; PRT; 14 AA.
AC P29263;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Prunasin beta-glucosidase I (EC 3.2.1.118) (Prunasin hydrolase
DE isozyme I) (PH I) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OC NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;

RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative Genomics of Salmonella enterica serovar Typhi strains Ty2
RT and C718.";
RL J. Bacteriol. 185:2330-2337(2003).
RN [10]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang X., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
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RN -----
DR EMBL; M10423; AAA23961.1; -;
DR EMBL; V00291; CAA23563.1; -;
DR EMBL; M13251; AAA24333.1; -;
DR EMBL; AB000266; AAC74785.1; -;
DR EMBL; AB016761; AN80571.1; -;
DR EMBL; AB005394; AAG56702.1; -;
DR EMBL; AF002558; BAB35845.1; -;
DR EMBL; AL627271; CAD02016.1; -;
DR EMBL; AB016838; AAC68872.1; -;
DR EMBL; AB015174; AAN43106.1; -;
DR PIR; B85780; B85780.
DR PIR; F90931; F90931.
DR PIR; S11551; LFECPFS.
DR EcoGene; EGI1272; phem.
KW Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1762 MW; 7031C48E006F0D4 CRC64;
Query Match 25.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FFF 4
Db 8 FFF 10

RESULT 26
CDNA_LITCE
ID CDNA_LITCE STANDARD; PRT; 15 AA.
AC P82076;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caeridin 4
OS Litoria caerulea (Green tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OC NCBI_TaxID=30344;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Parotoid gland;
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. Structures of the caeridins from
RT Litoria caerulea.";
RT J. Chem. Soc. Perkin Trans. 1:573-576(1993).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC -!- ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
CC glands.
CC -!- MASS SPECTROMETRY: MW=1504; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD RES 15 15
SQ SEQUENCE 15 AA; 1506 MW; 06F1BBFBBC5195F CRC64;
Query Match 25.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 NVL 11
Db 8 NVL 10

RESULT 27
CKX_WHEAT
ID CKX_WHEAT STANDARD; PRT; 15 AA.
AC P58763;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytokinin oxidase (EC 1.4.3.-) (CKO) (CKX) (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;

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OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RC SEQUENCE, AND CHARACTERIZATION.
RX STRAIN=cv. Samantha;
RX MEDLINE=21099312; PubMed=11168382;
RA Galuszka P., Frebort I., Sebelia M., Sauer P., Jacobsen S., Pec P.;
RT "Cytokinin oxidase or dehydrogenase? Mechanism of cytokinin
RT degradation in cereals.";
RL Eur. J. Biochem. 268:450-461(2001).
CC -!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-
CC substituted adenine derivatives that are plant hormones, where the
CC substituent is an isopentenyl group. Substrate preference is 2-(2-
CC Hydroxyethylamino)-9-methyl-N(6)-isopentenyladenine >>
CC isopentenyladenine > cis-zeatin = isopentenyladenosine = zeatin >>
CC zeatin riboside.
CC -!- CATALYTIC ACTIVITY: N(6)-(3-methylbut-2-enyl)adenine + H(2)O +
CC O(2) = adenine + 3-methylbut-2-enal + H(2)O(2).
CC -!- COFACTOR: FAD.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Extracellular (By similarity).
CC -!- MISCELLANEOUS: Optimal pH is 6.5.
CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
CC oxidoreductase family.
KW Oxidoreductase; Flavoprotein; FAD.
FT UNSURE 1
FT UNSURE 13 15
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1709 MW; 85B589BD53FCEDEF CRC64;

Query Match 25.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
DB [1]
DB 1 FLP 3

RESULT 28
ESTB_SCHGA
ID ESTB_SCHGA STANDARD; PRT; 15 AA.
AC P81011;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Esterase 56 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)
DE (Fragment).
OS Schizaphis graminum (Aphid).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphidoidea; Aphididae; Aphidini; Schizaphis.
OX NCBI_TaxID=13262;
RN [1]
RC SEQUENCE.
RX MEDLINE=97468499; PubMed=9327586;
RA Siegfried B.D., Ono M., Swanson J.J.;
RT "Purification and characterization of a carboxylesterase associated
RT with organophosphate resistance in the greenbug, Schizaphis graminum
RT (Homoptera: Aphididae).";
RL Arch. Insect Biochem. Physiol. 36:229-240(1997).
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR InterPro: IPR002018; CarboxylesteraseB.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
KW Hydrolase; Serine esterase.
FT UNTER 15
FT NON TER 15
SQ SEQUENCE 15 AA; 1609 MW; 1208B2BCCC969482 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PW 8
DB [1]
DB 2 PW 4

RESULT 29
LPP_ECOLI
ID LPP_ECOLI STANDARD; PRT; 15 AA.
AC P03057;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE PHE leader peptide (Attenuator peptide).
DE PHE OR PHEAF OR B2598 OR SF2658.
GN Escherichia coli, and
OS Escherichia coli, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 623;
RN [1]
RC SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=79033820; PubMed=360214;
RA Zurawski G., Brown K., Killingly D., Yanofsky C.;
RT "Nucleotide sequence of the leader region of the phenylalanine operon
RT of Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:4271-4275(1978).
RN [2]
RC SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=91072346; PubMed=2254312;
RA Gavini N., Davidson B.E.;
RT "phea mutants of Escherichia coli have a defective pheA attenuator.";
RL J. Biol. Chem. 265:21532-21535(1990).
RN [3]
RC SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97428617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1232-1244(1997).
RN [4]
RC SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue X., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF PHENYLALANINE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00314; CAA23600.1; -
DR EMBL; M10431; AAA24329.1; -
DR EMBL; M58024; AAA62783.1; -

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DR EMBL; AE000346; AAC75647.1; -.
DR EMBL; AE015281; AAN44154.1; -.
DR PIR; A03593; LFECE.
DR Ecogene; E011271; pHeL.
KW Leader peptide; Complete proteome.
SQ SEQUENCE 15 AA; 1924 MW; CFE14AE3BFF935E0 CRC64;

Query Match          25.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FFF 4
Db      |||
        6 FFF 8

RESULT 30
ID PH3_PRUSE STANDARD; PRT; 15 AA.
AC P29265;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Prunasin beta-glucosidase IIB (EC 3.2.1.118) (Prunasin hydrolase
DE isozyme IIB) (PH IIB) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-
CC glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1635 MW; 4F3D7F4FB90CFE4C CRC64;

Query Match          25.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PVV 8
Db      |||
        5 PVV 7

RESULT 31
UC08_MAIZE
ID UC08_MAIZE STANDARD; PRT; 15 AA.
AC P80614;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 159)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.

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RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Danerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.4, ITS MW IS: 38.8 kDa.
CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
CC family.
DR Maize-2DPAGE; P80614; COLEOPTILE.
DR MaizeDB; 123934; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1785 MW; 1978B1D6AB4DDF8D CRC64;

Query Match          25.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PVV 8
Db      |||
        9 PVV 11

RESULT 32
UP01_METAN
ID UP01_METAN STANDARD; PRT; 15 AA.
AC P83440;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Unknown protein (fragment).
OS Metarhizium anisopliae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocrymaceae; Hypocreales; Clavicipitaceae;
OC mitosporic Clavicipitaceae; Metarhizium.
OX NCBI_TaxID=5530;
RN [1]
RP SEQUENCE.
RC STRAIN=54A-1b;
RX MEDLINE=22343006; PubMed=12455610;
RA Kamp A.M., Bidochka M.J.;
RT "Protein analysis in a pleomorphically deteriorated strain of the
RT insect-pathogenic fungus Metarhizium anisopliae.";
RL Can. J. Microbiol. 48:787-792(2002).
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1651 MW; FBD76D669E1F0F4F CRC64;

Query Match          25.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PVV 8
Db      |||
        4 PVV 6

RESULT 33
PH2_PRUSE
ID PH2_PRUSE STANDARD; PRT; 16 AA.
AC P29264;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Prunasin beta-glucosidase IIA (EC 3.2.1.118) (Prunasin hydrolase
DE isozyme IIA) (PH IIA) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]

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RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-
CC glucose.
CC -!- SUBUNIT: Homodimer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1703 MW; FC4D7F4FB90CFE01 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8
DB |||

RESULT 34
BOL5 MEGPE STANDARD; PRT; 17 AA.
AC P07496;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin V.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=28643;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Argiolas A., Pisano J.J.;
RT "Bombolitin, a new class of mast cell degranulating peptides from
RT the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
CC -!- FUNCTION: Mast cell degranulating peptide.
DR PIR; E22595; E22595.
KW Mast cell degranulation.
SQ SEQUENCE 17 AA; 1731 MW; B076C091571606A5 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11
DB |||

RESULT 35
TPIS PINPS STANDARD; PRT; 17 AA.
AC P81656;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragments).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;

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RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RA MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
CC phosphate.
CC -!- PATHWAY: Plays an important role in several metabolic pathways.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- INDUCTION: By water stress.
CC -!- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
CC AND PLASTID.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT N139) IS: 5.9, ITS MW IS: 24 kDa.
CC -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR InterPro; IPR000652; Triophos. ismrse.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 1
FT NON_CONS 9
FT NON_TER 17
SQ SEQUENCE 17 AA; 2053 MW; 183DB41757AF13CB CRC64;

Query Match 25.0%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
DB |||

RESULT 36
AZM_OCTVU STANDARD; PRT; 18 AA.
AC P30800;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-2-macroglobulin homolog (Alpha-2-M) (Fragment).
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=5645;
RN [1]
RP SEQUENCE.
RX MEDLINE=92344633; PubMed=1379044;
RA Thøgersen I.B., Salvesen G., Brucato F.H., Pizzo S.V., Engild J.J.;
RT "Purification and characterization of an alpha-macroglobulin
RT proteinase inhibitor from the mollusc Octopus vulgaris.";
RL Biochem. J. 285:521-527(1992).
CC -!- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A
CC UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH,
CC CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES
CC FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT
CC REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH
CC TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST
CC LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR
CC WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE
CC BAIT REGION A THIOLESTER BOND IS HYDROLYZED AND MEDIATES THE
CC COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
DR PIR; S23971; S23971.
DR GO; GO:0016975; F.alpha-2 macroglobulin; NAS.
DR InterPro; IPR001599; MacroglobinA2.

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DR Pfam: PF00207; A2M; 1.
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
 KW Serine protease inhibitor; Glycoprotein; Plasma; Bait region;
 KW Thioester bond.
 FT NON TER 1 1 Isoglutamyl cysteine thioester (Cys-Gln).
 FT CROSSLINK 5 8
 FT NON TER 18 18
 SQ SEQUENCE 18 AA; 2011 MW; D8D61C473D901C9D CRC64;
 Query Match 25.0%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 NVL 11
 DB 16 NVL 18
 RESULT 37
 ALL2 CYDPO
 ID ALL2 CYDPO STANDARD; PRT; 18 AA.
 AC P82153;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 2.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily."
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 18 18
 SQ SEQUENCE 18 AA; 2169 MW; 8B66679C0C0F175C CRC64;
 Query Match 25.0%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LPV 7
 DB 11 LPV 13
 RESULT 38
 LUXB KRYAS
 ID LUXB KRYAS STANDARD; PRT; 18 AA.
 AC P18300;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alkanal monooxygenase beta chain (EC 1.14.14.3) (Bacterial luciferase
 DE beta chain) (Fragment).
 GN LUXB.
 OS Kryptophanon alfredi symbiont.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; light emitting symbionts of fish.
 OX NCBI_TaxID=28177;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91076680; PubMed=2256783;
 RA Haygood M.G.;
 RT "Relationship of the luminous bacterial symbiont of the Caribbean
 flashlight fish, Kryptophanon alfredi (family Anomalopidae) to

RT other luminous bacteria based on bacterial luciferase (luxA) genes.";
 RL Arch. Microbiol. 154:496-503(1990).
 CC -!- FUNCTION: LIGHT-EMITTING REACTION IN LUMINOUS BACTERIA. THE
 CC SPECIFIC ROLE OF THE BETA SUBUNIT IS UNKNOWN, BUT IT IS ABSOLUTELY
 CC REQUIRED FOR BIOLUMINESCENCE ACTIVITY.
 CC -!- CATALYTIC ACTIVITY: RCHO + FMN(2) + O(2) = RCOOH + FMN + H(2)O +
 CC light.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL: M36597; AAA91214.1;
 DR InterPro: IPR002103; Bac_luciferase.
 DR PROSITE: PS00494; BACTERIAL LUCIFERASE; PARTIAL.
 KW Photoprotein; Luminescence; Oxidoreductase; Monooxygenase;
 KW Flavoprotein; FMN.
 FT NON TER 18 18
 SQ SEQUENCE 18 AA; 2153 MW; 8CB3B6955CCB2E7A CRC64;
 Query Match 25.0%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPF 3
 DB 5 LPF 7
 RESULT 39
 COOT SARBU
 ID COOT SARBU STANDARD; PRT; 19 AA.
 AC Q09148;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE NEB-collcoostatin (Folliculostatin).
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95188911; PubMed=7883009;
 RA Bylemans D., Proost P., Samijn B., Borovsky D., Grauwels L.,
 RA Huybrechts R., van Damme J., van Beeumen J., de Loof A.;
 RT "Neb-collcoostatin, a second folliculostatin of the grey fleshfly,
 RT Neobellieria bullata.";
 RL Eur. J. Biochem. 228:45-49(1995).
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. IT INHIBITS YOLK SYNTHESIS SO
 CC INHIBITING THE SUBSEQUENT YOLK DEPOSITION IN PREVITELLOGENIC
 CC FOLLICLES.
 CC -!- SIMILARITY: TO THE NONHELICAL REGIONS OF THE COLLAGEN FAMILY.
 CC -!- CAUTION: NEB-COLLOOSTATIN MAY BE PROTEOLYTICALLY CLEAVED FROM
 CC COLLAGEN IV.
 DR PIR; S69153; S69153.
 SQ SEQUENCE 19 AA; 1880 MW; 41B6AF5F0CEB8251 CRC64;
 Query Match 25.0%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LPV 7
 DB 7 LPV 9

RESULT 40
MIFP_TRIMR
ID MIFP_TRIMR STANDARD; PRT; 19 AA.
AC P81530;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-dopachrome-methyl ester tautomerase (Macrophage migration inhibitory factor homolog) (Fragment).
OS Trichuris muris (Mouse whipworm).
OC Eukaryota; Metazoa; Nematoda; Enopalea; Trichocephalida; Trichuridae;
OC Trichuris.
OX NCBI_TaxID=70415;
RN [1]
RP SEQUENCE.
RX MEDLINE=99013685; Pubmed=9794786;
RA Pennock J.L., Behnke J.M., Bickle O.D., Devaney E., Grencis R.K., Isaac R.E., Joshua G.W.P., Selkirk M.E., Zhang Y., Meyer D.J.;
RT "Rapid purification and characterization of L-dopamine-methyl-ester tautomerase (macrophage migration inhibitory factor) from Trichinella spiralis, Trichuris muris and Brugia pahangi.";
RL Biochem. J. 335:495-498(1998).
CC -!- FUNCTION: TAUTOMERIZATION OF THE METHYL ESTER OF L-DOPACHROME.
CC -!- INDUCTION: INHIBITED BY FREE FATTY ACIDS AND HAEMATIN.
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
DR InterPro; IPR001398; MIF.
DR PROSITE; PS01159; MIF; PARTIAL.
KW Cytokine.
FT NON_TER
FT CYS
SQ SEQUENCE 19 AA; 2058 MW; F7D70C81D12F1234 CRC64;
Query Match 25.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 FFL 5
Db 17 FFL 19

RESULT 41
PSBN_SYNNU
ID PSBN_SYNNU STANDARD; PRT; 19 AA.
AC P12313;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Photosystem II reaction center N protein (fragment).
GN PSBN.
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX NCBI_TaxID=32053;
RN [1]
RP SEQUENCE.
RX MEDLINE=89338735; Pubmed=2503399;
RA Ikeuchi M., Koike H., Inoue Y.;
RT "N-terminal sequencing of low-molecular-mass components in cyanobacterial photosystem II core complex. Two components correspond to unidentified open reading frames of plant chloroplast DNA.";
RL FEBS Lett. 253:178-182(1989).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SIMILARITY: Belongs to the psbN family.
DR HAWAP; MF 00293; -; 1.
KW Photosystem II; Transmembrane.
FT MOD_RES 1 1 BLOCKED.
FT TRANSNM 6 >19 POTENTIAL.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2217 MW; A97C99B523106D14 CRC64;
Query Match 25.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
Db 16 LFF 18

RESULT 42
UP25_UPEIN
ID UP25_UPEIN STANDARD; PRT; 19 AA.
AC P82031;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 2.5.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104953;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C., Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the Australian floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -!- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST M.LUTEUS, L.MESENTERIOIDES AND S.UBERIS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1940; METHOD=FAB.
KW Amphibian defense peptide; Antibiotic.
SQ SEQUENCE 19 AA; 1941 MW; 5E94C6C757B463D9 CRC64;
Query Match 25.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 NVL 11
Db 15 NVL 17

RESULT 43
UP27_UPEMJ
ID UP27_UPEMJ STANDARD; PRT; 19 AA.
AC P82039;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 2.7.
OS Uperoleia mjobergii (Australian toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104954;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "New antibiotic uperin peptides from the dorsal glands of the Australian toadlet Uperoleia mjobergii.";
RL Aust. J. Chem. 49:1325-1331(1996).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1948; METHOD=FAB.
KW Amphibian defense peptide.
SQ SEQUENCE 19 AA; 1949 MW; 24E4F83A6BA35F21 CRC64;
Query Match 25.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11
Db 15 NVL 17

RESULT 44
UP28 UPEMJ
ID UP28 UPEMJ STANDARD; PRT; 19 AA.
AC P82040;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 2.8.
OS Uperoleia mjobergii (Australian toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104954;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "New antibiotic uperin peptides from the dorsal glands of the
RT Australian toadlet Uperoleia mjobergii.";
RL Aust. J. Chem. 49:1325-1331(1996).
CC -!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
CC S.EPIDERMIS AND S.UBERIS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1978; METHOD=FAB.
KW Amphibian defense peptide.
SQ SEQUENCE 19 AA; 1979 MW; 4E524822C8A340F9 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11
Db 15 NVL 17

RESULT 45
CISY STRY
ID CISY STRY STANDARD; PRT; 20 AA.
AC P20903;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Citrate synthase (EC 2.3.3.1) (Fragment).
GN GLTA.
OS Streptomyces hygroscopicus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1912;
RN [1]
RP SEQUENCE.
RC STRAIN=SF1293;
RA MEDLINE=90334852; PubMed=1368511;
RA Shimotohno K.W., Imai S., Murakami T., Seto H.;
RT "Purification and characterization of citrate synthase from
RT Streptomyces hygroscopicus SF-1293 and comparison of its properties
RT with those of 2-phosphomethylmalic acid synthase.";
RL Agric. Biol. Chem. 54:463-470(1990).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate = citrate +
CC CoA.
CC -!- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY NADH.
CC -!- PATHWAY: Tricarboxylic acid cycle.
CC -!- SUBUNIT: Homohexamer.
CC -!- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
CC CAPABLE OF OXIDATIVE METABOLISM.
CC -!- SIMILARITY: Belongs to the citrate synthase family.
PIR; PQ0046; PQ0046.

DR InterPro: IPR002020; Citrate synt.
DR PROSITE: PS00480; CITRATE SYNTHASE; PARTIAL.
KW Transferase; Tricarboxylic acid cycle; Allosteric enzyme.
FT NON TER 20
SQ SEQUENCE 20 AA; 2234 MW; C527EC7A87119597 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8
Db 17 PVV 19

RESULT 46
COGI PARCM
ID COGI PARCM STANDARD; PRT; 20 AA.
AC P20731;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collagenolytic protease 28 kDa (EC 3.4.21.32) (Fragment).
OS Paraliithodes camtschatica (Kamchatka crab) (Red king crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;
OC Lithodidae; Paraliithodes.
OX NCBI_TaxID=6741;
RN [1]
RP SEQUENCE.
RC TISSUE=Hepatopancreas;
EX MEDLINE=90165951; PubMed=2154979;
RA Klimova O.A., Borukhov S.I., Solovyeva N.I., Balaevskaya T.O.,
RA Strongin A.Y.;
RT "The isolation and properties of collagenolytic proteases from crab
RT hepatopancreas.";
RL Biochem. Biophys. Res. Commun. 166:1411-1420(1990).
CC -!- FUNCTION: THIS ENZYME IS A SERINE PROTEASE CAPABLE OF DEGRADING
CC THE NATIVE TRIPLE HELIX OF COLLAGEN.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins, with broad specificity
CC for peptide bonds. Degrades native collagen at about 75% of the
CC length of the molecule from the N-terminus. Low activity on small
CC molecule substrates of both trypsin and chymotrypsin.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR PIR; A34817; A34817.
DR MEROPS; S01.122; .
DR InterPro: IPR001254; Ser protease_Try.
DR Pfam; PF00089; trypsin; 1
DR PROSITE; PS50240; TRYPSIN_DOM; PARTIAL.
DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
KW Hydrolase; Serine protease; Collagen degradation.
FT NON TER 20
SQ SEQUENCE 20 AA; 2086 MW; 299BAC6FC8A99AA2 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
Db 18 LFF 20

RESULT 47
EFTU MYCSY
ID EFTU MYCSY STANDARD; PRT; 20 AA.
AC P81407;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor Tu (EF-Tu) (Fragment).
GN TUF.


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OS Mycoplasma synoviae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2109;
RN [1]
RP SEQUENCE.
RC STRAIN=ULB 925 / Isolate KP9.
RX MEDLINE=99237234; PubMed=10220885;
RA Bencina D., Narat M., Dovic P., Drobic-Valic M., Habe F., Kleven S.H.;
RT "The characterization of Mycoplasma synoviae EF-Tu protein and
RT proteins involved in hemagglutination and their N-terminal amino acid
RT sequences.";
RL FEMS Microbiol. Lett. 173:85-94 (1999).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
CC AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
CC BIOSYNTHESIS.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-TU/EF-1A SUBFAMILY.
DR HAMAP: MF 00118; -1.
DR InterPro: IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFATOR_GTP; PARTIAL.
RW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2222 MW; C3C92564B740ACC6 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VNV 10
Db 12 VNV 14

RESULT 48
FLA_VIBAL STANDARD; PRT; 20 AA.
ID FLA_VIBAL
AC P83150;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Flagellin (Outer membrane protein 38Va) (Omp38Va) (Fragment).
OS Vibrio alginolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=563;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 1903T;
RA Onji M., Hirabayashi J., Suzuki S.;
RT "Characterization of major outer membrane proteins of Vibrio
RT alginolyticus and the stability against proteases.";
RL Microbes Environ. 0:0-0 (2002).
CC -1- FUNCTION: Flagellin is the subunit protein which polymerizes to
CC form the filaments of bacterial flagella.
CC -1- SUBCELLULAR LOCATION: Flagellar.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
KW Flagella; Outer membrane.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2165 MW; 2BF12B5381E6GA085 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VNV 10
Db 2 VNV 4

RESULT 49
FRE3_LITIN

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ID FRE3_LITIN STANDARD; PRT; 20 AA.
AC P56249;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Frenatin 3
OS Litoria infrafracta (Giant tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=61195;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97368637; PubMed=9225251;
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "The structures of the frenatin peptides from the skin secretion of
RT the giant tree frog Litoria infrafracta.";
RL J. Pept. Sci. 2:117-124 (1996).
CC -1- FUNCTION: Wide spectrum antimicrobial peptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
CC glands.
KW Amphibian defense peptide; Antibiotic.
SQ SEQUENCE 20 AA; 1956 MW; 7B4AB30EAL7B20C CRC64;

Query Match 25.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVL 11
Db 12 NVL 14

RESULT 50
MDH_KIBAR STANDARD; PRT; 20 AA.
ID MDH_KIBAR
AC P19978;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).
OS MDH.
GN Kibdelosporangium aridum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardineae; Pseudonocardiaceae; Kibdelosporangium.
OX NCBI_TaxID=2030;
RN [1]
RP SEQUENCE.
RX MEDLINE=89374824; PubMed=2775496;
RA Rommel T.O., Hund H.-K., Speth A.R., Lingens F.;
RT "Purification and N-terminal amino-acid sequences of bacterial malate
RT dehydrogenases from six actinomycetales strains and from
RT phenyllobacterium immobile, strain E.";
RL Biol. Chem. Hoppe-Seyler 370:763-768 (1989).
CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
DR PIR; S04961; S04961.
DR InterPro; IPR001252; Mdh.
DR PROSITE; PS00068; MDH; PARTIAL.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 20
SQ SEQUENCE 20 AA; 1999 MW; 79587B6F58C00AC9 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VNV 10
Db 5 VNV 7

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RESULT 51
MIF_PIG
ID MIF_PIG STANDARD; PRT; 20 AA.
AC P80928;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Macrophage migration inhibitory factor (MIF) (Phenylpyruvate
DE tautomerase) (Glycosylation-inhibiting factor) (GIF) (Fragment).
GN MIF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RA Riviere S., Bouet F., Menez A., Galat A.;
RL Submitted (MAR-1997) to the SWISS-PROT data bank.
CC -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE (BY
CC SIMILARITY).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
DR HSP; P14174; IGIF.
DR InterPro: IPR001398; MIF.
DR Pfam; PF01187; MIF; 1.
DR PROSITE; PS01158; MIF; 1.
KW Isomerase; Macrophage; Inflammatory response; Cytokine.
FT ACT SITE 1 1 CATALYTIC BASE (BY SIMILARITY).
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2147 MW; 3517AF60F3012A61 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVN 9
DB 4 VVN 6

RESULT 52
TENB_ACTTE
ID TENB_ACTTE STANDARD; PRT; 20 AA.
AC P30834;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tenebrosin B (Fragment).
OS Actinia tenebrosa (Australian red waratah sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Actinia.
OX NCBI_TaxID=6105;
RN [1]
RP SEQUENCE.
EX MEDLINE=90232538; PubMed=1970442;
RA Norton R.S., Bobek G., Ivanov J.O., Thomson M., Fiala-Beer E.,
RA Moritz R.L., Simpson R.J.;
RT "Purification and characterisation of proteins with cardiac
RT stimulatory and haemolytic activity from the anemone Actinia
RT tenebrosa";
RL Toxicon 28:29-41(1990).
CC -!- FUNCTION: This cardiac stimulatory and hemolytic protein is a
CC channel-forming and/or membrane-penetrating protein.
CC -!- SUBCELLULAR LOCATION: Secreted; cnidocyst.
CC -!- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.
DR PIR; B34016; B34016.
KW Cytolysis; Hemolysis; Toxin; Cnidocyst; Transmembrane.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 1960 MW; FA32B426009FF5FA CRC64;

Query Match 25.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVN 9
DB 4 VVN 6

RESULT 53
FFKA_ANTEL
ID FFKA_ANTEL STANDARD; PRT; 4 AA.
AC P58705;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antho-Kaamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=61110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92028852; PubMed=1681803;
RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-Kaamide), a
RT novel neuropeptide from sea anemones.";
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RN FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Kaamide and Antho-Riamide.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
DR PIR; JQ1273; JQ1273.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FF 3
DB 1 FF 2

RESULT 54
FLRF_HIRME
ID FLRF_HIRME STANDARD; PRT; 4 AA.
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FLRamide.
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC Archyobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
OX NCBI_TaxID=6421, 27815;
RN [1]
RP SEQUENCE.
RX SPECIES=H.medicalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Fohl J., Kartsonis M.A., Calabrese R.L.;

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RT "Identification of Rfamidae neuropeptides in the medicinal leech.";
RL Peptides 12:897-908 (1991).
RN [2]
RP SEQUENCE.
RC SPECIES=H.trivoltis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRamide-related peptides from the kidney of the snail, Helisoma
trivoltis.";
RL Peptides 15:31-36 (1994).
CC -1- SIMILARITY: BELONGS TO THE FAMP (FMRFAMIDE RELATED PEPTIDE)
KW Neuropeptide; Amidation.
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FL 5
   ||
Db 1 FL 2

RESULT 55
FLRN ANTEL STANDARD; PRT; 4 AA.
ID AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthese; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;
RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414 (1990).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron-specific.
CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
DR PIR; A35779; A35779.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 1 L-3-PHENYLLACTYL.
FT MOD_RES 4 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FL 5
   ||
Db 1 FL 2

RESULT 56
PRCT PERAM STANDARD; PRT; 5 AA.
ID AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OX Periplaneta americana (American cockroach),

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OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
in insects.";
RL Life Sci. 17:1253-1256 (1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569 (1981).
RN [3]
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211 (1990).
RN [4]
RP SEQUENCE.
RC SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangler J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72 (1986).
CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LP 6
   ||
Db 3 LP 4

RESULT 57
RE11 LITRU STANDARD; PRT; 5 AA.
ID AC P82070;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;

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RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW Amphibian defense peptide.
FT MOD RES 5 6DD9C9CAB2A00000 CRC64;
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FF 3
Db 3 FF 4

RESULT 58
RE21 LITRU
ID RE21 LITRU STANDARD; PRT; 5 AA.
AC P82071;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]_TaxID=104895;
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW Amphibian defense peptide.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FF 3
Db 3 FF 4

RESULT 59
RE31 LITRU
ID RE31 LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;

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OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]_TaxID=104895;
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD RES 5 71A9C9CB10300000 CRC64;
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FF 3
Db 3 FF 4

RESULT 60
RE32 LITRU
ID RE32 LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]_TaxID=104895;
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FF 3
Db 3 FF 4

RESULT 61
UC22 MAIZE
ID UC22 MAIZE STANDARD; PRT; 5 AA.
AC P80628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:1997-1005(1996).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
 DR Maize-2DPAGE; P80628; COLEOPTILE.
 DR MaizedB; 123954; -.
 FT NON_TER 1 1 5
 FT NON_TER 1 1 5
 FT NON_TER 1 1 5
 SQ SEQUENCE 5 AA; 654 MW; 72CB19C0300000 CRC64;
 Query Match 16.7%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FF 3
 DB ||
 2 FF 3
 RESULT 62
 AC PH RABIT STANDARD; PRT; 6 AA.
 AC P25154;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
 DE (APH) (Acylaminoacyl-peptidase) (Fragment).
 GN APEH.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Muscle;
 RA Krishna R.G., Chin C.C.Q., Wold F.;
 RA MEDLINE=32222120; PubMed=1807161;
 RT "N-terminal sequence analysis of N alpha-acetylated proteins after
 RT unblocking with N-acylaminoacyl-peptide hydrolase.";
 RL Anal. Biochem. 199;45-50(1991).
 CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
 CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
 CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
 CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
 CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
 CC + peptide.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
 DR PIR; A49792; A49792.
 DR MEROPS; S09.004; -.
 DR InterPro; IPR002471; Prol_endopep_ser.
 DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
 KW Hydrolase; Acetylation.
 FT MOD_RES 1 1 1 ACETYLATION.
 FT NON_TER 1 1 6
 FT NON_TER 1 1 6
 SQ SEQUENCE 6 AA; 775 MW; 6732B6C40B16F000 CRC64;
 Query Match 16.7%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 VL 11
 DB ||
 5 VL 6
 RESULT 63
 FARP MONEX STANDARD; PRT; 6 AA.
 ID FARP MONEX
 AC P41956;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE FMRFamide-like neuropeptide GNFRF-amide.
 DE FMRFamide-like neuropeptide GNFRF-amide.
 OS Moniezia expansa (Sheep tapeworm).
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidae; Anoplocephalidae; Moniezia.
 OX NCBI_TaxID=28841;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=93312289; PubMed=8323531;
 RA Maule A.G., Shaw C., Halton D.W., Thim L.;
 RT "GNFRFamide: a novel FMRFamide-immunoreactive peptide isolated from
 RT the sheep tapeworm, Moniezia expansa.";
 RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR; A43129; A43129.
 KW Neuropeptide; Amidation.
 FT MOD_RES 6 6
 FT MOD_RES 6 6
 FT MOD_RES 6 6
 SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;
 Query Match 16.7%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FF 3
 DB ||
 3 FF 4
 RESULT 64
 TRPI_PSEPU STANDARD; PRT; 6 AA.
 ID TRPI_PSEPU
 AC F36414;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TrpBA operon transcriptional activator (Fragment).
 DE TRPI.
 GN Pseudomonas putida.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PpGI C15;
 RC MEDLINE=89335826; PubMed=2503057;
 RA Eberly L., Crawford I.P.;
 RA "DNA sequence of the tryptophan synthase genes of Pseudomonas
 RT putida.";
 RT Biochimie 71:521-531(1989).
 RL Biochimie 71:521-531(1989).
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
 CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
 CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
 CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 CC -----
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DR EMBL; X13299; CAA31660.1; --
 DR InterPro; IPR000947; HTH_LYSR.
 DR PROSITE; PS00044; HTH_LYSR_FAMILY; PARTIAL.
 KW Tryptophan biosynthesis; Transcription regulation; Activator;
 KW DNA-binding.
 FT NON TER
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LP 6
 ||
 DB 5 LP 6

RESULT 65
 FARI_HELTI
 ID FARI_HELTI STANDARD; PRT; 7 AA.
 AC P41871;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRamide-like neuropeptide GDPFLRF-amide.
 OS Helisoma trivolvis (Snail).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 CC Lymnaeidae; Planorbidae; Helisoma.
 OC NCBI_TaxID=27815;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRamide-related peptides from the kidney of the snail, Helisoma
 trivolvis";
 RL Peptides 15:31-36(1994).
 CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
 CC THE KIDNEY, MANTLE AND SKIN.
 CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FL 5
 ||
 DB 4 FL 5

RESULT 66
 FARI_MACRS
 ID FARI_MACRS STANDARD; PRT; 7 AA.
 AC P83274;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide FLPI (DKNFLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 CC Palaemonidae; Palaemonidae; Macrobrachium.
 OC NCBI_TaxID=79674;

RN SEQUENCE, AND MASS SPECTROMETRY.
 RP TISSUE=Eyestalk;
 RC Sithigorngul P., Saraithongkum W., Jaidechoey S., Longyant S.,
 RA Sithigorngul W.;
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
 RT freshwater prawn Macrobrachium rosenbergii.";
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -!- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC GO: GO:0007218; P:neuropeptide signaling pathway; TAS.
 DR Neuropeptide; Amidation.
 KW MOD RES 7
 SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540420 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FL 5
 ||
 DB 4 FL 5

RESULT 67
 FARI_PROCL
 ID FARI_PROCL STANDARD; PRT; 7 AA.
 AC P38499;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Cardioexcitatory FMRFamide homolog NF1.
 OS Procambarus clarkii (Red swamp crayfish).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 CC Astacidea; Cambaridae; Procambarus.
 OC NCBI_TaxID=6728;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pericardial organs;
 RX MEDLINE=93248032; PubMed=8387183;
 RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;
 RT "Isolation of two FMRamide-related peptides from crayfish
 RT pericardial organs";
 RL Peptides 14:137-143(1993).
 CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FL 5
 ||
 DB 4 FL 5

RESULT 68
 FARI_PROCL
 ID FARI_PROCL STANDARD; PRT; 7 AA.
 AC P38499;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Cardioexcitatory FMRFamide homolog DF2.
 OS Procambarus clarkii (Red swamp crayfish).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Astacoidea; Cambaridae; Procambarus.
 OX NCBI_TaxID=6728;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pericardial organs;
 RX MEDLINE=92248032; PubMed=8387183;
 RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;
 RT "Isolation of two FMRFamide-related peptides from crayfish
 RT pericardial organs.";
 RL Peptides 14:137-143(1993).
 CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD RES 7
 FT SEQUENCE 7 AA; 967 MW; 69040729C4540AC0 CRC64;
 SQ
 Query Match 16.7%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 FL 5
 Db 4 FL 5

RESULT 69
 PPH2_LYCES
 ID _PPH2_LYCES STANDARD; PRT; 7 AA.
 AC P83379;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Purple acid phosphatase isozyme LeSP2 (EC 3.1.3.2) (Fragment).
 OS Lycopersicon esculentum (tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
 RP GLYCOSYLATION.
 RC STRAIN=cv. Moneymaker; TISSUE=Seed;
 RX MEDLINE=22361242; PubMed=12473124;
 RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
 RT "Purification and characterization of two secreted purple acid
 RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon
 RT esculentum) cell cultures.";
 RL Eur. J. Biochem. 269:6278-6286(2002).
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 CC alcohol + phosphate.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- FM: Glycosylated.
 CC -!- MISCELLANEOUS: In L.esculentum there are at least two isozymes of
 CC purple acid phosphatase.
 KW Hydrolase; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;
 Query Match 16.7%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 FL 5
 Db 1 FL 2

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Astacoidea; Cambaridae; Procambarus.
 OX NCBI_TaxID=6728;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pericardial organs;
 RX MEDLINE=92248032; PubMed=8387183;
 RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;
 RT "Isolation of two FMRFamide-related peptides from crayfish
 RT pericardial organs.";
 RL Peptides 14:137-143(1993).
 CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD RES 7
 FT SEQUENCE 7 AA; 967 MW; 69040729C4540AC0 CRC64;
 SQ
 Query Match 16.7%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 FL 5
 Db 4 FL 5

RESULT 70
 UN06_PINPS
 ID _UN06_PINPS STANDARD; PRT; 7 AA.
 AC P81675;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of needles (N141) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=1647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
 FT NON_TER 1
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 823 MW; 69D7672448B5740 CRC64;
 Query Match 16.7%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 LP 6
 Db 5 LP 6

RESULT 71
 AKHG_GRYBI
 ID _AKHG_GRYBI STANDARD; PRT; 8 AA.
 AC P14086;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Adipokinetic hormone G (AKH-G) (RO II).
 OS Gryllus bimaculatus (Two-spotted cricket), and
 OS Romalea microptera (Lubber grasshopper).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllinae;
 OC Gryllus.
 OX NCBI_TaxID=6999, 7007;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
 RX MEDLINE=88106553; PubMed=3426616;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary sequence analysis by fast atom bombardment mass spectrometry
 RT of a peptide with adipokinetic activity from the corpora cardiaca of
 RT the cricket Gryllus bimaculatus.";
 RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
 RX MEDLINE=89145002; PubMed=3226948;
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
 RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
 RT the lubber grasshopper, Romalea microptera.";
 RL Peptides 9:681-688(1988).
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -!- SIMILARITY: BELONGS TO THE AKH / RPCH FAMILY.

```
DR PIR: A28004; A28004.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VN 9
Db 2 VN 3

RESULT 72
AKH LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetin hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
GAede G.;
RA "The putative ancestral peptide of the adipokinetin/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483 (1990).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR: S10596; S10596.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VN 9
Db 2 VN 3

RESULT 73
ALL6_CYPDO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydia statin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=92600;

[1]
RN SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309 (1997).
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LP 6
Db 1 LP 2

RESULT 74
CADI_ENTFA STANDARD; PRT; 8 AA.
AC P13268;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CADI.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85051889; PubMed=6437872;
RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the bacterial sex pheromone, CADI, that
RT induces plasmid transfer in Streptococcus faecalis.";
RL FEBS Lett. 178:97-100 (1984).
CC -!- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PAD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LF 2
Db 1 LF 2

RESULT 75
CLP_THICU STANDARD; PRT; 8 AA.
AC P80488;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chemolithotroph-specific protein (fragment).
OS Thiobacillus cuprinus.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Thiomonas.
OX NCBI_TaxID=36860;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 5494;
RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
RL Submitted (SEP-1995) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
```


CC CHEMOLITHOTROPHICALLY.
FT NON TER 8
SQ SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;
Query Match 16.7%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PV 7
Db 2 PV 3

Search completed: November 25, 2003, 18:17:25
Job time : 7.80851 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 28.9149 Seconds
(without alignments)
107.095 Million cell updates/sec

Title: US-09-641-801-4
Perfect score: 12
Sequence: 1 LFFFLPWNVLP 12

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database:

SPTREMBL_23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	5	41.7	17	11	Q9ERZ2
2	4	33.3	9	3	Q9PBE5
3	4	33.3	13	11	Q9QVK6
4	4	33.3	15	4	Q9UQU2
5	4	33.3	15	7	Q9TNQ1
6	4	33.3	17	12	Q65373
7	4	33.3	19	4	Q15610
8	4	33.3	19	8	Q9ZYW7
9	4	33.3	19	12	O11338
10	4	33.3	20	11	Q9QUX7
11	3	25.0	4	11	O08433
12	3	25.0	7	2	O50556
13	3	25.0	8	3	O13591
14	3	25.0	8	4	Q15901
15	3	25.0	8	6	Q9TRX8
16	3	25.0	8	10	Q40530

17	3	25.0	9	2	P82568
18	3	25.0	9	6	Q8MJT7
19	3	25.0	9	6	Q8MJT8
20	3	25.0	9	8	Q9GD36
21	3	25.0	9	15	Q64972
22	3	25.0	10	2	Q9RSN2
23	3	25.0	10	2	Q9RSN1
24	3	25.0	10	2	Q9RSN3
25	3	25.0	10	2	Q9AE19
26	3	25.0	10	4	Q9H1I5
27	3	25.0	10	5	P82383
28	3	25.0	10	8	Q8WBR7
29	3	25.0	10	11	Q9ESU5
30	3	25.0	10	12	Q39952
31	3	25.0	10	12	Q39952
32	3	25.0	10	13	Q8JFE7
33	3	25.0	10	13	Q8JJ33
34	3	25.0	11	6	Q9TQSO
35	3	25.0	11	12	O39951
36	3	25.0	12	8	Q9GI96
37	3	25.0	12	10	P82329
38	3	25.0	12	11	Q62966
39	3	25.0	12	13	P82820
40	3	25.0	13	8	Q9GCU0
41	3	25.0	13	11	O88176
42	3	25.0	13	12	Q9WMG5
43	3	25.0	13	13	P82880
44	3	25.0	13	13	P82881
45	3	25.0	13	13	P82882
46	3	25.0	13	13	P82883
47	3	25.0	13	13	P82884
48	3	25.0	13	13	P82830
49	3	25.0	13	13	P82848
50	3	25.0	14	2	Q9R224
51	3	25.0	14	2	Q45876
52	3	25.0	14	2	Q9R225
53	3	25.0	14	2	Q9X715
54	3	25.0	14	2	Q9WW79
55	3	25.0	14	2	Q45872
56	3	25.0	14	4	O95179
57	3	25.0	14	5	Q9TWW0
58	3	25.0	14	5	P82216
59	3	25.0	14	8	Q8M099
60	3	25.0	14	10	Q9S8X6
61	3	25.0	14	10	P82340
62	3	25.0	14	11	Q9QVF3
63	3	25.0	14	11	O70599
64	3	25.0	14	13	P82832
65	3	25.0	14	16	Q8ZDW9
66	3	25.0	15	2	Q8RKN0
67	3	25.0	15	2	O68425
68	3	25.0	15	4	Q9UCH4
69	3	25.0	15	6	Q9TRA6
70	3	25.0	15	7	Q9TNQ5
71	3	25.0	15	8	O78794
72	3	25.0	15	8	Q8HIF8
73	3	25.0	15	8	Q8HIF6
74	3	25.0	15	16	Q8XFF4
75	3	25.0	15	16	Q8X2E0
76	3	25.0	15	16	Q8FEZ7
77	3	25.0	16	2	Q44610
78	3	25.0	16	2	Q8VNS8
79	3	25.0	16	4	Q9UC52
80	3	25.0	16	6	Q9TR60
81	3	25.0	16	9	Q37853
82	3	25.0	16	12	Q9WMG6
83	3	25.0	16	13	Q9PT90
84	3	25.0	16	16	Q8D183
85	3	25.0	17	2	Q9R4C4
86	3	25.0	17	2	Q93UW3
87	3	25.0	17	4	Q9UML8
88	3	25.0	17	4	Q95794
89	3	25.0	17	4	Q95794

P82568 streptococ
Q8mj77 eulemur ful
Q8mj78 eulemur ful
Q9gd36 juncus effu
Q64972 avian rous-
Q9rsn2 clostridium
Q9rsn1 clostridium
Q9rsn3 clostridium
Q9ae19 streptococ
Q9h1i5 homo sapien
P82383 drosophila
Q8wbr7 chaitophoru
Q9esu5 mus musculu
Q39952 hepatitis g
Q9wle4 hepatitis g
Q8jfe7 ficedula al
Q8jj33 ficedula hy
Q9tqso bos taurus
Q39951 hepatitis g
Q9g196 sargassum p
P82329 pisum sativ
Q62966 rattus norv
P82820 rana catesb
Q9gcu0 xyris sp. c
O88176 mus musculu
Q9wmg5 sigma virus
P82880 rana clamit
P82881 rana clamit
P82882 rana clamit
P82883 rana clamit
P82884 rana clamit
P82830 rana luteiv
P82848 rana pipien
Q9r224 campylobact
Q45876 clostridium
Q9r225 campylobact
Q9x715 campylobact
Q9ww79 campylobact
Q45872 clostridium
Q95179 homo sapien
Q9tww0 trypanosoma
P82216 bombyx mori
Q8m099 tockus nasu
Q9s8x6 glycine max
P82340 pisum sativ
Q9gvf3 rattus sp.
O70599 rattus norv
P82832 rana luteiv
Q8zdw9 yersinia pe
Q8rkn0 escherichia
O68425 buchnera ap
Q9uch4 homo sapien
Q9tra6 bos taurus
Q9tng5 mus sp. maj
O78794 pylaiaella l
Q8hif8 arthroderma
Q8hif6 trichophyto
Q8xf44 salmonella
O8x2e0 escherichia
Q8fez7 escherichia
Q44610 buchnera ap
Q8vns8 escherichia
Q9uc52 homo sapien
Q9tr60 bos taurus
Q37853 bacterioph
Q9wmg6 sigma virus
Q9pt90 gallus gall
Q8d183 yersinia pe
Q9r4c4 agrobacteri
Q93uw3 agrobacteri
Q6800 saccharomyc
Q9uml8 homo sapien
Q95794 homo sapien

90 3 25.0 17 4 Q95795 O95795 homo sapien
 91 3 25.0 17 5 Q9TW16 Q9TW16 ceratitidis c
 92 3 25.0 17 5 Q17203 Q17203 bombyx mori
 93 3 25.0 17 6 Q9TRY8 Q9TRY8 sus sp. ins
 94 3 25.0 17 6 Q9TRU8 Q9TRU8 bos taurus
 95 3 25.0 17 8 Q95F78 Q95F78 hizikia fus
 96 3 25.0 17 8 Q8HKH3 Q8HKH3 boophilus a
 97 3 25.0 17 8 Q8HKH2 Q8HKH2 boophilus d
 98 3 25.0 17 11 Q62547 Q62547 mus spretus
 99 3 25.0 17 12 Q8V9K6 Q8V9K6 human papil
 100 3 25.0 18 3 Q9P897 Q9P897 emericella

ALIGNMENTS

RESULT 1

Q9ERZ2 ID Q9ERZ2 PRELIMINARY; PRT; 17 AA.
 AC Q9ERZ2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Protein tyrosine phosphatase RPTP-GMC1 (Fragment).
 GN PTPRO.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Wright M.B., Foernzler D., Pech M.;
 RT "Organization of the mouse Ptpq gene encoding protein-tyrosine
 phosphatase RPTP-GMC1";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF265561; AAG22700.1; -.
 FT NON TER 17
 SQ SEQUENCE 17 AA; 2001 MW; 834A1F2920F07DBF CRC64;

Query Match 41.7%; Score 5; DB 11; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFL 5
 |||||
 Db 4 LFFFL 8

RESULT 2

Q9P8E5 ID Q9P8E5 PRELIMINARY; PRT; 9 AA.
 AC Q9P8E5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE HIS4 protein (Fragment).
 GN HIS4.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL-Y1140;
 RX MEDLINE=99448382; PubMed=10518937;
 RA Lamas-Maceiras M., Esperanza Cardan E., Freire-Picos M.A.;
 RT "Kluyveromyces lactis HIS4 transcriptional regulation: similarities
 and differences to Saccharomyces cerevisiae HIS4 gene.";
 RL FEBS Lett. 458:72-76(1999).
 DR EMBL; AJ238494; CAB87125.1; -.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

Query Match 33.3%; Score 4; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
 |||||
 Db 2 LPVV 5

RESULT 3

Q9QVK6 ID Q9QVK6 PRELIMINARY; PRT; 13 AA.
 AC Q9QVK6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Phosphoglycerate mutase P29 (EC 2.7.5.3) (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91373341; PubMed=1832670;
 RA Hoppner W., Becker L., Buck F., Seitz H.J.;
 RT "Is the p29 protein involved in the rapid regulation of
 phosphoenolpyruvate carboxykinase (GTP)?";
 RL J. Biol. Chem. 266:17257-17260(1991).
 SQ SEQUENCE 13 AA; 1456 MW; 39099D8CBB6D2D7 CRC64;

Query Match 33.3%; Score 4; DB 11; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
 |||||
 Db 5 LPVV 8

RESULT 4

Q9UQJ2 ID Q9UQJ2 PRELIMINARY; PRT; 15 AA.
 AC Q9UQJ2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Prorelaxin H2 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Garibay-Tupas J.;
 RT "Characterization of the human relaxins H1 and H2 5'-flanking
 regions";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF104935; AAD21961.1; -.
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1806 MW; E9AFA622F3A86818 CRC64;

Query Match 33.3%; Score 4; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF 4
 |||||
 Db 4 LFFF 7

RESULT 5

Q9TNQ1

```
ID Q9TNQ1 PRELIMINARY; PRT; 15 AA.
AC Q9TNQ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta 2M- class I-binding PEPTIDE-MAJOR histocompatibility complex
DE H-2KB-specific molecule POORLY associated with beta 2-microglobulin
DE (Fragment).
DE Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE
RX MEDLINE=94240094; PubMed=8193884;
RA Joyce S., Kuzushima K., Kepes G., Angeletti R.H., Nathenson S.G.;
RT "Characterization of an incompletely assembled major
RT histocompatibility class I molecule (H-2Kb) associated with unusually
RT long peptides: implications for antigen processing and presentation.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149(1994).
KW MHC.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1754 MW; 2CEACDA0F1180DC7 CRC64;

Query Match 33.3%; Score 4; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8
Db 7 LPVV 10

RESULT 6
Q65373
ID Q65373 PRELIMINARY; PRT; 17 AA.
AC Q65373;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE ORF 2 minigene.
OS Orgyia pseudotsugata single capsid nuclear polyhedrosis virus
OS (OpSNPV). dsDNA viruses, no RNA stage; Baculoviridae;
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10450;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93286576; PubMed=8389803;
RA Russell R.L., Rohmann G.F.;
RT "Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia
RT pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.";
RL J. Gen. Virol. 74:1191-1195(1993).
DR EMBL; D13375; BAA02640.1; -.
SQ SEQUENCE 17 AA; 1882 MW; BFECA959495FE6A CRC64;

Query Match 33.3%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VNVL 11
Db 5 VNVL 8

RESULT 7
Q15610
ID Q15610 PRELIMINARY; PRT; 19 AA.
AC Q15610;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
```

```
DE Topoisomerase I (Fragment).
GN TOP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91099302; PubMed=2176592;
RA Kunze N., Klein M., Richter A., Knippers R.;
RT "Structural characterisation of the human DNA topoisomerase I gene
RT promoter.";
RL Eur. J. Biochem. 194:323-330(1990).
DR EMBL; X52601; CAA36834.1; -.
KW Isomerase.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2236 MW; 47BDB36F4FFEEFB CRC64;

Query Match 33.3%; Score 4; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4
Db 12 LFFF 15

RESULT 8
Q9ZYW7
ID Q9ZYW7 PRELIMINARY; PRT; 19 AA.
AC Q9ZYW7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Cytochrome oxidase II (Fragment).
OS Aphidius rosae.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonicoidea;
OC Braconidae; Aphidinae; Aphidius.
OX NCBI_TaxID=64817;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152621; PubMed=10028295;
RA Dowton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the hymenoptera.";
RL Mol. Biol. Evol. 16:298-309(1999).
DR EMBL; AF034594; AAC79742.1; -.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 19 AA; 2361 MW; B624CD9DF26536C3 CRC64;

Query Match 33.3%; Score 4; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4
Db 9 LFFF 12

RESULT 9
O11338
ID O11338 PRELIMINARY; PRT; 19 AA.
AC O11338;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE H1-7-1 protein (Fragment).
GN H1-7-1.
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
```

OC Molluscipoxvirus.
 OX NCBI_TaxID=10280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
 RA Lopez-Esteban J.L., Esteban M., Martin-Gallardo A.,
 RT "A Random DNA Sequencing, Computer-Based Approach for the Generation
 of a Gene Map of Molluscum Contagiosum Virus.",
 RL Virus Genes 0:0-0(1997).
 DR EMBL; U86916; AAB57971.1; -.
 DR InterPro; IPR004900; Pox_P35.
 DR Pfam; PF03213; Pox_P35; 1.
 FT NON TER 19
 SQ SEQUENCE 19 AA; 2018 MW; 1ECAF898F95ED65 CRC64;
 Query Match 33.3%; Score 4; DB 12; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LPVV 8
 DB 13 LPVV 16
 RESULT 10
 O9QUX7 PRELIMINARY; PRT; 20 AA.
 AC O9QUX7
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Carboxylesterase isozyme (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=96170127; PubMed=8597091;
 RA Satoh I., Hosokawa M.;
 RT "Molecular aspects of carboxylesterase isoforms in comparison with
 other esterases.",
 RL Toxicol. Lett. 82:439-445(1995).
 SQ SEQUENCE 20 AA; 2133 MW; 435160FFA80E086D CRC64;
 Query Match 33.3%; Score 4; DB 11; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PVVN 9
 DB 6 PVVN 9
 RESULT 11
 Q08433 PRELIMINARY; PRT; 4 AA.
 AC Q08433
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE Bilirubin UDP-glucuronosyltransferase (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Gunn;
 RX MEDLINE=91282758; PubMed=1840486;
 RA Sato H., Aono S., Kashiwamata S., Koizumi O.;
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
 hyperbilirubinemic Gunn rat.",

RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
 DR EMBL; S38636; AAB19259.1; -.
 KW Transferase.
 FT NON TER 1
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;
 Query Match 25.0%; Score 3; DB 11; Length 4;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 NVL 11
 DB 1 NVL 3
 RESULT 12
 O50556 PRELIMINARY; PRT; 7 AA.
 AC O50556
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE GlyA (Fragment).
 GN GLYA
 OS Actinobacillus actinomycetemcomitans (Haemophilus
 actinomycetemcomitans).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Actinobacillus.
 OX NCBI_TaxID=714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=ATCC 33384;
 RX MEDLINE=96355846; PubMed=8751884;
 RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
 RA Kraig E.;
 RT "cis Elements and trans factors are both important in strain-specific
 regulation of the leukotoxin gene in Actinobacillus
 actinomycetemcomitans.",
 RL Infect. Immun. 64:3451-3460(1996).
 DR EMBL; U51862; AAB88721.1; -.
 FT NON TER 1
 SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;
 Query Match 25.0%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LPV 7
 DB 3 LPV 5
 RESULT 13
 O13591 PRELIMINARY; PRT; 8 AA.
 AC O13591
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE ORF YNL337W (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Obermaier B., Piravandi E., Rinke M.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z71612; CAA96271.2; -.

FT NON_TER 1 1
SQ SEQUENCE 8 AA; 1005 MW; 5CA441E449C9C720 CRC64;
Query Match 25.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
Db 2 LFF 4

RESULT 14

Q15901 ID Q15901 PRELIMINARY; PRT; 8 AA.
AC Q15901;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP7B11B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32080; AAA73891.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 860 MW; 37D72878676729CB CRC64;

Query Match 25.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
Db 2 FLP 4

RESULT 15

Q9TRX8 ID Q9TRX8 PRELIMINARY; PRT; 8 AA.
AC Q9TRX8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Osteopontin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91282766; PubMed=1676261;
RA Prince C.W., Dickie D., Krumdieck C.L.;
RT "Osteopontin, a substrate for transglutaminase and factor XIII
RT activity."
RL Biochem. Biophys. Res. Commun. 177:1205-1210(1991).
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 920 MW; 05DAFAF76322D767 CRC64;

Query Match 25.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 LPV 7
Db 1 LPV 3

RESULT 16

Q40530 ID Q40530 PRELIMINARY; PRT; 8 AA.
AC Q40530;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE P20 n with a leader peptide.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87089808; PubMed=3540612;
RA Herman L.M.F., Montagu M.C.V., Depicker A.G.;
RT "Isolation of tobacco DNA segments with plant promoter activity."
RL Mol. Cell. Biol. 6:4486-4492(1986).
DR EMBL; M14685; AAA34090.1; -.
SQ SEQUENCE 8 AA; 1109 MW; E257205B19C9C6 CRC64;

Query Match 25.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4
Db 2 FFF 4

RESULT 17

P82568 ID P82568 PRELIMINARY; PRT; 9 AA.
AC P82568;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=13114;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC STRAIN=JRS4;
RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
RA vanSogelen R.A.;
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT proteins."
RL Submitted (MAY-2000) to the SWISS-PROT data bank.
CC -!- MASS SPECTROMETRY; MW=22592.04; METHOD=ELECTROSPRAY.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPV 7
Db 1 LPV 3

RESULT 18

Q8MJT7
ID Q8MJT7 PRELIMINARY; PRT; 9 AA.
AC Q8MJT7
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hemopexin (fragment).
OS Eulemur fulvus (brown lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemnidae; Eulemur.
OX NCBI_TaxID=13515;
RN [1]
RP SEQUENCE FROM N.A.
RA Wyner Y.M., Johnson S.E., Stumpf R., DeSalle R.;
RT "A genetic assessment of a red-fronted/white-collared lemur hybrid
zone at Andringitra, Madagascar."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258049; AAM43870.1; -.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1110 MW; 738CC9C720587B1B CRC64;
Query Match 25.0%; Score 3; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LFF 3
Db 6 LFF 8
RESULT 19
ID Q8MJT8 PRELIMINARY; PRT; 9 AA.
AC Q8MJT8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hemopexin (fragment).
OS Eulemur fulvus albocollaris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemnidae; Eulemur.
OX NCBI_TaxID=122224;
RN [1]
RP SEQUENCE FROM N.A.
RA Wyner Y.M., Johnson S.E., Stumpf R., DeSalle R.;
RT "A genetic assessment of a red-fronted/white-collared lemur hybrid
zone at Andringitra, Madagascar."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258028; AAM43849.1; -.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1110 MW; 738CC9C720587B1B CRC64;
Query Match 25.0%; Score 3; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LFF 3
Db 6 LFF 8
RESULT 20
ID Q9GD36 PRELIMINARY; PRT; 9 AA.
AC Q9GD36
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ribosomal protein S16 (fragment).
GN RPS16.
OS Juncus effusus (Soft rush).

OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Juncaceae; Juncus.
OX NCBI_TaxID=13579;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Asmussen C.B., Chase M.W.;
RT "Coding and noncoding plastid DNA in palm systematics."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ404962; CAC17904.1; -.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1135 MW; 8DCCC9D2C046CB41 CRC64;
Query Match 25.0%; Score 3; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FFF 4
Db 7 FFF 9
RESULT 21
ID Q64972 PRELIMINARY; PRT; 9 AA.
AC Q64972
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rous associated virus type 1 (RAV-1) mil protein, 3' end, and env
protein (fragment).
OS Avian rous-associated virus type 1.
OC Viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11950;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89037349; PubMed=2846875;
RA Marx M., Crisanti P., Eychene A., Bechade C., Laugier D.,
Gysdael J., Peseac B., Calothy G.;
RT "Activation and transduction of c-mil sequences in chicken neuroretina
cells induced to proliferate by infection with avian lymphomatosis
virus."
RL J. Virol. 62:4627-4633(1988).
DR EMBL; M25399; AAA42548.1; -.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1033 MW; 83AED7673411B5A1 CRC64;
Query Match 25.0%; Score 3; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 LPV 7
Db 6 LPV 8
RESULT 22
ID Q9RSN2 PRELIMINARY; PRT; 10 AA.
AC Q9RSN2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Neurotoxin type A HN+ 57 kDa SUBUNIT=SAMPLE 2 (fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.

```

RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
RT without hemagglutinating activity: do they share common amino acid
RT sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1225 MW; EC3DE932D366C1BA CRC64;

Query Match 25.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db 7 VLP 9

RESULT 23
ID Q9R5N1 PRELIMINARY; PRT; 10 AA.
AC Q9R5N1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Neurotoxin type A HN+ 57 kDa subunit (Fragment)
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
RT without hemagglutinating activity: do they share common amino acid
RT sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1172 MW; ESDAE932D416C1BA CRC64;

Query Match 25.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db 7 VLP 9

RESULT 24
ID Q9R5N3 PRELIMINARY; PRT; 10 AA.
AC Q9R5N3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Neurotoxin type B HN+ 57 kDa subunit (Fragment)
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
RT without hemagglutinating activity: do they share common amino acid
RT sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1172 MW; ESDAE932D416C1BA CRC64;

Query Match 25.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db 7 VLP 9

RESULT 25
ID Q9AE19 PRELIMINARY; PRT; 10 AA.
AC Q9AE19;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Laminin-binding surface protein (Fragment)
GN LMB.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A5;
RX MEDLINE=21172873; PubMed=11274116;
RA Granlund M., Michel F., Norgren M.;
RT "Mutually exclusive distribution of IS1548 and GBS11, an active group
RT II intron identified in human isolates of group b streptococci.";
RL J. Bacteriol. 183:2560-2569(2001).
DR EMBL; AJ290953; CAC35987.1; -.
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1204 MW; 4965EF9729C9C873 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFL 5
Db 5 FFL 7

RESULT 26
ID Q9H1I5 PRELIMINARY; PRT; 10 AA.
AC Q9H1I5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Mutant beta-globin (Fragment)
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Z., Chu J., Ban G., Shi L., Huang X., Lin K., Tao Y.;
RT "Molecular characterization of beta thalassemia in Yunnan, China.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY013300; AAG46183.1; -.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1042 MW; 2210B2A2C732C448 CRC64;

Query Match 25.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db 7 VLP 9

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QY      9 NVL 11
Db      4 NVL 6

RESULT 27
P82383      PRELIMINARY;      PRT;      10 AA.
ID P82383
AC P82383;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Larval cuticle LCP2A protein (Minor band protein) (Fragment).
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE
RC STRAIN=OREGON-R; TISSUE=LARVA;
RA Chihara C.J.;
RT "Third instar cuticle proteins.";
RL DIS 83:0-0(2000).
CC -1- FUNCTION: COMPONENT OF THE CUTICLE OF THE LARVA OF FRUIT FLY.
DR FlyBase; FBgn0061208; Lcp2a.
DR InterPro; IPR000618; Insect_cuticle.
DR PROSITE; PS00233; CUTICLE; PARTIAL.
KW Cuticle; Structural protein.
FT NON TER 10
SQ SEQUENCE 10 AA; 1100 MW; 9DCF320732C44DDA CRC64;

Query Match 25.0%; Score 3; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 NVL 11
Db      5 NVL 7

RESULT 28
Q8WBK7      PRELIMINARY;      PRT;      10 AA.
ID Q8WBK7
AC Q8WBK7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN COI
OS Chaitophorus leucomelas.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphidoidea; Drepanosiphidae; Chaitophorus.
OX NCBI_TaxID=136351;
RN [1]
RP SEQUENCE FROM N.A.
RA Shingleton A.W.; Stern D.L.;
RT "Molecular phylogenetic evidence for multiple origins of ant mutualism
RT within the aphid genus Chaitophorus.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF44288; AAL38565.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 10 AA; 1194 MW; 6E553D5042D7672B CRC64;

Query Match 25.0%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 LpV 7
Db      1
|||

RESULT 29
Q9ESU5      PRELIMINARY;      PRT;      10 AA.
ID Q9ESU5
AC Q9ESU5;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Fas death receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He;
RX MEDLINE=20127858; PubMed=10660538;
RA Munsch D.; Watanabe-Fukunaga R.; Bourdon J.C.; Nagata S.; May E.;
RA Yonish-Rouach E.; Reisdorf P.;
RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a
RT p53-responsive element that is activated by p53 mutants unable to
RT induce apoptosis.";
RL J. Biol. Chem. 275:3867-3872(2000).
DR EMBL; AF282865; AAG02410.1; -.
KW Receptor.
FT NON TER 10
SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;

Query Match 25.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 VLP 12
Db      7 VLP 9
|||

RESULT 30
Q39952      PRELIMINARY;      PRT;      10 AA.
ID Q39952
AC Q39952;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
OS Hepatitis GB virus C.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=39839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Edinburgh haemophilic;
RX MEDLINE=97368412; PubMed=9225026;
RA Smith D.B.; Cuceanu N.; Davidson P.; Jarvis L.M.; Mokili J.L.;
RA Hamid S.; Ludlam C.A.; Simmonds P.;
RT "Discrimination of hepatitis G virus/GBV-C geographical variants by
RT analysis of the 5' non-coding region.";
RL J. Gen. Virol. 78:1533-1542(1997).
DR EMBL; AF003170; AAC57981.1; -.
KW NON TER 10
SQ SEQUENCE 10 AA; 1152 MW; CC88F0C9C7272732 CRC64;

Query Match 25.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LFF 3
Db      6 LFF 8
|||

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RESULT 31
ID Q9WLE4 PRELIMINARY; PRT; 10 AA.
AC Q9WLE4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula hypoleuca.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=46689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Op86;
RX MEDLINE=21918460; PubMed=11918793;
RA Primmer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454216; AAC22904.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1152 MW; CC88FOC9C7272732 CRC64;

Query Match 25.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
Db 6 LFF 8

RESULT 32
ID Q8JFE7 PRELIMINARY; PRT; 10 AA.
AC Q8JFE7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula albicollis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=59894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bc5, and Bc8;
RX MEDLINE=21918460; PubMed=11918793;
RA Primmer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454217; AAC22903.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1206 MW; 1FAAC9676732C86B CRC64;

Query Match 25.0%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db 5 VLP 7

RESULT 33
ID Q8JUJ3 PRELIMINARY; PRT; 10 AA.
AC Q8JUJ3;

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula hypoleuca.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=46689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Op86;
RX MEDLINE=21918460; PubMed=11918793;
RA Primmer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454216; AAC22902.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1206 MW; 1FAAC9676732C86B CRC64;

Query Match 25.0%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db 5 VLP 7

RESULT 34
ID Q9TQSO PRELIMINARY; PRT; 11 AA.
AC Q9TQSO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE C-KIT (Fragment).
GN KIT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC Olsen H.G., Vage D.I., Lien S., Klungland H.;
RT "A polymorphism in the bovine c-kit gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243424; CAB60775.1; -.
DR EMBL; AJ243060; CAB60774.1; -.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 25.0%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8
Db 5 PVV 7

RESULT 35
ID O39951 PRELIMINARY; PRT; 11 AA.
AC O39951;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).

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OS Hepatitis GB virus C.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV Group.
OX NCBI_TaxID=39839;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Edinburgh haemophilic;
RC MEDLINE=97369412; PubMed=9225026;
RA Smith D.B., Cuccaneu N., Davidson P., Jarvis L.M., Mokili J.L.,
RA Hamid S., Ludlam C.A., Simmonds P.;
RT "Discrimination of hepatitis G virus/GBV-C geographical variants by
RT analysis of the 5' non-coding region.";
RL J. Gen. Virol. 78:1533-1542(1997).
FT EMBL; AF003169; AAC57980.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1281 MW; 45DC88F0C9C72727 CRC64;

Query Match 25.0%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
Db 6 LFF 8

RESULT 36
O9GI96 PRELIMINARY; PRT; 12 AA.
ID O9GI96
AC O9GI96
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
DE (Fragment).
GN RBCS
OS Sargassum polycystum.
OG Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
OC Sargassum.
OX NCBI_TaxID=127578;
CX [1]
RN [1] SEQUENCE FROM N.A.
RP STRAIN=nepl27;
RC STRAIN=nepl27;
RA Phillips N.E.; Smith C.M., Morden C.W.;
RT "Testing the systematics of the genus Sargassum (Fucales,
RT Phaeophyceae) with the Rubisco operon.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244344; AAF98114.1; -.
KW Chloroplast.
FT NON TER 12
SQ SEQUENCE 12 AA; 1379 MW; 373D121250CEB867 CRC64;

Query Match 25.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 10 FLP 12

RESULT 37
P82329 PRELIMINARY; PRT; 12 AA.
ID P82329
AC P82329;

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DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT111) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3886;
RN [1]
RN SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RP STRAIN=cv. DE GRACE; TISSUE=LEAF;
RC MEDLINE=20181728; PubMed=10715320;
RA Paltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson P.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.5, ITS MW IS: 24.1 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON TER 12
SQ SEQUENCE 12 AA; 1244 MW; CBE0AD74B3D5B862 CRC64;

Query Match 25.0%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 8 FLP 10

RESULT 38
Q62966 PRELIMINARY; PRT; 12 AA.
ID Q62966
AC Q62966;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interstitial collagenase (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley;
RC MEDLINE=96408720; PubMed=9813727;
RA Rajakumar R.A., Quinn C.O.;
RT "Parathyroid hormone induction of rat interstitial collagenase mRNA in
RT osteosarcoma cells is mediated through an AP-1-binding site.";
RL Mol. Endocrinol. 10:867-878(1996).
DR EMBL; U53605; AAB47407.1; -.
KW Collagen.
FT NON TER 12
SQ SEQUENCE 12 AA; 1432 MW; 148A4DFEE8ADD720 CRC64;

Query Match 25.0%; Score 3; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4
Db 9 FFF 11

RESULT 39
P82820 PRELIMINARY; PRT; 12 AA.
ID P82820
AC P82820;

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DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE RANATUERIN 5.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia, Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN;
 RX MEDLINE=98422096; PubMed=9751476;
 RA Goraya J., Knoop F.C., Conlon J.M.;
 RT "Ranaturins: antimicrobial peptides isolated from the skin of the
 American bullfrog, Rana catesbeiana."
 RL Biochem. Biophys. Res. Commun. 250:589-592(1998).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 SQ SEQUENCE 12 AA; 1335 MW; C8531D12A92735BD CRC64;
 Query Match 25.0%; Score 3; DB 13; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 FLP 6
 Db |||
 1 FLP 3
 RESULT 40
 Q9GCU0 PRELIMINARY; PRT; 13 AA.
 ID Q9GCU0
 AC Q9GCU0
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Ribosomal protein S16 (Fragment).
 GN RPS16.
 OS Xyris sp. Chase 154.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Xyridaceae; Xyris.
 OX NCBI_TaxID=120079;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Rasmussen C.B., Chase M.W.;
 RT "Coding and noncoding plastid DNA in palm systematics."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ404965; CAC18098.1;
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1593 MW; 6F7948EFB7A55EA4 CRC64;
 Query Match 25.0%; Score 3; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FFF 4
 Db |||
 10 FFF 12
 RESULT 41
 O88176 PRELIMINARY; PRT; 13 AA.
 ID O88176
 AC O88176
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Neural cell adhesion molecule (Fragment).
 GN NCAM1 OR NCAM.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb-C; TISSUE=Liver;
 RX MEDLINE=98250618; PubMed=9582442;
 RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
 RT "A cis-acting regulatory element that affects the alternative splicing
 of a muscle-specific exon in the mouse NCAM gene."
 RL Biochim. Biophys. Acta 1397:305-315(1998).
 DR EMBL; AB001873; BAA31275.1; -.
 DR MGI; MGI:97281; Ncam1.
 FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;
 Query Match 25.0%; Score 3; DB 11; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LPV 7
 Db |||
 4 LPV 6
 RESULT 42
 Q9WMG5 PRELIMINARY; PRT; 13 AA.
 ID Q9WMG5
 AC Q9WMG5
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE 3 protein (Fragment).
 GN GENE 3.
 OS Sigma virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; unclassified Rhabdoviridae.
 OX NCBI_TaxID=11301;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212481; PubMed=8384742;
 RA Teninges D., Bras F., Dezelee S.;
 RT "Genome organization of the sigma rhabdovirus: six genes and a gene
 overlap."
 RL Virology 193:1018-1023(1993).
 DR EMBL; S57850; AAD40700.1; -.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1456 MW; 9AF4F3FDE75E32D5 CRC64;
 Query Match 25.0%; Score 3; DB 12; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 VLP 12
 Db |||
 7 VLP 9
 RESULT 43
 P82880 PRELIMINARY; PRT; 13 AA.
 ID P82880
 AC P82880
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE Temporin-1CA.
 OS Rana clamitans (green frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=145282;
 RN [1]
 RP SEQUENCE.

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RC TISSUE=Skin;
RX MEDLINE=20283865; PubMed=10822101;
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
RT "Purification and characterization of antimicrobial peptides from the
RL skin of the North American green frog Rana clamitans.";
RL Peptides 21:469-476(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MASS SPECTROMETRY: MW=1430.0; MW ERR=0.02; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1432 MW; CC18532F8DFE533D CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 1 FLP 3

RESULT 44
P82881 ID P82881 PRELIMINARY; PRT; 13 AA.
AC P82881;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE Temporin-1CB.
OS Rana clamitans (green frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=145282;
RN [1]
RP SEQUENCE.
RX MEDLINE=20283865; PubMed=10822101;
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
RT "Purification and characterization of antimicrobial peptides from the
RL skin of the North American green frog Rana clamitans.";
RL Peptides 21:469-476(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MASS SPECTROMETRY: MW=1430.0; MW ERR=0.02; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1432 MW; CAA71A765A8935BD CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 1 FLP 3

RESULT 45
P82882 ID P82882 PRELIMINARY; PRT; 13 AA.
AC P82882;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE Temporin-1CB.
OS Rana clamitans (green frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=145282;
RN [1]
RP SEQUENCE.
RX MEDLINE=20283865; PubMed=10822101;
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
RT "Purification and characterization of antimicrobial peptides from the
RL skin of the North American green frog Rana clamitans.";
RL Peptides 21:469-476(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MASS SPECTROMETRY: MW=1461.0; MW ERR=0.02; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1462 MW; CC18586F8DF935BD CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 1 FLP 3

RESULT 46
P82883 ID P82883 PRELIMINARY; PRT; 13 AA.
AC P82883;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE Temporin-1CD.
OS Rana clamitans (green frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=145282;
RN [1]
RP SEQUENCE.
RX MEDLINE=20283865; PubMed=10822101;
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
RT "Purification and characterization of antimicrobial peptides from the
RL skin of the North American green frog Rana clamitans.";
RL Peptides 21:469-476(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MASS SPECTROMETRY: MW=1447.0; MW ERR=0.02; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1448 MW; CC18586B9DF935BD CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 1 FLP 3

RESULT 47
P82884 ID P82884 PRELIMINARY; PRT; 13 AA.
AC P82884;

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Temporin-1CE.
OS Rana clamitans (green frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=145282;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=20283865; PubMed=10822101;
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
RT "Purification and characterization of antimicrobial peptides from the
RT skin of the North American green frog Rana clamitans.";
RL Peptides 21:469-476(2000).
CC -1- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- MASS SPECTROMETRY: MW=1461.0; MW_ERR=0.02; METHOD=ELECTROSPRAY.
CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1482 MW; CC18586B9DF931AD CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
Db |||
1 FLP 3

RESULT 48
P82830 PRELIMINARY; PRT; 13 AA.
AC P82830;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Temporin-1LA.
OS Rana luteiventris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=58176;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=SKIN;
RX MEDLINE=20117700; PubMed=10651828;
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
RA Conlon J.M.;
RT "Peptides with antimicrobial activity from four different families
RT isolated from the skins of the North American frogs Rana luteiventris,
RT Rana berlandieri and Rana pipiens.";
RL Eur. J. Biochem. 267:894-900(2000).
CC -1- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -1- MASS SPECTROMETRY: MW=1366.8; METHOD=ELECTROSPRAY.
CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1368 MW; 92541A7649A3D685 CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db |||
1 VLP 3

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RESULT 49
P82848 PRELIMINARY; PRT; 13 AA.
ID P82848
AC P82848;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Temporin-1P.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=SKIN;
RX MEDLINE=20117700; PubMed=10651828;
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
RA Conlon J.M.;
RT "Peptides with antimicrobial activity from four different families
RT isolated from the skins of the North American frogs Rana luteiventris,
RT Rana berlandieri and Rana pipiens.";
RL Eur. J. Biochem. 267:894-900(2000).
CC -1- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -1- MASS SPECTROMETRY: MW=1368; METHOD=ELECTROSPRAY.
CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1370 MW; 3EF3402B9DF92338 CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
Db |||
1 FLP 3

RESULT 50
Q9R2Z4 PRELIMINARY; PRT; 14 AA.
ID Q9R2Z4
AC Q9R2Z4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Flagellin A (fragment).
GN FLAA.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RA Studer E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Studer E., Dohnke M., Wegmueller B., Luethy J., Schmid S.,
RA Candrian U.;
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter
RT coli PCR products amplified directly from environmental samples.";
RL Food Sci. Technol. 31:337-345(1998).
DR EMBL; AJ133577; CAB39387.1; -.
DR EMBL; AJ133572; CAB39382.1; -.
DR EMBL; AJ133573; CAB39383.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1599 MW; C7C4BBB7A1739156 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 14;

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Best Local Similarity 100.0%; Pred. No. 1.1e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

Qy 9 NVL 11
|||
Db 8 NVL 10

RESULT 51
Q45876 PRELIMINARY; PRT; 14 AA.
AC Q45876;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HA-II protein (Fragment).
GN HA-II.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 7273;
RA East A.K., Stacey J.M., Collins M.D.;
RT "Cloning and sequencing of a hemagglutinin component of the botulinum neurotoxin complex encoded by Clostridium botulinum types A and B.";
RL Syst. Appl. Microbiol. 17:306-312(1994).
DR EMBL; X79102; CAA55711.1; -.
FT NON TER 14
RN 14
SQ SEQUENCE 14 AA; 1628 MW; CD689B0937D75E29 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
4 FLP 6
|||
7 FLP 9

Qy 4 FLP 6
|||
Db 7 FLP 9

RESULT 52
Q9R2Z5 PRELIMINARY; PRT; 14 AA.
AC Q9R2Z5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Flagellin A (Fragment).
GN FLAA.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RA Studer E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,
RA Candrian U.;
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter coli PCR products amplified directly from environmental samples.";
RL Food Sci. Technol. 31:337-345(1998).
DR EMBL; AJ133567; CAB55353.1; -.
DR EMBL; AJ133568; CAB39378.1; -.
DR EMBL; AJ133569; CAB39379.1; -.
DR EMBL; AJ133570; CAB39380.1; -.
DR EMBL; AJ133571; CAB39381.1; -.
DR EMBL; AJ133574; CAB39384.1; -.
DR EMBL; AJ133575; CAB39385.1; -.
DR EMBL; AJ133576; CAB39386.1; -.

FT NON TER 1 1
SQ SEQUENCE 14 AA; 1611 MW; C7C0EFB7A1739156 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
9 NVL 11
|||
8 NVL 10

Qy 9 NVL 11
|||
Db 8 NVL 10

RESULT 53
Q9X715 PRELIMINARY; PRT; 14 AA.
AC Q9X715;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Flagellin A (Fragment).
GN FLAA.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RA Studer E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,
RA Candrian U.;
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter coli PCR products amplified directly from environmental samples.";
RL Food Sci. Technol. 31:337-345(1998).
DR EMBL; AJ133578; CAB39388.1; -.
FT NON TER 1 1
RN 1
SQ SEQUENCE 14 AA; 1595 MW; C7C0F96DA1739156 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
9 NVL 11
|||
8 NVL 10

Qy 9 NVL 11
|||
Db 8 NVL 10

RESULT 54
Q9WW79 PRELIMINARY; PRT; 14 AA.
AC Q9WW79;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Flagellin A (Fragment).
GN FLAA.
OS Campylobacter coli.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=195;
RN [1]
RP SEQUENCE FROM N.A.
RA Studer E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,
RA Candrian U.;
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter coli PCR products amplified directly from environmental samples.";
RL Food Sci. Technol. 31:337-345(1998).

DR EMBL; AJ133579; CAB39377.1; -.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1611 MW; C7C0EPB7A1739156 CRC64;
 Query Match 25.0%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11
 Db 8 NVL 10

RESULT 55
 Q45872 PRELIMINARY; PRT; 14 AA.
 AC Q45872; Q45869;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last annotation update)
 DE (NCTC 7272 type A) HA-33 and P-21 genes (Fragment).
 GN HA-II.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCTC 7272, TYPE A, and 178;
 RA East A.K., Stacey J.W., Collins M.D.;
 RL Syst. Appl. Microbiol. 17:306-312(1994).
 DR EMBL; X79104; CAA55719.1; -.
 DR EMBL; X79103; CAA55715.1; -.
 FT NON TER 14
 SQ SEQUENCE 14 AA; 1656 MW; CD689B1BBCD75E29 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
 Db 7 FLP 9

RESULT 56
 Q95179 PRELIMINARY; PRT; 14 AA.
 AC Q95179;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Glucose-6-phosphatase hydrolytic subunit (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99156747; PubMed=10024523;
 RA Schmolli D., Washer C., Hinds C.J., Allan B.B., Walther R.,
 RA Burchell A.;
 RT "Identification of a cAMP response element within the glucose-6-phosphatase hydrolytic subunit gene promoter which is involved in the transcriptional regulation by cAMP and glucocorticoids in H4IIE hepatoma cells";
 RL Biochem. J. 338:457-463(1999).
 DR EMBL; AF051355; AAD11621.1; -.
 FT NON TER 14
 SQ SEQUENCE 14 AA; 1666 MW; A6B78EEF99F7FD46 CRC64;

Query Match 25.0%; Score 3; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11
 Db 8 NVL 10

RESULT 57
 Q9TWW0 PRELIMINARY; PRT; 14 AA.
 AC Q9TWW0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Histone C (Fragment).
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93064852; PubMed=1437281;
 RA Bender K., Betschart B., Schaller J., Kampfer U., Hecker H.;
 RT "Sequence differences between histones of procyclic Trypanosoma brucei and higher eukaryotes.";
 RL Parasitology 105:97-104(1992).
 SQ SEQUENCE 14 AA; 1480 MW; 460FF4E8876C4EC7 CRC64;

Query Match 25.0%; Score 3; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
 Db 8 VLP 10

RESULT 58
 P82216 PRELIMINARY; PRT; 14 AA.
 AC P82216;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;
 RX MEDLINE=21177481; PubMed=11280994;
 RA Zhong B.X.;
 RT "Protein database for several tissues derived from five instar of silkworm.";
 RL I Chuan Hsueh Pao 28:217-224(2001).
 CC -1- SIMILARITY: TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
 FT NON TER 14
 SQ SEQUENCE 14 AA; 1619 MW; 86C63995B983BC45 CRC64;

Query Match 25.0%; Score 3; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8
 Db 4 PVV 6

RESULT 59
 Q8M099 PRELIMINARY; PRT; 14 AA.
 ID Q8M099


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AC Q8M099;
DE 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE NADH dehydrogenase subunit 6 (Fragment).
OS Tockus nasutus (African grey hornbill).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Bucerotiformes; Bucerotidae; Tockus.
OX NCBI_TaxID=118205;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2024936; PubMed=12029361;
RA Delport W., Ferguson J.W.H., Bloomer P.;
RT "Characterization and evolution of the mitochondrial DNA control
RT region in hornbills (Bucerotiformes).";
RL J. Mol. Evol. 54:794-806(2002).
DR EMBL; AY027933; AAK31783.1; -.
KW Mitochondrion.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1638 MW; DFAE115DFA724E29 CRC64;

Query Match 25.0%; Score 3; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFL 5
DB 6 FFL 8

RESULT 60
Q9S8X6 PRELIMINARY; PRT; 14 AA.
AC Q9S8X6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Vegetative storage protein 94 peptide 1, VS994=LIPOXYGENASE
DE (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE.
RX MEDLINE=92361246; PubMed=1822994;
RA Tranbarger T.J., Franceschi V.R., Hildebrand D.F., Grimes H.D.;
RT "The soybean 94-kilodalton vegetative storage protein is a
RT lipoxigenase that is localized in paraveinal mesophyll cell
RT vacuoles.";
RL Plant Cell 3:973-987(1991).
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1541 MW; 98EB730EA6AE785A CRC64;

Query Match 25.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11
DB 4 NVL 6

RESULT 61
P82340 PRELIMINARY; PRT; 14 AA.
ID P82340;
AC P82340;
DT 01-JUN-2000 (TReMBLrel. 14, Created)
DT 01-JUN-2000 (TReMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)

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DE Unknown protein from 2D-page of thylakoid lumen (SPOT204) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1505 MW; 2EABFAF980F3D7D7 CRC64;

Query Match 25.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8
DB 7 PVV 9

RESULT 62
Q9QVF3 PRELIMINARY; PRT; 14 AA.
ID Q9QVF3
AC Q9QVF3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE TRANSFERRIN=PEPTIDE 35 (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92165927; PubMed=1791188;
RA Cavanaugh P.G., Nicolson G.L.;
RT "Lung-derived growth factor that stimulates the growth of lung-
RT metastasizing tumor cells: identification as transferrin.";
RL J. Cell. Biochem. 47:261-271(1991).
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin, 1.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1499 MW; 01AE8289E54E3224 CRC64;

Query Match 25.0%; Score 3; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8
DB 10 PVV 12

RESULT 63
O70599 PRELIMINARY; PRT; 14 AA.
ID O70599
AC O70599;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Thymidine kinase (EC 2.7.1.21) (Fragment).
OS Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Sauer M.;
 RL Thesis (1999), University of Vienna, Inst. of Molecular Biology.
 DR EMBL; AJ006455; CAA07030.1; -.
 KW Kinase; Transferase.
 FT NON TER 14
 SQ SEQUENCE 14 AA; 1579 MW; 294979C45CB2E887 CRC64;
 25.0%; Score 3; DB 11; Length 14;
 Query Match
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 10 VLP 12
 |||
 9 VLP 11
 |||
 RESULT 64
 P82832 PRELIMINARY; PRT; 14 AA.
 AC P82832;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Temporin-1LC.
 OS Rana luteiventris.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=58176;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=SKIN;
 RX MEDLINE=20117700; PubMed=10651828;
 RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
 RA Conlon J.M.;
 RT "Peptides with antimicrobial activity from four different families
 RT isolated from the skins of the North American frogs *Rana luteiventris*,
 RT *Rana berlandieri* and *Rana pipiens*.";
 RL Eur. J. Biochem. 267:894-900(2000).
 CC -1- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
 CC S.AUREUS. WEAK ACTIVITY AGAINST GRAM-NEGATIVE BACTERIUM E.COLI AND
 CC THE YEAST C.ALBICANS.
 CC -1- MASS SPECTROMETRY: MW=1603.1; METHOD=ELECTROSPRAY.
 CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 CC FAMILY.
 KW Antibiotic; Amidation; Fungicide.
 FT MOD RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA; 1604 MW; 0B540E1B7FCA8924 CRC64;
 25.0%; Score 3; DB 13; Length 14;
 Query Match
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 4 FLP 6
 |||
 1 FLP 3
 |||
 RESULT 65
 Q8ZDW9 PRELIMINARY; PRT; 14 AA.
 AC Q8ZDW9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Phenylalanyl-tRNA synthetase operon leader peptide (Phenylalanyl-tRNA
 DE synthetase (pheST) operon leader peptide).
 GN PHEW OR YF02429A OR Y1906.

OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whithead S., Barrell B.G.;
 RT "Genome sequence of *Yersinia pestis*, the causative agent of plague.";
 RL Nature 413:523-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5 / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of *Yersinia pestis* KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 DR EMBL; AJ414152; CAC91234.1; -.
 DR EMBL; AE013793; AAM85473.1; -.
 KW Aminoacyl-tRNA synthetase; Complete proteome.
 SQ SEQUENCE 14 AA; 1813 MW; 6141D61508FEF0D4 CRC64;
 25.0%; Score 3; DB 16; Length 14;
 Query Match
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2 FFF 4
 |||
 8 FFF 10
 |||
 RESULT 66
 Q8RKN0 PRELIMINARY; PRT; 15 AA.
 AC Q8RKN0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative transposase ORF1005 (Fragment).
 GN ORF1005.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=743-D;
 RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,
 RA Prats G.;
 RT "A novel complex sul1-type integron in *Escherichia coli* carrying the
 RT bla(CTX-M-9) gene.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY092058; AAM15719.1; -.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1751 MW; 2D706E3A12001249 CRC64;
 25.0%; Score 3; DB 2; Length 15;
 Query Match
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 5 LPV 7
 |||

Db 10 LPV 12

RESULT 67

O68425 PRELIMINARY; PRT; 15 AA.

AC O68425;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Hypothetical 1.8 kDa protein (Fragment).

OS Buchnera aphidicola.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Buchnera.

OX NCBI_TaxID=9;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98290710; PubMed=9625791;

RA Baumann L., Baumann P., Moran N.A.;

RT "News & notes: the endosymbiont (Buchnera) of the aphid diuraphis

RT noxia contains all the genes of the cryptophan biosynthetic pathway.";

RL Curr. Microbiol. 37:58-59(1998).

DR EMBL; AF038565; AAC27732.1; -.

KW Hypothetical protein.

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1795 MW; 54A3D5B40D326E1E CRC64;

Query Match 25.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3

Db 9 LFF 11

RESULT 68

Q9UCH4 PRELIMINARY; PRT; 15 AA.

ID Q9UCH4;

AC Q9UCH4;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Natural killer enhancing factor, NKEF (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=93215001; PubMed=8462106;

RA Shau H., Gupta R.K., Golub S.H.;

RT "Identification of a natural killer enhancing factor (NKEF) from human

RT erythroid cells.";

RL Cell. Immunol. 147:1-11(1993).

FT NON_TER 1 1

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1738 MW; 4909D4A793D382BF CRC64;

Query Match 25.0%; Score 3; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VNV 10

Db 9 VNV 11

RESULT 69

Q9TRA6 PRELIMINARY; PRT; 15 AA.

ID Q9TRA6

AC Q9TRA6;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE PA700 subunit P31=ATP-dependent 20 S proteasome activator

DE (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RX MEDLINE=94342244; PubMed=8063704;

RA DeMartino G.N., Moomaw C.R., Zagnitko O.P., Proske R.J., Chu-Ping M.,

RA Afendis S.J., Swaffield J.C., Slaughter C.A.;

RT "PA700, an ATP-dependent activator of the 20 S proteasome, is an

RT ATPase containing multiple members of a nucleotide-binding protein

RT family.";

RL J. Biol. Chem. 269:20878-20884(1994).

FT NON_TER 1 1

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1659 MW; D189812B9389B755 CRC64;

Query Match 25.0%; Score 3; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6

Db 8 FLP 10

RESULT 70

Q9TNQ5 PRELIMINARY; PRT; 15 AA.

AC Q9TNQ5;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Major histocompatibility complex class II bound peptide

DE (Fragment).

OS Mus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10095;

RN [1]

RP SEQUENCE.

RX MEDLINE=94082939; PubMed=8260091;

RA Freed J.H., Marrack P.;

RT "Tissue-specific expression of self peptides bound by major

RT histocompatibility complex class II molecules.";

RL Chem. Immunol. 57:88-112(1993).

KW MHC.

FT NON_TER 1 1

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1607 MW; CBE93F7B8C5E7425 CRC64;

Query Match 25.0%; Score 3; DB 7; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPV 7

Db 10 LPV 12

RESULT 71

O78794 PRELIMINARY; PRT; 15 AA.

ID O78794;

AC O78794;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE Mitochondrial ribosomal protein S14 (Fragment).

DR EMBL; AE008921; AAL21555.1; -.
DR EMBL; AL627276; CAD05845.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 15 AA; 1959 MW; CFE1598393ED35E0 CRC64;

Query Match 25.0%; Score 3; DB 16; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4
|||
Db 6 FFF 8

RESULT 75
Q8X2E0 PRELIMINARY; PRT; 15 AA.
AC Q8X2E0;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Leader peptide of chorismate mutase-P-prephenate
DE dehydratase.
GN ECS3461.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIND 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AP002562; BAB36884.1; -.
SQ SEQUENCE 15 AA; 1912 MW; CFE14AF996F935E0 CRC64;

Query Match 25.0%; Score 3; DB 16; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4
|||
Db 6 FFF 8

Search completed: November 25, 2003, 18:25:17
Job time : 31.9649 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 38.8723 Seconds
(without alignments)
48.999 Million cell updates/sec

Title: US-09-641-801-4

Perfect score: 12

Sequence: 1 LFFFLPVNVLP 12

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A_Geneseq_19Jun03.*

Rank	Query Match	Score	Length	ID	Description
1	12	100.0	12	22	Colostrinin derive
2	12	100.0	12	22	Colostrinin peptid
3	12	100.0	12	22	Colostrinin peptid
4	12	100.0	12	22	Ewe colostrinin pe
5	12	100.0	12	23	Colostrinin consti
6	12	100.0	12	23	Colostrinin consti
7	12	100.0	12	23	Neural cell regula
8	12	100.0	14	22	Ewe colostrinin pe
9	6	50.0	6	22	Colostrinin peptid

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	100.0	12	22	Colostrinin derive
2	12	100.0	12	22	Colostrinin peptid
3	12	100.0	12	22	Colostrinin peptid
4	12	100.0	12	22	Ewe colostrinin pe
5	12	100.0	12	23	Colostrinin consti
6	12	100.0	12	23	Colostrinin consti
7	12	100.0	12	23	Neural cell regula
8	12	100.0	14	22	Ewe colostrinin pe
9	6	50.0	6	22	Colostrinin peptid

Rank	Query Match	Score	Length	ID	Description
10	6	50.0	7	22	Modified colostrin
11	6	50.0	9	19	Human bcl2 proto-o
12	5	41.7	5	19	Peptide #21 useful
13	5	41.7	5	19	Peptide #27 useful
14	5	41.7	5	21	Natural beta amyl
15	5	41.7	5	22	APP70 abeta peptid
16	5	41.7	5	24	Natural beta-amyl
17	5	41.7	9	21	Arabidopsis thalia
18	5	41.7	11	19	Peptide SEQ ID No:
19	5	41.7	11	20	ste2 agonist pepti
20	5	41.7	11	21	MF-alpha-1 express
21	5	41.7	11	21	Peptide encoded by
22	5	41.7	11	22	Amino acid sequenc
23	5	41.7	11	22	Amino acid sequenc
24	5	41.7	14	22	Human peptide #61
25	5	41.7	14	22	Human peptide #156
26	5	41.7	14	22	Human peptide #156
27	5	41.7	15	22	Ribosomal protein
28	5	41.7	15	22	Human gene 11 enco
29	5	41.7	17	23	Human albumin fusi
30	5	41.7	19	22	Complement inhibit
31	5	41.7	19	23	A thaliana recepto
32	5	41.7	20	19	Apolipoprotein B t
33	5	41.7	20	20	Apolipoprotein fra
34	5	41.7	20	20	Alipoprotein B try
35	4	33.3	4	21	Human E3 ubiquitin
36	4	33.3	5	19	Peptide #17 useful
37	4	33.3	5	19	Peptide #15 useful
38	4	33.3	5	19	Peptide #16 useful
39	4	33.3	5	21	Natural beta amyl
40	4	33.3	5	21	Natural beta amyl
41	4	33.3	5	21	Natural beta amyl
42	4	33.3	5	22	APP70 abeta peptid
43	4	33.3	5	22	APP70 abeta peptid
44	4	33.3	5	22	APP70 abeta peptid
45	4	33.3	5	22	Beta-amylloid pepti
46	4	33.3	5	22	Beta-amylloid pepti
47	4	33.3	5	22	Beta-amylloid pepti
48	4	33.3	5	23	Peptide #16 capabl
49	4	33.3	5	23	Peptide #17 capabl
50	4	33.3	5	23	Peptide #18 capabl
51	4	33.3	5	23	Human HGF receptor
52	4	33.3	5	23	Human HGF receptor
53	4	33.3	5	23	Peptide #5 related
54	4	33.3	5	24	Natural beta-amyl
55	4	33.3	5	24	Natural beta-amyl
56	4	33.3	5	24	Natural beta-amyl
57	4	33.3	6	5	Sequence of substa
58	4	33.3	6	5	Transcriptional ac
59	4	33.3	6	19	Beta-amylloid pepti
60	4	33.3	6	21	Beta-amylloid pepti
61	4	33.3	6	21	Beta-amylloid pepti
62	4	33.3	6	21	Peptide encoded by
63	4	33.3	6	21	Feline human TRFP
64	4	33.3	6	21	TRFP derived pepti
65	4	33.3	6	21	Human TRFP derived
66	4	33.3	7	16	Peralkylated oligo
67	4	33.3	7	16	Peralkylated oligo
68	4	33.3	7	16	Peralkylated oligo
69	4	33.3	7	21	Hsp47-binding phag
70	4	33.3	8	15	PLP peptide 74, po
71	4	33.3	8	18	HIV-1 pol peptide
72	4	33.3	8	21	Peptide linker #23
73	4	33.3	8	22	HIV A03 super moti
74	4	33.3	8	22	HIV A03 motif pol
75	4	33.3	8	22	Vascular dementia-
76	4	33.3	8	22	AB56001
77	4	33.3	8	23	AAU77974
78	4	33.3	9	15	AAU77974
79	4	33.3	9	15	AAU77974
80	4	33.3	9	15	AAU77974
81	4	33.3	9	15	AAU77974
82	4	33.3	9	15	AAU77974

83 4 33.3 9 18 AAW43839 Specific human leu
84 4 33.3 9 20 AAY06041 Human cancer antig
85 4 33.3 9 21 AAB23686 Cytotoxic T lympho
86 4 33.3 9 22 ABP15973 HIV A24 super moti
87 4 33.3 9 22 ABP23687 HIV A11 motif pol
88 4 33.3 9 22 ABP24323 HIV A24 motif pol
89 4 33.3 9 22 AAM95552 Vaccine related MH
90 4 33.3 9 22 AAG67192 Cancer testis tumo
91 4 33.3 9 22 AAB69924 Human NY-ESO-1 HLA
92 4 33.3 9 23 AAE31375 Human MUC1 peptide
93 4 33.3 9 23 ABG79052 Human Gp100 class
94 4 33.3 9 23 ABG66788 Tumour antigen Gp1
95 4 33.3 9 23 AAU94300 Human novel protei
96 4 33.3 9 23 AAU94307 Human novel protei
97 4 33.3 9 23 AAU94469 Human novel protei
98 4 33.3 9 23 AAU94507 Human novel protei
99 4 33.3 9 23 AAU94677 Human novel protei
100 4 33.3 9 23 AAU94712 Human novel protei

ALIGNMENTS

RESULT 1
AAB72249
XX ID AAB72249 standard; peptide; 12 AA.
XX AC AAB72249;
XX DT 14-MAY-2001 (first entry)
XX DE Colostrinin derived cytokine inducing peptide SEQ ID 4.
XX KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX OS Synthetic.
XX WO200111937-A2.
XX 22-FEB-2001.
XX 17-AUG-2000; 2000WO-US22818.
XX 17-AUG-1999; 99US-0149311.
XX (TEXA) UNIV TEXAS SYSTEM.
XX (REGE-) REGEN THERAPEUTICS PLC.
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX WPI; 2001-202804/20.
XX Inducing a cytokine and modulating an immune response, useful for
XX treating central nervous system diseases and bacterial and viral
XX infections, comprises administering colostrinin as an immunological
XX regulator -
XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
XX a proline rich polypeptide aggregate contained in colostrum. The
XX peptides have immune response modulatory activity, and are capable of
XX inducing cytokines. Colostrinin and its derived peptides are useful for
XX inducing cytokine production, for modulating an immunological response
XX and for inducing blood cell proliferation. The peptides are useful in the
XX treatment of disorders of the central nervous system, neurological
XX disorders, mental disorders, dementia, neurodegenerative diseases,
XX Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
XX disorders of the immune system, bacterial and viral infections and
XX acquired immunological deficiencies.

XX SQ Sequence 12 AA;
XX Query Match 100.0%; Score 12; DB 22; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-06;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 LFFFLPVNVLP 12
XX |||||
XX 1 LFFFLPVNVLP 12
XX
XX RESULT 2
XX AAB72503
XX ID AAB72503 standard; Peptide; 12 AA.
XX AC AAB72503;
XX DT 09-MAY-2001 (first entry)
XX DE Colostrinin peptide #4.
XX KW Dermatological; oxidative stress regulator; colostrinin.
XX OS Unidentified.
XX WO200112650-A2.
XX 22-FEB-2001.
XX 17-AUG-2000; 2000WO-US22665.
XX 17-AUG-1999; 99US-0149310.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Stanton GJ, Hughes TK, Boldogh I;
XX WPI; 2001-218342/22.
XX Modulating oxidative stress level in a cell, involves contacting the
XX cell with an oxidative stress regulator selected from colostrinin, its
XX constituent peptide, analog or their combinations -
XX Claim 6; Page 25; 48pp; English.
XX The present invention relates to a method for modulating the oxidative
XX stress level in a cell or a patient, comprising contacting the cell with,
XX or administering to the patient, an oxidative stress regulator selected
XX from colostrinin, or its constituent peptide (e.g. the present peptide),
XX to change the level of an oxidising species in the cell. The method can
XX be used to treat oxidative damage to skin, by decreasing or preventing an
XX increase in the level of damage to a biomolecule of the patient.
XX SQ Sequence 12 AA;
XX Query Match 100.0%; Score 12; DB 22; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-06;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 LFFFLPVNVLP 12
XX |||||
XX 1 LFFFLPVNVLP 12
XX
XX RESULT 3
XX AAB72535
XX ID AAB72535 standard; Peptide; 12 AA.
XX AC AAB72535;
XX DT 09-MAY-2001 (first entry)
XX

DE Colostrinin peptide #4.
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX Unidentified.
 OS
 PN WO200112651-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22774.
 XX
 PR 17-AUG-1999; 99US-0149633.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Boldogh I;
 XX
 XX WPI; 2001-226545/23.
 XX
 XX Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 12; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LFFFLPVNVLP 12
 Db |||||
 1 LFFFLPVNVLP 12

RESULT 4
 AAB59323
 ID AAB59323 standard; Peptide; 12 AA.
 XX
 AC AAB59323;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Ewe colostrinin peptide fragment B-8.
 XX
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 XX Ovis sp.
 OS
 PN WO200075173-A2.
 XX
 PD 14-DEC-2000.
 XX
 DF 02-JUN-2000; 2000WO-GB02128.
 XX
 XX 02-JUN-1999; 99GB-0012852.
 PR
 XX (REGG-) REGEN THERAPEUTICS PLC.
 PA
 XX Georgiades JA;
 PI
 XX WPI; 2001-071058/08.
 DR
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 XX characterized by amyloid plaques -
 PS Claim 7; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 12; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LFFFLPVNVLP 12
 Db |||||
 1 LFFFLPVNVLP 12

RESULT 5
 AAE20231
 ID AAE20231 standard; peptide; 12 AA.
 XX
 AC AAE20231;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Colostrinin constituent peptide #4.
 XX
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnary.
 XX
 OS Unidentified.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 12
 FT /note= "Optionally C-terminal amide"
 XX
 PN WO200213850-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US22776.
 XX
 PR 17-AUG-2000; 2000WO-US22776.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Stanton GJ, Hughes TK, Boldogh I;
 PI
 XX WPI; 2002-269151/31.
 DR
 XX
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 XX
 XX Claim 6; Page 25; 51pp; English.
 PS
 XX The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX Sequence 12 AA;

Query Match 100.0%; Score 12; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFLPVNVLP 12
 |||||
 Db 1 LFFFLPVNVLP 12

RESULT 6

AA014580
 ID AAM51039 standard; Peptide; 12 AA.

XX AAM51039;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide.

KW Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 12 /note= "optional C-terminal amidation"

FN WO200213849-A1.

XX 21-FEB-2002.

PR 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

PA (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

PS Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is preferred for use as an immunological regulator and as a
 CC blood cell regulator in claimed methods of the invention. It is
 CC classified as having a beta-casein homologue precursor. Methods
 CC are claimed for: inducing a cytokine in a cell by contact with an
 CC immunological regulator, where the cell is present in a cell
 CC culture, a tissue, an organ or an organism, and the cell is
 CC mammalian, including human; modulating an immune response in a cell
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a
 CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator
 CC is administered topically or as part of a dietary supplement, and
 CC where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation
 CC by contacting blood cells with a blood cell regulator, where the
 CC blood cells are present in a cell culture or an organism, are
 CC mammalian or human, and where the blood cells are increased in
 CC number or differentiated; and a method for modulating blood cell
 CC proliferation in a patent. A claimed cytokine-inducing composition
 CC comprises a pharmaceutical carrier and an active agent such as the
 CC present peptide. Cytokines induced by this peptide in human
 CC leucocyte cultures include interferon-gamma, tumour necrosis
 CC factor-alpha, interleukin-6 and interleukin-10.

SQ Sequence 12 AA;

Query Match 100.0%; Score 12; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFLPVNVLP 12
 |||||
 Db 1 LFFFLPVNVLP 12

RESULT 7

AA014580

ID AAO14580 standard; peptide; 12 AA.

XX AAO14580;

DT 27-MAY-2002 (first entry)

DE Neural cell regulatory colostrinin peptide 4.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

OS Unidentified.

XX Key Location/Qualifiers

FT Modified-site 12 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

PR 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

PS Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention.

XX SQ Sequence 12 AA;

Query Match
Best Local Similarity 100.0%; Score 12; DB 23; Length 12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVNVNLP 12
|||||

Db 1 LFFFLPVNVNLP 12

RESULT 8
AAB59353
ID AAB59353 standard; Peptide; 14 AA.
XX AC AAB59353;
XX DT 21-MAR-2001 (first entry)
DE Ewe colostrinin peptide fragment derived sequence #13.
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX Ovis sp.
XX WO200075173-A2.
XX 14-DEC-2000.
XX 02-JUN-2000; 2000WO-GB02128.
XX 02-JUN-1999; 99GB-0012852.
XX (REGE-) REGEN THERAPEUTICS PLC.
XX Georgiades JA;
XX WPI; 2001-071058/08.
XX Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX Claim 8; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.

XX SQ Sequence 14 AA;

Query Match
Best Local Similarity 100.0%; Score 12; DB 22; Length 14;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVNVNLP 12
|||||

Db 2 LFFFLPVNVNLP 13

RESULT 9
AAE07186

ID AAE07186 standard; peptide; 6 AA.
XX AC AAE07186;
XX DT 06-NOV-2001 (first entry)
DE Colostrinin peptide 2.
XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
KW central nervous system disorder; neurodegenerative disorder; weight loss;
KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
KW acquired immunological deficiency; neurological disorder; dementia;
KW antiviral.
XX Unidentified.
XX WO200155199-A1.
XX PN 02-AUG-2001.
XX PD 26-JAN-2001; 2001WO-GB00329.
XX PF 26-JAN-2000; 2000GB-0001825.
XX PR (REGE-) REGEN THERAPEUTICS PLC.
XX PA Georgiades JA;
XX PI WPI; 2001-488775/53.
XX DR Peptide useful as an inter alia in the treatment of e.g. disorders of
PT the immune system and the central nervous system comprises ten
PT amino-terminal amino acid sequence derived from peptides present in
PT colostrinin -
XX Claim 1; Page 15; 40pp; English.

CC The invention relates to colostrinin peptide fragments which are useful,
CC inter alia, in the treatment of chronic disorders of the immune system
CC and the central nervous system. Colostrinin peptides are used as a
CC medicament in the treatment of neurological disorders e.g., dementia,
CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
CC neurosis, in acquired immunological deficiencies, chronic bacterial and
CC viral infections and diseases characterised by the presence of beta-
CC amyloid plaques and as a dietary supplement for babies, small children,
CC adults and senile persons, who have been subjected to chemotherapy or
CC have suffered from cachexia or weight loss due to the chronic disease.
CC Colostrinin peptides are also used as food additives and as an auxiliary
CC withdrawal treatment for drug addicts, after a period of detoxification
CC and in persons dependent on stimulants. Colostrinin peptides are used to
CC prepare antibodies and to treat emotional disturbances, e.g. emotional
CC disturbances of psychiatric patients in a state of depression. These
CC colostrinin peptides improves the development of immune system in a new
CC born child and to correct the immunological deficiencies in a child.
CC The present sequence is colostrinin peptide 2 related to the invention.

XX SQ Sequence 6 AA;

Query Match
Best Local Similarity 100.0%; Score 6; DB 22; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPVVN 9
|||||

Db 1 FLPVVN 6

RESULT 10
AAE07196
ID AAE07196 standard; peptide; 7 AA.
XX

AAE07196;
 06-NOV-2001 (first entry)
 Modified colostrinin cyclic peptide #2.
 Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 central nervous system disorder; neurodegenerative disorder; weight loss;
 beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 acquired immunological deficiency; neurological disorder; dementia;
 antiviral; cyclic.
 Synthetic.
 Key Location/Qualifiers
 Modified-site 1
 /note= "N-terminal acetyl; this residue forms a cyclic
 linkage with Asn found at the C-terminal end"
 WO200155199-A1.
 02-AUG-2001.
 26-JAN-2001; 2001WO-GB00329.
 26-JAN-2000; 2000GB-0001825.
 (REG-) REGEN THERAPEUTICS PLC.
 Georgiades JA;
 WPI; 2001-488775/53.
 Peptide useful as an inter alia in the treatment of e.g. disorders of
 the immune system and the central nervous system comprises ten
 amino-terminal amino acid sequence derived from peptides present in
 colostrinin -
 Example 2; Page 8; 40pp; English.
 The invention relates to colostrinin peptide fragments which are useful,
 inter alia, in the treatment of chronic disorders of the immune system
 and the central nervous system. Colostrinin peptides are used as a
 medicament in the treatment of neurological disorders e.g., dementia,
 neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 neurosis, in acquired immunological deficiencies, chronic bacterial and
 viral infections and diseases characterised by the presence of beta-
 amyloid plaques and as a dietary supplement for babies, small children,
 adults and senile persons, who have been subjected to chemotherapy or
 have suffered from cachexia or weight loss due to the chronic disease.
 Colostrinin peptides are also used as food additives and as an auxiliary
 withdrawal treatment for drug addicts, after a period of detoxification
 and in persons dependent on stimulants. Colostrinin peptides are used to
 prepare antibodies and to treat emotional disturbances, e.g. emotional
 disturbances of psychiatric patients in a state of depression. These
 colostrinin peptides improves the development of immune system in a new
 born child and to correct the immunological deficiencies in a child.
 The present sequence is modified colostrinin cyclic peptide #2 related to
 the invention.
 Sequence 7 AA;
 Query Match 50.0%; Score 6; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

AAAY21194
 ID AAY21194 standard; Protein; 9 AA.
 XX
 AC AAY21194;
 XX
 DT 22-JUL-1999 (first entry)
 XX
 DE Human bcl2 proto-oncogene mutant protein fragment 42.
 XX
 KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 frameshift mutation; age-related disease; neurodegenerative disorder;
 Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 Huntington's disease; multiple sclerosis; alcoholic liver disease;
 diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 high mobility group protein-C; neuroendocrine specific protein A.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9845322-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 02-APR-1998; 98WO-IB00705.
 XX
 PR 10-APR-1997; 97US-0043163.
 XX
 PA (UYUT-) RIJKSUNIV UTRECHT.
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 XX
 PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
 XX
 DR WPI; 1998-609901/51.
 DR N-PSDB; AAX75766.
 XX
 PT Diagnosing disease by detecting frameshift mutations in RNA or
 corresponding protein mutations - used to diagnose cancer and
 neurological diseases, particularly Alzheimer's disease, and also
 for treatment and prevention with specific ribozymes or wild-type
 RNA
 XX
 PS Disclosure; Figure 15; 258pp; English.
 XX
 CC This invention describes a novel method for the diagnosis of a disease
 caused by, or associated with, an RNA molecule that has a frameshift
 mutation. The method is used to diagnose age-related diseases, especially
 cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 and many others listed) or susceptibility to these disorders. The method
 allows a definitive diagnosis of Alzheimer's disease in living patients,
 at an early stage. It is based on the observation that disease may be
 caused by mutations in RNA rather than DNA. The invention describes the
 use of neuronal system RNA molecules, specifically proteins including
 beta-amyloid precursor protein (beta-APP), the microtubule associated
 proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 protein-C (HMGP-C) and neuroendocrine specific protein A.
 XX
 SQ Sequence 9 AA;
 Query Match 50.0%; Score 6; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFFLPV 7
 DB 4 FFFLPV 9

RESULT 12
 AAW51338
 ID AAW51338 standard; peptide; 5 AA.
 AC AAW51338;
 XX
 DT 14-AUG-1998 (first entry)
 DE Peptide #21 useful as modulator of beta-amyloid peptide aggregation.
 KW Natural beta-amyloid peptide; aggregation; D-amino acid;
 KW Alzheimer's disease; beta-amyloidosis.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Modified-site /note= "D-form residue, C-terminal amide"
 FT
 XX
 PN WO9808868-A1.
 XX
 PD 05-MAR-1998.
 XX
 PF 27-AUG-1997; 97WO-US15166.
 XX
 PR 21-JUL-1997; 97US-0897342.
 PR 27-AUG-1996; 96US-0703675.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PI Arico-muendel CC, Chin J, Findeis MA, Geftter ML;
 PI Hayward NJ, Kelley M, Komar-panicucci S, Lee J, Molineaux S;
 PI Musso G, Phillips K, Signer ER, Wakefield J;
 XX WPI; 1998-216936/19.
 XX
 PT Peptide compounds which are preferably based on beta-amyloid
 PT peptide(s) - are useful in treatment of disorders related to
 PT beta-amyloidosis, especially Alzheimer's disease
 XX
 PS Claim 8; Page 78; 92pp; English.
 XX
 CC The invention relates to peptides that modulate natural beta-amyloid
 CC peptide aggregation. The modulators of the invention comprise a peptide
 CC preferably based on a beta-amyloid peptide, that is comprised entirely
 CC of D-amino acids. Preferably the peptide comprises 3-5 D-amino acid
 CC residues and includes at least two D-amino acid residues independently
 CC selected from the group consisting of D-leucine, D-phenylalanine and
 CC D-valine. Preferred amino-terminal modifying groups include cyclic,
 CC heterocyclic, polycyclic and branched alkyl groups. Preferred
 CC carboxy-terminal modifying groups include an amide group, an alkyl amide
 CC group, an aryl amide group or a hydroxy group. The peptides may be used
 CC to treat disorders associated with beta-amyloidosis, especially
 CC Alzheimer's disease. They may also be used in methods for detecting the
 CC presence of beta-amyloid peptides in biological samples. The present
 CC sequence represents a specifically claimed peptide.
 XX
 SQ Sequence 5 AA;

Query Match 41.7%; Score 5; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFL 5
 DB 1 LFFFL 5

RESULT 13
 AAW51344
 ID AAW51344 standard; peptide; 5 AA.
 XX
 AC AAW51344;
 XX
 DT 14-AUG-1998 (first entry)
 DE Peptide #27 useful as modulator of beta-amyloid peptide aggregation.
 KW Natural beta-amyloid peptide; aggregation; D-amino acid;
 KW Alzheimer's disease; beta-amyloidosis.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "D-form residue, N-terminal acetyl"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Modified-site /note= "D-form residue, C-terminal amide"
 FT
 XX
 PN WO9808868-A1.
 XX
 PD 05-MAR-1998.
 XX
 PF 27-AUG-1997; 97WO-US15166.
 XX
 PR 21-JUL-1997; 97US-0897342.
 PR 27-AUG-1996; 96US-0703675.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PI Arico-muendel CC, Chin J, Findeis MA, Geftter ML;
 PI Hayward NJ, Kelley M, Komar-panicucci S, Lee J, Molineaux S;
 PI Musso G, Phillips K, Signer ER, Wakefield J;
 XX WPI; 1998-216936/19.
 XX
 PT Peptide compounds which are preferably based on beta-amyloid
 PT peptide(s) - are useful in treatment of disorders related to
 PT beta-amyloidosis, especially Alzheimer's disease
 XX
 PS Claim 8; Page 80; 92pp; English.
 XX
 CC The invention relates to peptides that modulate natural beta-amyloid
 CC peptide aggregation. The modulators of the invention comprise a peptide
 CC preferably based on a beta-amyloid peptide, that is comprised entirely
 CC of D-amino acids. Preferably the peptide comprises 3-5 D-amino acid
 CC residues and includes at least two D-amino acid residues independently
 CC selected from the group consisting of D-leucine, D-phenylalanine and
 CC D-valine. Preferred amino-terminal modifying groups include cyclic,
 CC heterocyclic, polycyclic and branched alkyl groups. Preferred
 CC carboxy-terminal modifying groups include an amide group, an alkyl amide
 CC group, an aryl amide group or a hydroxy group. The peptides may be used
 CC to treat disorders associated with beta-amyloidosis, especially
 CC Alzheimer's disease. They may also be used in methods for detecting the

CC modulate the aggregation of natural beta-AP and/or inhibit the cyto-
CC toxicity of natural beta-Aps. The beta-amyloid modulator compounds of
CC the invention comprise a peptide, preferably based on beta-AP, that is
CC composed entirely of D-amino acids. The modulators of the invention are
CC useful for treating a disorder associated with beta-amyloidosis such as
CC Alzheimer's disease. The present sequence is an inversed isomer mutant
CC (W18F; A41L) of Abeta peptide. Beta AP is a cleavage product of beta
CC amyloid precursor protein (APP-770; residues 17-21).

XX Sequence 5 AA;

Query Match 41.7%; Score 5; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFL 5
|
|
|
|
Db 1 LFFFL 5

RESULT 16

ABG73485
ID ABG73485 standard; Peptide; 5 AA.

XX AC ABG73485;

XX DT 10-MAY-2003 (first entry)

XX DE Natural beta-amyloid peptide modulator compound #28.

XX KW Natural beta-amyloid peptide; aggregation inhibition; beta-amyloidosis;
KW Alzheimer's disease; beta-amyloid deposition; Down's syndrome;
KW hereditary cerebral haemorrhage with amyloidosis-Dutch-type; HCHWA-D;
KW neurological impairment; neuroprotective; nootropic.

XX OS Synthetic.

XX FN US2002103134-A1.

XX PD 01-AUG-2002.

XX PF 29-JUN-2001; 2001US-0895443.

XX PR 27-AUG-1997; 97US-0920162.

XX PR 19-JUL-1999; 99US-0356931.

XX PR 27-OCT-1995; 95US-0548998.

XX PR 14-MAR-1996; 96US-0616081.

XX PR 27-AUG-1996; 96US-0703675.

XX PR 21-JUL-1997; 97US-0897342.

XX FA (PRAE-) PRAECIS PHARM INC.

XX FI Findeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;

PI Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;

PI Arico-Muendel CC, Phillips K, Hayward NJ;

XX WPI; 2003-298609/29.

XX Novel compound that modulate natural beta-amyloid peptide aggregation,
PT is useful for treating amyloidogenic diseases e.g. Alzheimer's disease
PT -

XX PS Claim 8; Page 36; 42pp; English.

XX The invention relates to a compound that modulates natural beta-amyloid
CC peptide aggregation. The peptide is useful for inhibiting aggregation of
CC natural beta-amyloid peptides and for treating a disorder associated with
CC beta-amyloidosis, e.g. Alzheimer's disease. The compound is also useful
CC for detecting the presence or absence of natural beta-amyloid peptides in
CC a biological sample, by contacting the biological sample with the
CC compound in vitro, where the compound is labelled with a detectable
CC substance and detecting the compound bound to natural beta-amyloid
CC peptides to thus detect the presence or absence of natural beta-amyloid

CC peptides. The compound is preferably labelled with radioactive technetium
CC or radioactive iodine and is administered to the subject. The compound is
CC also useful for prophylactically or therapeutically treating other
CC clinical occurrences of beta-amyloid deposition such as in Down's
CC syndrome individuals and in patients with hereditary cerebral haemorrhage
CC with amyloidosis-Dutch-type (HCHWA-D), and for therapeutically allowing
CC for the sequestration of beta-amyloid proteins at sites that do not lead
CC to neurological impairment. This sequence represents a natural
CC beta-amyloid peptide modulator compound of the invention.

XX Sequence 5 AA;

Query Match 41.7%; Score 5; DB 24; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFL 5
|
|
|
|
Db 1 LFFFL 5

RESULT 17

AAG61675

ID AAG61675 standard; Protein; 9 AA.

XX AC AAG61675;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 80031.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX OS Arabidopsis thaliana.

XX FN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

XX PR 08-APR-1999; 99US-0128714.

XX PR 16-APR-1999; 99US-0129845.

XX PR 19-APR-1999; 99US-0130077.

XX PR 21-APR-1999; 99US-0130449.

XX PR 23-APR-1999; 99US-0130510.

XX PR 23-APR-1999; 99US-0130831.

XX PR 28-APR-1999; 99US-0131449.

XX PR 30-APR-1999; 99US-0132048.

XX PR 30-APR-1999; 99US-0132407.

XX PR 04-MAY-1999; 99US-0132484.

XX PR 05-MAY-1999; 99US-0132485.

XX PR 06-MAY-1999; 99US-0132486.

XX PR 06-MAY-1999; 99US-0132487.

XX PR 07-MAY-1999; 99US-0132863.

XX PR 11-MAY-1999; 99US-0134256.

XX PR 14-MAY-1999; 99US-0134218.

XX PR 14-MAY-1999; 99US-0134219.

XX PR 14-MAY-1999; 99US-0134221.

XX PR 14-MAY-1999; 99US-0134370.

XX PR 18-MAY-1999; 99US-0134768.

XX PR 19-MAY-1999; 99US-0134941.

XX PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 05-OCT-1999; 99US-0157117.
PR 06-OCT-1999; 99US-0157753.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 14-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.

PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 41.7%; Score 5; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9, 3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6
 DB 1 FFFLP 5
 |||||

RESULT 18

AAW69637
 ID AAW69637 standard; peptide; 11 AA.

AC AAW69637;

XX DT 19-OCT-1998 (first entry)

DE Peptide SEQ ID NO:57 from US5789184 Example 5.

XX Yeast; Saccharomyces cerevisiae; pheromone; alpha factor; receptor;
 KW surrogate; screening; selection.

XX OS Synthetic.

XX PN US5789184-A.

XX PD 04-AUG-1998.

XX PF 05-JUN-1995; 95US-0464531.

XX PR 05-JUN-1995; 95US-0464531.

XX PR 31-MAR-1993; 93US-0041431.

XX PR 31-JAN-1994; 94US-0190328.

XX PR 20-SEP-1994; 94US-0309313.

XX PR 13-OCT-1994; 94US-0322137.

XX (CADU-) CADUS PHARM CORP.

XX PI Broach J, Fowlkes DM, Klein C, Manfredi J, Murphy AJ;

XX PI Paul J, Trueheart J;

XX DR WPI; 1998-446076/38.

XX DR N-PSDB; AAV50008.

XX PT Recombinant yeast cells - containing gene encoding yeast pheromone
 PT system protein surrogate and gene encoding peptide modulator

XX PS Example 5; Column 125; 93pp; English.

XX CC The present invention describes a yeast cell having a pheromone system,
 CC in which the cell comprises: (a) a first heterologous gene encoding a
 CC heterologous surrogate of a yeast pheromone system protein, the surrogate
 CC being a kinase and performing in the pheromone system of the yeast cell
 CC a function naturally performed by the corresponding yeast pheromone
 CC system protein; and (b) a second heterologous gene encoding a
 CC heterologous peptide, where the heterologous peptide modulates the
 CC interaction of the surrogate with the pheromone system in the yeast cell,
 CC and the modulation is a selectable or screenable event. The yeast cells
 CC are used in assaying a peptide for modulation of the activity of a non-
 CC yeast surrogate for a pheromone system protein and determining by
 CC detecting a change in the selectable or screenable event whether the
 CC pheromone signal pathway is activated or inhibited by the interaction of
 CC the surrogate and the peptide. The present sequence represents a
 XX peptide which is used in an example of the present invention.

XX SQ Sequence 11 AA;

Query Match 41.7%; Score 5; DB 19; Length 11;

AAW20744

Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6
 DB 6 FFFLP 10
 |||||

RESULT 19

AAW74434
 ID AAW74434 standard; peptide; 11 AA.

XX AC AAW74434;

XX DT 20-MAR-2003 (updated)

XX DT 10-MAY-1999 (first entry)

XX DE Ste2 agonist peptide sequence.

XX KW Yeast pheromone; Ste2 agonist; cognate yeast pheromone system protein;
 KW farnesyl transferase; anticancer therapy.

XX OS Synthetic.

XX PN US5876951-A.

XX PD 02-MAR-1999.

XX PF 05-JUN-1995; 95US-0461598.

XX PR 05-JUN-1995; 95US-0461598.

XX PR 31-MAR-1993; 93US-0041431.

XX PR 31-JAN-1994; 94US-0190328.

XX PR 20-SEP-1994; 94US-0309313.

XX PR 13-OCT-1994; 94US-0322137.

XX (CADU-) CADUS PHARM CORP.

XX PI Broach J, Fowlkes DM, Klein C, Manfredi J, Murphy AJ;

XX PI Paul J, Trueheart J;

XX DR WPI; 1999-189631/16.

XX DR N-PSDB; AAX18224.

XX PT Yeast cells having an engineered pheromone system - useful for
 PT identifying drugs which can inhibit or activate pheromone system
 PT protein, e.g. to develop anti-cancer therapies

XX PS Example 5; Column 61; 93pp; English.

XX CC This sequence represents an Ste2 agonist peptide sequence.
 CC The invention relates to Yeast cells engineered to express an exogenous
 CC protein capable of substituting for a yeast protein involved in the
 CC post-translational modification, transport, recognition or signal
 CC transduction of a yeast pheromone. The system can be used to identify
 CC drugs which inhibit or activate the ability of the surrogate to
 CC substitute for the cognate yeast pheromone system protein. Inhibitors of
 CC farnesyl transferase identified can be used for anticancer therapies.
 CC (Updated on 20-MAR-2003 to correct PF field.)

XX SQ Sequence 11 AA;

Query Match 41.7%; Score 5; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6
 DB 6 FFFLP 10
 |||||

RESULT 20

AAW20744


```
ID XX AAB20744 standard; Peptide; 11 AA.
AC XX AAB20744;
DT 21-DEC-2000 (first entry)
DE XX MF-alpha-1 expression construct peptide SEQ ID NO:57.
KW Yeast; pheromone; alpha-factor; transporter; pheromone receptor;
KW G alpha subunit; MF alpha 1; Mfal; STE2; STE3; C5a receptor; GPAL1;
KW G protein coupled receptor; mutagenesis; amplification; screening;
KW hybrid; agonist; antagonist; signal transduction; detection;
KW identification.
XX
OS Saccharomyces cerevisiae.
OS Synthetic.
XX
PN US6100042-A.
XX
PD 08-AUG-2000.
XX
PF 13-OCT-1994; 94US-0322137.
XX
PR 31-MAR-1993; 93US-0041431.
XX
PR 31-JAN-1994; 94US-0190328.
XX
PR 20-SEP-1994; 94US-0309313.
XX
PA (CADU-) CADUS PHARM CORP.
XX
XX Fowlkes DM, Broach J, Klein C, Murphy AJ, Paul J, Trueheart J;
PI Manfredi J;
XX
XX WPI; 2000-531665/48.
XX
XX Mixture of recombinant yeast cells comprising a heterologous G protein
PT coupled receptor whose signal transduction activity is modulated by a
PT heterologous polypeptide which provides a detectable signal on
PT modulation.
XX
XX Example 5; Column 63; 95pp; English.
XX
XX The present invention describes recombinant yeast cell mixtures (I).
XX Each (I) has a heterologous G protein coupled receptor (GPCR) expressed
XX in the cell membrane such that signal transduction (ST) activity via
XX GPCR is modulated by interaction of extracellular region (ER) of GPCR
XX with a heterologous polypeptide (P) which interacts with ER of GPCR.
XX Modulation of the ST activity by (P) provides a detectable signal.
XX Also described is a recombinant yeast cell (II) that has a cell membrane
XX which comprises a GPCR such that ST activity via GPCR is modulated by
XX interaction of an ER of GPCR with an extracellular signal, and a (P)
XX which is transported to a location allowing interaction with ER of GPCR.
XX (I) is used for identifying a modulator of (P) expressed by the yeast
XX cell which involves providing (I) which comprises heterologous GPCR and
XX a heterologous test polypeptide, allowing the cells within the mixture
XX to generate a detectable signal, and then identifying the heterologous
XX test peptide as a modulator of the heterologous receptor protein
XX expressed by the yeast cell. The yeast cells may be used to identify
XX drugs which inhibit or activate, to a detectable degree, the ability of
XX the surrogate to substitute for the cognate yeast pheromone system
XX proteins. The yeast cell is also used to screen agonists and
XX antagonists. The present sequence is used in the exemplification of
XX the present invention.
SQ Sequence 11 AA;
Query Match 41.7%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FFFLP 6
Db 6 FFFLP 10
RESULT 22
AAG79162
ID AAG79162 standard; peptide; 11 AA.
XX
XX AC AAG79162;
XX
XX DT 03-JAN-2002 (first entry)
XX
XX DE Amino acid sequence of an improved a-factor variant.
XX
```

```
RESULT 21
AAY93630
ID AAY93630 standard; peptide; 11 AA.
XX
XX AC AAY93630;
XX
XX DT 25-SEP-2000 (first entry)
XX
XX DE Peptide encoded by the insert of an a-factor variant.
XX
XX KW Surrogate ligand; formyl peptide receptor like-1 receptor;
XX FPRL-1 receptor; signal transduction; cellular receptor; a-factor;
XX ABC transporter; ion channel.
XX
XX OS Synthetic.
XX
XX PN WO200031261-A2.
XX
XX PD 02-JUN-2000.
XX
XX PF 24-NOV-1999; 99WO-US27909.
XX
XX PR 25-NOV-1998; 98US-0109902.
XX
XX PR 30-NOV-1998; 98US-0201396.
XX
XX PA (CADU-) CADUS PHARM CORP.
XX
XX Klein CA, Murphy AJ, Paul J;
PI WPI; 2000-400071/34.
XX
XX Recombinant cell used to identify modulators of heterologous formyl
PT peptide receptor like-1 (FPRL-1) receptor, comprising FPRL-1 receptor
PT expressed in the cell membrane, and a FPRL-1 receptor ligand agonist -
XX
XX Example 5; Page 88; 156pp; English.
XX
XX AAY93628-31 represent peptides encoded by the inserts of a-factor
XX variants identified from random peptide libraries. These variants have
XX utility as improved substrates of ABC transporters expressed in yeast.
XX The specification describes a method for screening and identifying
XX pharmacologically effective compounds which specifically interact with
XX and modulate the activity of a cellular receptor or ion channel. The
XX method uses a cells which expresses a heterologous formyl peptide
XX receptor like-1 (FPRL-1) receptor in the cell membrane, so
XX that extracellular signal interaction with the receptors extracellular
XX region modulates signal transduction via the receptor. The cell is
XX used in a method to screen and identify pharmaceutically effective
XX compounds which specifically interact with and modulate the activity
XX of a cellular receptor or ion channel, especially the FPRL-1 receptor.
XX
XX SQ Sequence 11 AA;
Query Match 41.7%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FFFLP 6
Db 6 FFFLP 10
RESULT 22
AAG79162
ID AAG79162 standard; peptide; 11 AA.
XX
XX AC AAG79162;
XX
XX DT 03-JAN-2002 (first entry)
XX
XX DE Amino acid sequence of an improved a-factor variant.
XX
```

KW Cellular receptor; ion channel; cellular activity; drug discovery;
 KW orphan receptor ligand; a-factor; ABC transporter.
 XX Synthetic.
 XX US2001026926-A1.
 XX 04-OCT-2001.
 PD
 XX
 PF 21-DEC-2000; 2000US-0747774.
 XX
 PR 17-JAN-1996; 96US-0582333.
 PR 31-MAR-1993; 93US-0041431.
 PR 31-JAN-1994; 94US-0190328.
 PR 20-SEP-1994; 94US-0309313.
 PR 13-OCT-1994; 94US-0322137.
 PR 05-JUN-1995; 95US-0461383.
 PR 05-JUN-1995; 95US-0461598.
 PR 05-JUN-1995; 95US-0463181.
 PR 05-JUN-1995; 95US-0464531.
 XX
 PA (CADU-) CADUS PHARM CORP.
 XX
 PI Klein CA, Murphy AJ, Fowlkes DM, Broach J, Manfredi J, Paul J;
 PI Trueheart J;
 XX
 DR WPI; 2001-615870/71.
 DR N-PSDB; AA165751.
 XX
 PT Identification of compounds modulating cellular receptor activity
 PT useful for identifying and screening for ligands for orphan receptors,
 PT comprises using recombinant cells comprising both receptors and test
 PT polypeptide -
 XX
 PS Example 5; Page 34; 50pp; English.
 XX
 CC The specification describes an assay for screening and identifying
 CC pharmacaceutically effective compounds that specifically interact with
 CC and modulate the activity of a cellular receptor or ion channel. The
 CC assay uses a mixture of recombinant cells, each comprising a receptor
 CC protein whose signal transduction activity is modulated by an
 CC interaction with an extracellular signal, a recombinant gene encoding
 CC a potential receptor polypeptide, and a reporter gene construct. The
 CC assay is useful for rapid screening of large numbers of polypeptides to
 CC identify polypeptides antagonizing or agonizing receptor activity, and
 CC to identify drugs for modulating cellular activity. It is especially
 CC useful to identify ligands for orphan receptors, especially ligands for
 CC orphan cell surface receptors, which are useful in drug discovery. The
 CC present sequence represents an improved a-factor variant, which is a
 CC better substrate for ABC transporters. The variant was identified using
 CC the assay of the invention.
 XX
 SQ Sequence 11 AA;
 Query Match 41.7%; Score 5; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FFFLP 6
 |||||
 Db 6 FFFLP 10
 XX
 DE
 XX
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 XX Homo sapiens.
 XX OS

KW G protein coupled receptor; GPCR; cellular receptor; ion channel;
 KW surrogate ligand; orphan receptor; pheromone analogue.
 XX Synthetic.
 XX US255059-B1.
 XX 03-JUL-2001.
 PD
 XX
 PF 17-JAN-1996; 96US-0582333.
 XX
 PR 31-MAR-1993; 93US-0041431.
 PR 31-JAN-1994; 94US-0190328.
 PR 20-SEP-1994; 94US-0309313.
 PR 13-OCT-1994; 94US-0322137.
 PR 05-JUN-1995; 95US-0463181.
 XX
 PA (CADU-) CADUS PHARM CORP.
 XX
 PI Klein CA, Murphy AJM, Fowlkes DM, Broach J, Manfredi J, Paul J;
 PI Trueheart J;
 XX
 DR WPI; 2001-396979/42.
 DR N-PSDB; AAH27821.
 XX
 PT Identifying a ligand for an orphan G protein coupled receptor comprises
 PT using an recombinant yeast expression library -
 XX
 PS Example 5; Column 63; 128pp; English.
 XX
 CC The specification describes a method for identifying a ligand for
 CC an orphan G protein coupled receptor (GPCR). The method comprises
 CC rapidly screening large numbers of polypeptides in a yeast expression
 CC library to identify those polypeptides which induce or antagonise
 CC receptor bioactivity. The method is useful for screening and identifying
 CC pharmacaceutically effective compounds that specifically interact with
 CC and modulate the activity of a cellular receptor or ion channel. The
 CC assay is particularly amenable for identifying surrogate ligands for
 CC orphan receptors. The present sequence represents a pheromone analogue,
 CC identified using the method of the invention.
 XX
 SQ Sequence 11 AA;
 Query Match 41.7%; Score 5; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FFFLP 6
 |||||
 Db 6 FFFLP 10
 XX
 DE
 XX
 XX
 XX
 DE
 XX
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 XX Homo sapiens.
 XX OS

PR 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX (CURA-) CURAGEN CORP.
 PA Shimkets RA, Leach M;
 XX WPI; 2001-465210/50.
 DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 XX oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX Disclosure; Page 4011; 4143pp; English.
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinases, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms.
 XX Sequence 14 AA;
 SQ

Query Match 41.7%; Score 5; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFL 5
 DB 6 LFFFL 10

RESULT 27
 AAG64341
 ID AAG64341 standard; Peptide; 15 AA.
 AC AAG64341;
 XX 24-SEP-2001 (first entry)
 DE Ribosomal protein L2-11 peptide fragment.
 XX Ribosomal protein L2-11; cytostatic; haemostatic; virucide;
 KW immunomodulatory; antiinflammatory; gene therapy; malignant tumour;
 KW haemopathy; HIV infection; immunological disease; inflammation.
 XX Unidentified.
 OS WO200147990-A1.
 PN 05-JUL-2001.
 PD 18-DEC-2000; 2000WO-CN00630.
 XX 24-DEC-1999; 99CN-0125768.
 PR (BIOW-) BIOWINDOW GENE DEV INC.
 PA Mao Y, Xie Y;
 PI WPI; 2001-425641/45.
 XX

PT Ribosomal protein L2-11 and encoded polynucleotide, used in diagnosis
 PT and treatment of malignant tumors, hemopathy, human immunodeficiency
 PT virus infection, immunological diseases and inflammation -
 XX Example 6; Page 14; 35pp; Chinese.
 PS The present invention relates to ribosomal protein L2-11 and its coding
 XX sequence (see AAH49665 and AAG64340). The ribosomal protein and its
 CC coding sequence are useful in the diagnosis and treatment of malignant
 CC tumour, haemopathy, HIV infection, immunological diseases and various
 CC inflammations. The present sequence is a N-terminal peptide fragment of
 CC the ribosomal protein, which was used in an example from the present
 CC invention.
 XX Sequence 15 AA;
 SQ

Query Match 41.7%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLPV 7
 DB 4 FFLPV 8

RESULT 28
 AAE01592
 ID AAE01592 standard; peptide; 17 AA.
 XX AAE01592;
 AC 17-JUL-2001 (first entry)
 XX Human gene 11 encoded secreted protein fragment HMVDP35, SEQ ID NO:142.
 DE Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder;
 KW endocrine disorder; infection; wound healing; vulnerability;
 KW cell culture; chemotaxis; food additive;
 KW binding partner identification; gene therapy.
 XX Homo sapiens.
 OS WO200134623-A1.
 PN 17-MAY-2001.
 PD 01-NOV-2000; 2000WO-US30037.
 XX 05-NOV-1999; 99US-0163577.
 PR 30-JUN-2000; 2000US-0215137.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Ruben SM, Komatsoulis GA, Moore PA;
 PI WPI; 2001-316490/33.
 DR N-PSDB; AAD05435.
 XX Nucleic acids encoding 29 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX Claim 11; Page 495-496; 535pp; English.
 PS AAD05389-AAD05473 represent cDNAs corresponding to 29 human secreted
 CC protein genes, and AAE01546-AAE01630 represent the proteins they encode.

CC AAE01631-AAE01660 represent human secreted protein fragments or variants.
 CC The secreted proteins and their genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 29 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angogenic disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein fragment of the invention.
 XX
 SQ Sequence 17 AA;

Query Match 41.7%; Score 5; DB 22; Length 17;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFL 5
 |||||
 Db 5 LFFFL 9

RESULT 29
 ABG63823
 ID ABG63823 standard; Protein; 17 AA.

AC ABG63823;

DT 27-AUG-2002 (first entry)

DE Human albumin fusion protein #498.

KW Albumin fusion protein; therapeutic protein X; human albumin; HA;
 KW human serum albumin; HSA; cancer; reproductive disorder;
 KW digestive disorder; immune disorder; endocrine disorder;
 KW haematopoietic disorder; neural disorder; connective disorder;
 KW cytosolic; antifertility; antitumour; inflammatory; antiulcer;
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
 KW osteopathic; antiarthritic.

OS Homo sapiens.
 OS Synthetic.

PN WO200177137-A1.

PD 18-OCT-2001.

XX 12-APR-2001; 2001WO-US11988.

XX 12-APR-2000; 2000US-229350P.

PR 25-APR-2000; 2000US-199384P.

PR 21-DEC-2000; 2000US-256931P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Haseltine WA;

XX WPI; 2002-010886/01.

XX New fusion protein for treating disease e.g. diabetes comprises an
 PT albumin fused to a therapeutic protein -

XX Claim 1; Page 848; 2102pp; English.

XX The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein X and human albumin (HA, also known as human serum
 CC albumin, HSA). The proteins are useful for treating a disease or
 CC disorder that may be modulated by therapeutic protein X. The albumin
 CC extends the shelf-life of protein X, and may increase its biological
 CC in vitro/in vivo activity. The protein is useful for treating and
 CC diagnosing disorders such as cancer, reproductive disorders, digestive
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
 CC (e.g. diabetes), haematopoietic disorders, neural disorders
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders
 CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin
 CC fusion proteins of the invention.

XX Sequence 17 AA;

Query Match 41.7%; Score 5; DB 23; Length 17;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFL 5
 |||||
 Db 5 LFFFL 9

RESULT 30
 AAB91942

ID AAB91942 standard; Peptide; 19 AA.

AC AAB91942;

DT 22-JUN-2001 (first entry)

XX Complement inhibitor peptide SEQ ID NO:1118.

DE Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
 OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity

XX

PS Disclosure; Page 561; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX

SQ Sequence 19 AA;
 Query Match 41.7%; Score 5; DB 22; Length 19;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VNVLP 12
 Db 15 VNVLP 19
 |||||

RESULT 31
 AAO17268
 ID AAO17268 standard; Protein; 19 AA.
 AC AAO17268;
 DT 08-JUL-2002 (first entry)
 XX
 DE A thaliana receptor kinase RKX8 peptide fragment.
 XX
 KW Vegetative propagation; plant; phytochrome; receptor kinase-like SERK;
 KW RKS.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1094113-A1.
 XX
 PD 25-APR-2001.
 XX
 PF 22-OCT-1999; 99EP-0203480.
 XX
 PR 22-OCT-1999; 99EP-0203480.
 XX
 PA (GENE-) GENETWISTER TECHNOLOGIES BV.
 XX
 PI Schmidt BDL, Van Der Kop DAM, De Boer AD;
 XX
 DR WPI; 2002-228902/29.
 XX
 PT In vitro culture propagation of a plant from plant starting material,
 PT comprises stimulating root/shoot initiation by introducing a
 PT recombinant gene product into the starting material, thus reducing
 PT phytochrome addition to culture -
 XX
 PS Disclosure; Page 86; 171pp; English.
 XX
 CC The present invention relates to a culture method for propagating a plant
 CC from a plant starting material, where root or shoot initiation is
 CC stimulated by introducing a gene into the starting material which allows
 CC the reduction or absence of phytochrome addition to the culture. The
 CC method is used for the propagation (preferably, seedless propagation) of
 CC a plant from a plant starting material in an in vitro culture method.
 CC Nucleic acids encoding receptor-like kinases are useful in the method.

CC The present sequence is a receptor-like kinase protein.
 XX

SQ Sequence 19 AA;
 Query Match 41.7%; Score 5; DB 23; Length 19;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
 Db 2 FFFLP 6
 |||||

RESULT 32
 AAW47343
 ID AAW47343 standard; peptide; 20 AA.
 AC AAW47343;
 XX
 DT 01-JUN-1998 (first entry)
 XX
 DE Apolipoprotein B tryptic peptide.
 XX
 KW Binding inhibitor; low-density lipoprotein; LDL; vascular wall;
 KW vascular injury; elastin; collagen; prevention; treatment;
 KW vascular disease; atherosclerosis; apolipoprotein B; apoB;
 KW tryptic peptide.
 XX
 OS Homo sapiens.
 XX
 PN US5726153-A.
 XX
 PD 10-MAR-1998.
 XX
 PF 06-JUN-1995; 95US-0468543.
 XX
 PR 06-JUN-1995; 95US-0469692.
 PR 02-MAY-1988; 88US-0189130.
 PR 03-MAY-1990; 90US-0518142.
 PR 03-MAY-1990; 90US-0518215.
 PR 02-MAY-1991; 91US-0694929.
 PR 16-APR-1993; 93US-0048569.
 PR 24-FEB-1994; 94US-0201057.
 PR 28-FEB-1995; 95US-0398046.
 PR 06-JUN-1995; 95US-0468543.
 XX
 PA (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
 XX
 PI Findeis MA, Fischman A, Lees AM, Lees RS, Shih I;
 XX
 DR WPI; 1998-192802/17.
 XX
 PT Inhibiting binding of low-density lipoprotein to vascular walls - by
 PT administering peptide with affinity for vascular injury sites
 XX
 PS Disclosure; Column 10; 31pp; English.
 XX
 CC A novel method for inhibiting the binding of a low-density
 CC lipoprotein (LDL) to vascular walls in vivo, comprises
 CC administering a synthetic water soluble peptide containing an
 CC amphiphilic domain and having affinity for sites of vascular
 CC injury, e.g. derived from the present peptide.
 CC The peptide inhibits the binding of LDL to vascular wall
 CC components, e.g. elastin and collagen, and so can be used to
 CC prevent or treat vascular diseases, e.g. atherosclerosis.
 XX
 SQ Sequence 20 AA;
 Query Match 41.7%; Score 5; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PVNVV 10

```

Db      11 PVNV 15
|||||
RESULT 33
AAV5885
ID AAV5885 standard; peptide; 20 AA.
XX
AC AAV5885;
XX
DT 01-FEB-2000 (first entry)
XX
DE Apolipoprotein fragment peptide #35 for vascular disease imaging.
XX
KW Diagnosis; water soluble; amphiphilic domain; affinity; vascular injury;
KW detection; imaging; disease; atherosclerosis; apolipoprotein.
XX
OS Synthetic.
OS Homo sapiens.
PN US5972890-A.
XX
PD 26-OCT-1999.
XX
PF 28-FEB-1995; 95US-0398046.
XX
PR 02-MAY-1991; 91US-0694929.
PR 16-APR-1993; 93US-0048569.
PR 24-FEB-1994; 94US-0201057.
PR 02-MAY-1988; 88US-0189130.
PR 03-MAY-1990; 90US-0518142.
PR 03-MAY-1990; 90US-0518142.
XX
PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
XX
PI Lees AM, Fischman A, Shih I, Findeis MA, Lees RS;
XX
DR WPI; 1999-632641/54.
XX
PT New diagnostic synthetic peptides which have affinity for and
PT accumulate at a site of vascular injury useful for detection and
PT imaging of vascular disease such as atherosclerosis -
XX
PS Disclosure; Column 10; 30pp; English.
XX
CC The peptides AAV5851-Y5889 represent examples of diagnostic, synthetic
CC peptides which carry a detectable label, contain 30 or fewer amino
CC acids, are water soluble, contain an amphiphilic domain and have affinity
CC for, and propensity to accumulate at, a site of vascular injury. They
CC are preferably derived from the amino acid sequence of apolipoprotein.
CC The peptides can be used for the detection or imaging of a vascular
CC injury or disease, e.g. atherosclerosis.
XX
SQ Sequence 20 AA;
Query Match 41.7%; Score 5; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVNV 10
|||||
Db 11 PVNV 15

RESULT 34
AAV33110
ID AAV33110 standard; peptide; 20 AA.
XX
AC AAV33110;
XX
DT 15-NOV-1999 (first entry)
XX
DE Alipoprotein B tryptic peptide 6.

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XX
KW Alipoprotein B; alipoprotein AI; elastin; vascular imaging; detection;
KW injury; vascular system; atherosclerosis; re-endothelizing; noninvasive;
KW aortic lesion; trauma; lipoprotein accumulation.
XX
OS Synthetic.
XX
PN US5955055-A.
XX
PD 21-SEP-1999.
XX
PF 06-JUN-1995; 95US-0469692.
XX
PR 02-MAY-1991; 91US-0694929.
PR 02-MAY-1988; 88US-0189130.
PR 03-MAY-1990; 90US-0518142.
PR 03-MAY-1990; 90US-0518215.
PR 16-APR-1993; 93US-0048569.
PR 24-FEB-1994; 94US-0201057.
PR 28-FEB-1995; 95US-0398046.
PR 06-JUN-1995; 95US-0469692.
XX
PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
XX
PI Findeis MA, Fischman A, Lees AM, Lees RS, Shih I;
XX
DR WPI; 1999-539543/45.
XX
PT Detecting vascular injuries using a labeled peptide useful for the
PT diagnosis and monitoring of atherosclerosis
XX
PS Disclosure; Column 31-32; 31pp; English.
XX
CC This invention describes a novel method (I) for detecting injuries in a
CC vascular system using a labeled synthetic peptide with an affinity for,
CC and propensity to accumulate at, a site of vascular injury. The method
CC is particularly suitable for detecting and monitoring atherosclerosis.
CC It has been found that the synthetic peptide accumulates at the healing
CC (re-endothelizing) edge of aortic lesions produced by trauma. These
CC lesions resemble human arteriosclerosis in many important respects
CC (including accumulation of lipoproteins and other pathological changes).
CC The ability of the synthetic peptides to localize at the trauma site,
CC and to permit imaging, may be used to visualize vascular disease. The
CC method is noninvasive and the peptides used to target vascular lesions
CC may be produced inexpensively, quickly and in large quantities.
CC AAV3088-Y33114 represent synthetic peptides derived from alipoprotein B,
CC alipoprotein AI and elastin which are used in the method of the
CC invention.
XX
SQ Sequence 20 AA;
Query Match 41.7%; Score 5; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVNV 10
|||||
Db 11 PVNV 15

RESULT 35
AAV96713
ID AAV96713 standard; peptide; 4 AA.
XX
AC AAV96713;
XX
DT 26-SEP-2000 (first entry)
XX
DE Human E3 ubiquitin ligase peptide sequence tag.
XX
E3 ubiquitin ligase; beta-TrCP; P-box; WD protein; I-kappa-B; inhibitor;
KW nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
KW anti-inflammatory; immunosuppressive; cytostatic.

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XX OS Homo sapiens.
XX PN WO200034447-A2.
XX PD 15-JUN-2000.
XX PF 10-DEC-1999; 99WO-US9371.
XX PR 10-DEC-1998; 98US-0210060.
XX PA (SIGN-) SIGNAL PHARM INC.
XX PA (YISS ) YISSUM RES & DEV CO.
XX PI Manning AM, Mercurio F, Amit S, Ben-eriah Y, Davis M, Hatzubai A;
XX PI Lavon I, Yaron A;
XX PR WPI; 2000-431294/37.
XX DR
XX PT Polypeptide enhancing phosphorylated lkappaB ubiquitination useful for
XX PT treating disorder associated with NF-kappaB activation e.g. cancer,
XX PT comprising amino acid sequence of human E3 ubiquitin ligase or its
XX PT variant
XX PS Example 5; Page 33; 77pp; English.
XX CC This peptide sequence tag was derived from fragmentation spectra of
XX CC trypsin digested human E3 ubiquitin ligase (E3). Further spectra
XX CC identified peptides shown in AAY96714-18, of which the first four are
XX CC also present within human F-box/WD protein beta-TrCP. The fifth peptide
XX CC matches that of a peptide from the broscophila Slimb protein, which is
XX CC highly homologous to the human beta-TrCP. E3 enhances ubiquitination
XX CC of phosphorylated I-kappa-B, an inhibitor protein of nuclear factor
XX CC kappa-B (NF-kappa-B). Understanding I-kappa-B degradation via the
XX CC ubiquitin pathway is useful for identifying modulators of this process
XX CC for use in treating diseases associated with activation of NF-kappa-B.
XX CC In vitro analysis suggests that deletion of the F-box results in a
XX CC protein that functions as a dominant negative molecule in vivo.
XX CC Transient over-expression of delta-beta-TrCP (a deletion mutant)
XX CC inhibited the degradation of endogenous I-kappa-B-alpha in stimulated
XX CC Jurkat cells, resulting in accumulation of phosphorylated
XX CC I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B
XX CC activity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat
XX CC inflammatory diseases, autoimmune diseases, cancer and viral
XX CC infections.
XX SQ Sequence 4 AA;
Query Match 33.3%; Score 4; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 VVNV 10
Db 1 VVNV 4
RESULT 36
AAW51334
ID AAW51334 standard; peptide; 5 AA.
XX AC AAW51334;
XX DT 14-AUG-1998 (first entry)
XX DE Peptide #17 useful as modulator of beta-amyloid peptide aggregation.
XX KW Natural beta-amyloid peptide; aggregation; D-amino acid;
XX KW Alzheimer's disease; beta-amyloidosis.
XX OS Synthetic.
XX OS Homo sapiens.

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PH FT Modified-site 1 Location/Qualifiers
FT FT /note= "D-form residue, N-terminal modifying group"
FT FT Misc-difference 2 /note= "D-form residue"
FT FT Misc-difference 3 /note= "D-form residue"
FT FT Misc-difference 4 /note= "D-form residue"
FT FT Misc-difference 5 /note= "D-form residue"
FT FT Modified-site 5 /note= "D-form residue, C-terminal modifying group"
XX PN WO9808868-A1.
XX PD 05-MAR-1998.
XX PR 27-AUG-1997; 97WO-US15166.
XX PR 21-JUL-1997; 97US-0897342.
XX PR 27-AUG-1996; 96US-0703675.
XX PA (PRAE-) PRAECIS PHARM INC.
XX PI Arico-muendel CC, Chin J, Pindeis MA, Geftter ML;
XX PI Hayward NJ, Kelley M, Komar-panicucci S, Lee J, Molineaux S;
XX PI Musso G, Phillips K, Signer ER, Wakefield J;
XX PR WPI; 1998-216936/19.
XX PT Peptide compounds which are preferably based on beta-amyloid
XX PT peptide(s) - are useful in treatment of disorders related to
XX PT beta-amyloidosis, especially Alzheimer's disease
XX PS Claim 1; Page 76; 92pp; English.
XX CC The invention relates to peptides that modulate natural beta-amyloid
XX CC peptide aggregation. The modulators of the invention comprise a peptide
XX CC preferably based on a beta-amyloid peptide, that is comprised entirely
XX CC of D-amino acids. Preferably the peptide comprises 3-5 D-amino acid
XX CC residues and includes at least two D-amino acid residues independently
XX CC selected from the group consisting of D-leucine, D-phenylalanine and
XX CC D-valine. Preferred amino-terminal modifying groups include cyclic,
XX CC heterocyclic, polycyclic and branched alkyl groups. Preferred
XX CC carboxy-terminal modifying groups include an amide group, an alkyl amide
XX CC group, an aryl amide group or a hydroxy group. The peptides may be used
XX CC to treat disorders associated with beta-amyloidosis, especially
XX CC Alzheimer's disease. They may also be used in methods for detecting the
XX CC presence of beta-amyloid peptides in biological samples. The present
XX CC sequence represents a specifically claimed peptide.
XX SQ Sequence 5 AA;
Query Match 33.3%; Score 4; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FFEL 5
Db 2 FFEL 5
RESULT 37
AAW51332
ID AAW51332 standard; peptide; 5 AA.
XX AC AAW51332;
XX DT 14-AUG-1998 (first entry)
XX DE Peptide #15 useful as modulator of beta-amyloid peptide aggregation.
XX KW Natural beta-amyloid peptide; aggregation; D-amino acid;
XX KW Alzheimer's disease; beta-amyloidosis.

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XX OS Synthetic.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT Modified-site 1 /note= "D-form residue, N-terminal modifying group"
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 3 /note= "D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT Misc-difference 5 /note= "D-form residue"
FT Modified-site 5 /note= "D-form residue, C-terminal modifying group"
XX FT WO9808868-A1.
XX PD 05-MAR-1998.
XX PF 27-AUG-1997; 97WO-US15166.
XX PR 21-JUL-1997; 97US-0897342.
XX PR 27-AUG-1996; 96US-0703675.
XX PA (PRAE-) PRAECIS PHARM INC.
XX PI Arico-muendel CC, Chin J, Findeis MA, Geffer ML;
XX PI Hayward NJ, Kelley M, Komar-panicucci S, Lee J, Molineaux S;
XX PI Musso G, Phillips K, Signer ER, Wakefield J;
XX DR WPI; 1998-216936/19.
XX PS Peptide compounds which are preferably based on beta-amyloid
XX PT peptide(s) - are useful in treatment of disorders related to
XX PT beta-amyloidosis, especially Alzheimer's disease
XX PS Claim 1; Page 76; 92pp; English.
XX CC The invention relates to peptides that modulate natural beta-amyloid
XX CC peptide aggregation. The modulators of the invention comprise a peptide
XX CC preferably based on a beta-amyloid peptide, that is comprised entirely
XX CC of D-amino acids. Preferably the peptide comprises 3-5 D-amino acid
XX CC residues and includes at least two D-amino acid residues independently
XX CC selected from the group consisting of D-leucine, D-phenylalanine and
XX CC D-valine. Preferred amino-terminal modifying groups include cyclic,
XX CC heterocyclic, polycyclic and branched alkyl groups. Preferred
XX CC carboxy-terminal modifying groups include an amide group, an alkyl amide
XX CC group, an aryl amide group or a hydroxy group. The peptides may be used
XX CC to treat disorders associated with beta-amyloidosis, especially
XX CC Alzheimer's disease. They may also be used in methods for detecting the
XX CC presence of beta-amyloid peptides in biological samples. The present
XX CC sequence represents a specifically claimed peptide.
XX SQ Sequence 5 AA;
XX Query Match 33.3%; Score 4; DB 19; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FFPL 5
DB 1 FFPL 4
XX RESULT 38
XX AAWS1333
XX ID AAWS1333 standard; peptide; 5 AA.
XX AC AAWS1333;
XX XX
XX DT 14-AUG-1998 (first entry)
XX XX

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DE Peptide #16 useful as modulator of beta-amyloid peptide aggregation.
XX Natural beta-amyloid peptide; aggregation; D-amino acid;
XX Alzheimer's disease; beta-amyloidosis.
XX OS Synthetic.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT Modified-site 1 /note= "D-form residue, N-terminal modifying group"
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 3 /note= "D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT Misc-difference 5 /note= "D-form residue"
FT Modified-site 5 /note= "D-form residue, C-terminal modifying group"
XX FT WO9808868-A1.
XX PD 05-MAR-1998.
XX PF 27-AUG-1997; 97WO-US15166.
XX PR 21-JUL-1997; 97US-0897342.
XX PR 27-AUG-1996; 96US-0703675.
XX PA (PRAE-) PRAECIS PHARM INC.
XX PI Arico-muendel CC, Chin J, Findeis MA, Geffer ML;
XX PI Hayward NJ, Kelley M, Komar-panicucci S, Lee J, Molineaux S;
XX PI Musso G, Phillips K, Signer ER, Wakefield J;
XX DR WPI; 1998-216936/19.
XX PS Peptide compounds which are preferably based on beta-amyloid
XX PT peptide(s) - are useful in treatment of disorders related to
XX PT beta-amyloidosis, especially Alzheimer's disease
XX PS Claim 1; Page 76; 92pp; English.
XX CC The invention relates to peptides that modulate natural beta-amyloid
XX CC peptide aggregation. The modulators of the invention comprise a peptide
XX CC preferably based on a beta-amyloid peptide, that is comprised entirely
XX CC of D-amino acids. Preferably the peptide comprises 3-5 D-amino acid
XX CC residues and includes at least two D-amino acid residues independently
XX CC selected from the group consisting of D-leucine, D-phenylalanine and
XX CC D-valine. Preferred amino-terminal modifying groups include cyclic,
XX CC heterocyclic, polycyclic and branched alkyl groups. Preferred
XX CC carboxy-terminal modifying groups include an amide group, an alkyl amide
XX CC group, an aryl amide group or a hydroxy group. The peptides may be used
XX CC to treat disorders associated with beta-amyloidosis, especially
XX CC Alzheimer's disease. They may also be used in methods for detecting the
XX CC presence of beta-amyloid peptides in biological samples. The present
XX CC sequence represents a specifically claimed peptide.
XX SQ Sequence 5 AA;
XX Query Match 33.3%; Score 4; DB 19; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FFPL 5
DB 2 FFPL 5
XX RESULT 39
XX AAY49991
XX ID AAY49991 standard; peptide; 5 AA.
XX XX

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```

AC AAY49991;
XX
DT 04-FEB-2000 (first entry)
XX
DE Natural beta amyloid peptide aggregation modulating peptide #19.
XX
KW Beta amyloid peptide aggregation; modulation; D-amino acid; diagnosis;
KW retro-inverso isomer; amyloidogenic disease; Alzheimer's disease;
KW Down's syndrome; hereditary cerebral haemorrhage; HCHWA-D;
KW amyloidosis-Dutch-type.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..5 /note= "D-form residues"
XX
XX US5985242-A.
XX
PD 16-NOV-1999.
XX
XX 27-AUG-1997; 97US-0920162.
XX
PR 27-OCT-1995; 95US-0548998.
PR 14-MAR-1996; 96US-0616081.
PR 27-AUG-1996; 96US-0703675.
PR 21-JUL-1997; 97US-0897342.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX
PI Wakefield J, Molineaux S, Signer ER, Kelley M, Komar-Panicucci S;
PI Musso G, Phillips K, Hayward NJ, Geftter ML, Findeis MA, Lee J;
PI Arico-Muendel CC, Chin J;
XX
XX WPI; 2000-022266/02.
XX
XX Compound comprising a peptidic structure, an amino-terminal modifying
XX group and a carboxy-terminal modifying group, useful for treating
XX Alzheimer's disease -
XX
XX Claim 1; Column 61; 40pp; English.
XX
CC The present invention describes a compound of formula A-(Xaa)-B,
CC comprising a peptidic structure (Xaa), an amino-terminal modifying
CC group (A), and a carboxy-terminal modifying group (B). AAY49973 to
CC AAY49994 represent specifically claimed examples of (Xaa). Also
CC described is a method for inhibiting aggregation of natural beta-amyloid
CC peptides and treating Alzheimer's disease, comprising contacting the
CC amyloid peptides with A-(Xaa)-B; and a method for detecting the presence
CC of natural beta-amyloid peptides in a biological sample by contacting
CC with A-(Xaa)-B. The compound is useful for treating Alzheimer's disease
CC and for detecting the presence of natural beta-amyloid peptides in a
CC biological sample. The compound can also be used prophylactically or
CC therapeutically to treat other clinical occurrences of beta-amyloid
CC deposition, such as in Down's syndrome individuals and in patients with
CC hereditary cerebral haemorrhage with amyloidosis-Dutch-type (HCHWA-D).
XX
SQ Sequence 5 AA;
Query Match 33.3%; Score 4; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FFFL 5
Db 1 FFFL 4
RESULT 40
AAY49992
ID AAY49992 standard; peptide; 5 AA.
XX

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AC AAY49992;
XX
DT 04-FEB-2000 (first entry)
XX
DE Natural beta amyloid peptide aggregation modulating peptide #20.
XX
KW Beta amyloid peptide aggregation; modulation; D-amino acid; diagnosis;
KW retro-inverso isomer; amyloidogenic disease; Alzheimer's disease;
KW Down's syndrome; hereditary cerebral haemorrhage; HCHWA-D;
KW amyloidosis-Dutch-type.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..5 /note= "D-form residues"
XX
XX US5985242-A.
XX
PD 16-NOV-1999.
XX
XX 27-AUG-1997; 97US-0920162.
XX
PR 27-OCT-1995; 95US-0548998.
PR 14-MAR-1996; 96US-0616081.
PR 27-AUG-1996; 96US-0703675.
PR 21-JUL-1997; 97US-0897342.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX
PI Wakefield J, Molineaux S, Signer ER, Kelley M, Komar-Panicucci S;
PI Musso G, Phillips K, Hayward NJ, Geftter ML, Findeis MA, Lee J;
PI Arico-Muendel CC, Chin J;
XX
XX WPI; 2000-022266/02.
XX
XX Compound comprising a peptidic structure, an amino-terminal modifying
XX group and a carboxy-terminal modifying group, useful for treating
XX Alzheimer's disease -
XX
XX Claim 1; Column 61; 40pp; English.
XX
CC The present invention describes a compound of formula A-(Xaa)-B,
CC comprising a peptidic structure (Xaa), an amino-terminal modifying
CC group (A), and a carboxy-terminal modifying group (B). AAY49973 to
CC AAY49994 represent specifically claimed examples of (Xaa). Also
CC described is a method for inhibiting aggregation of natural beta-amyloid
CC peptides and treating Alzheimer's disease, comprising contacting the
CC amyloid peptides with A-(Xaa)-B; and a method for detecting the presence
CC of natural beta-amyloid peptides in a biological sample by contacting
CC with A-(Xaa)-B. The compound is useful for treating Alzheimer's disease
CC and for detecting the presence of natural beta-amyloid peptides in a
CC biological sample. The compound can also be used prophylactically or
CC therapeutically to treat other clinical occurrences of beta-amyloid
CC deposition, such as in Down's syndrome individuals and in patients with
CC hereditary cerebral haemorrhage with amyloidosis-Dutch-type (HCHWA-D).
XX
SQ Sequence 5 AA;
Query Match 33.3%; Score 4; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FFFL 5
Db 2 FFFL 5
RESULT 41
AAY49993
ID AAY49993 standard; peptide; 5 AA.
XX

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AC AAY49993;
 XX 04-FEB-2000 (first entry)
 DT
 XX
 DE Natural beta amyloid peptide aggregation modulating peptide #21.
 XX
 KW Beta amyloid peptide aggregation; modulation; D-amino acid; diagnosis;
 KW retro-inverso isomer; amyloidogenic disease; Alzheimer's disease;
 KW Down's syndrome; hereditary cerebral haemorrhage; HCHWA-B;
 KW amyloidosis-Dutch-type.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..5
 FT /note= "D-form residues"
 FT
 XX US5985242-A.
 XX 16-NOV-1999.
 XX
 XX 27-AUG-1997; 97US-0920162.
 XX
 XX 27-OCT-1995; 95US-0548998.
 PR 14-MAR-1996; 96US-0616081.
 PR 27-AUG-1996; 96US-0703675.
 PR 21-JUL-1997; 97US-0897342.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PI Wakefield J, Molineaux S, Signer ER, Kelley M, Komar-Panicucci S;
 PI Musso G, Phillips K, Hayward NJ, Gefter ML, Findeis MA, Lee J;
 PI Arico-Muendel CC, Chin J;
 XX
 DR WPI; 2000-022266/02.
 XX
 XX Compound comprising a peptidic structure, an amino-terminal modifying
 PT group and a carboxy-terminal modifying group, useful for treating
 PT Alzheimer's disease -
 XX
 PS Claim 1; Column 61; 40pp; English.
 XX
 CC The present invention describes a compound of formula A-(Xaa)-B
 CC comprising a peptidic structure (Xaa), an amino-terminal modifying
 CC group (A), and a carboxy-terminal modifying group (B). AAY49973 to
 CC AAY49994 represent specifically claimed examples of (Xaa). Also
 CC described is a method for inhibiting aggregation of natural beta-amyloid
 CC peptides and treating Alzheimer's disease, comprising contacting the
 CC of natural beta-amyloid peptides in a biological sample by contacting
 CC with A-(Xaa)-B. The compound is useful for treating Alzheimer's disease
 CC and for detecting the presence of natural beta-amyloid peptides in a
 CC biological sample. The compound can also be used prophylactically or
 CC therapeutically to treat other clinical occurrences of beta-amyloid
 CC deposition, such as in Down's syndrome individuals and in patients with
 CC hereditary cerebral haemorrhage with amyloidosis-Dutch-type (HCHWA-D).
 XX
 SQ Sequence 5 AA;
 Query Match 33.3%; Score 4; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FFPL 5
 DB 2 FFPL 5
 RESULT 42
 AA012530
 ID AA012530 standard; peptide; 5 AA.
 XX

AC AA012530;
 XX 03-JAN-2002 (first entry)
 DT
 XX
 DE APP70 abeta peptide (residues 17-21) inverso isomer mutant.
 XX
 KW Beta-amyloid peptide; beta-AP; Abeta peptide; therapy; beta-amyloidosis;
 KW Alzheimer's disease; neuroprotective; beta-amyloid precursor protein;
 KW APP-770; nontropic; mutant; mutein.
 XX
 OS Unidentified.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..5
 FT /note= "D-form residues"
 FT Misc-difference 1
 FT /note= "Wild-type Ala substituted with Phe; corresponds
 FT to position 21 of natural Abeta peptide"
 FT
 FT Misc-difference 4
 FT /note= "Wild-type Val substituted with Leu; corresponds
 FT to position 18 of natural Abeta peptide"
 FT
 FT Misc-difference 5
 FT /note= "Wild-type Leu substituted with Val; corresponds
 FT to position 17 of natural Abeta peptide; Optionally
 FT C-terminal amide"
 XX
 PN US6277826-B1.
 XX 21-AUG-2001.
 XX
 XX 19-JUL-1999; 99US-0356931.
 XX
 XX 27-AUG-1997; 97US-0920162.
 PR 27-AUG-1996; 96US-0703675.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA
 XX Findeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;
 PI Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;
 PI Arico-Muendel CC, Phillips K, Hayward NJ;
 XX
 DR WPI; 2001-637856/73.
 XX
 XX Modulator compound for treating disorders associated with
 PT beta-amyloidosis e.g. Alzheimer's disease, comprises a beta-amyloid
 PT peptide containing D-amino acids -
 XX
 PS Example 11; Column 48; 41pp; English.
 XX
 CC The patent discloses compounds and pharmaceutical compositions thereof,
 CC that can bind to natural beta amyloid peptide (beta-AP; Abeta peptide),
 CC modulate the aggregation of natural beta-AP and/or inhibit the cyto-
 CC toxicity of natural beta-APs. The beta-amyloid modulator compounds of
 CC the invention comprise a peptide, preferably based on beta-AP, that is
 CC composed entirely of D-amino acids. The modulators of the invention are
 CC useful for treating a disorder associated with beta-amyloidosis such as
 CC Alzheimer's disease. The present sequence is an inverso isomer mutant
 CC (L17V; V18L; A21F) of Abeta peptide. Beta AP is a cleavage product of
 CC beta amyloid precursor protein (APP-770; residues 17-21).
 XX
 SQ Sequence 5 AA;
 Query Match 33.3%; Score 4; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FFPL 5
 DB 1 FFPL 4
 RESULT 43
 AA012531

ID	AAE12531	standard; peptide; 5 AA.
XX	AAE12531;	
XX	AAE12531;	
XX	03-JAN-2002	(first entry)
XX	APP70	abeta peptide (residues 17-21) inverse isomer mutant (V18F; A21F).
XX	Beta-amyloid peptide; beta-AP; Abeta peptide; therapy; beta-amyloidosis; Alzheimer's disease; neuroprotective; beta-amyloid precursor protein; APP-770; nootropic; mutant; mutein.	
XX	Unidentified.	
XX	Key	Location/Qualifiers
XX	Misc-difference 1..5	/note= "D-form residues"
XX	Misc-difference 1	/note= "Wild-type Val substituted with Phe; corresponds to position 21 of natural Abeta peptide"
XX	Misc-difference 4	/note= "Wild-type Val substituted with Phe; corresponds to position 18 of natural Abeta peptide"
XX	Modified-site 5	/note= "Optionally C-terminal amide"
XX	US6277826-B1.	
XX	21-AUG-2001.	
XX	19-JUL-1999;	99US-0356931.
XX	27-AUG-1997;	97US-0920162.
XX	27-AUG-1996;	96US-0703675.
XX	(PRAE-) PRACIS PHARM INC.	
XX	Findeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;	
XX	Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;	
XX	Arico-Muendel CC, Phillips K, Hayward NJ;	
XX	WPI; 2001-637856/73.	
XX	Modulator compound for treating disorders associated with beta-amyloidosis e.g. Alzheimer's disease, comprises a beta-amyloid peptide containing D-amino acids	
XX	Example 11; Column 48; 41pp; English.	
XX	The patent discloses compounds and pharmaceutical compositions thereof, that can bind to natural beta amyloid peptide (beta-AP; Abeta peptide), modulate the aggregation of natural beta-AP and/or inhibit the cytotoxicity of natural beta-APs. The beta-amyloid modulator compounds of the invention comprise a peptide, preferably based on beta-AP, that is composed entirely of D-amino acids. The modulators of the invention are useful for treating a disorder associated with beta-amyloidosis such as Alzheimer's disease. The present sequence is an inverse isomer mutant (V18F; A21F) of Abeta peptide. Beta AP is a cleavage product of beta amyloid precursor protein (APP-770; residues 17-21).	
XX	Sequence	5 AA;
XX	Query Match	33.3%; Score 4; DB 22; Length 5;
XX	Best Local Similarity	100.0%; Pred. No. 9.3e+05;
XX	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	QY	2 FFFL 5
XX	Db	2 FFFL 5
XX	RESULT 44	
XX	AAE12532	standard; peptide; 5 AA.
XX	AAE12532;	
XX	03-JAN-2002	(first entry)
XX	APP70	abeta peptide (residues 17-21) retro inverse isomer mutant (V18F).
XX	Beta-amyloid peptide; beta-AP; Abeta peptide; therapy; beta-amyloidosis; Alzheimer's disease; neuroprotective; beta-amyloid precursor protein; APP-770; nootropic; mutant; mutein.	
XX	Unidentified.	
XX	Key	Location/Qualifiers
XX	Misc-difference 1..5	/note= "D-form residues"
XX	Misc-difference 1	/note= "Wild-type Val substituted with Phe; corresponds to position 21 of natural Abeta peptide"
XX	Misc-difference 4	/note= "Wild-type Val substituted with Phe; corresponds to position 18 of natural Abeta peptide"
XX	Modified-site 5	/note= "Optionally C-terminal amide"
XX	US6277826-B1.	
XX	21-AUG-2001.	
XX	19-JUL-1999;	99US-0356931.
XX	27-AUG-1997;	97US-0920162.
XX	27-AUG-1996;	96US-0703675.
XX	(PRAE-) PRACIS PHARM INC.	
XX	Findeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;	
XX	Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;	
XX	Arico-Muendel CC, Phillips K, Hayward NJ;	
XX	WPI; 2001-637856/73.	
XX	Modulator compound for treating disorders associated with beta-amyloidosis e.g. Alzheimer's disease, comprises a beta-amyloid peptide containing D-amino acids	
XX	Example 11; Column 48; 41pp; English.	
XX	The patent discloses compounds and pharmaceutical compositions thereof, that can bind to natural beta amyloid peptide (beta-AP; Abeta peptide), modulate the aggregation of natural beta-AP and/or inhibit the cytotoxicity of natural beta-APs. The beta-amyloid modulator compounds of the invention comprise a peptide, preferably based on beta-AP, that is composed entirely of D-amino acids. The modulators of the invention are useful for treating a disorder associated with beta-amyloidosis such as Alzheimer's disease. The present sequence is an inverse isomer mutant (V18F; A21F) of Abeta peptide. Beta AP is a cleavage product of beta amyloid precursor protein (APP-770; residues 17-21).	
XX	Sequence	5 AA;
XX	Query Match	33.3%; Score 4; DB 22; Length 5;
XX	Best Local Similarity	100.0%; Pred. No. 9.3e+05;
XX	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	QY	2 FFFL 5
XX	Db	2 FFFL 5
XX	RESULT 45	
XX	AAE10004	
XX	ID	AAE10004 standard; peptide; 5 AA.
XX	AAE10004;	

XX DT 29-NOV-2001 (first entry)
 XX AC Beta-amyloid peptide derivative #19.
 XX DE
 XX KW Drug bioavailability; beta-amyloid peptide derivative; CNS disorder;
 KW central nervous system; multidrug resistance; liver cirrhosis;
 KW cardiovascular disorder; neuromuscular disorder; Parkinson's disease;
 KW neurodegenerative disorder; Alzheimer's disease; multiple sclerosis;
 KW cancer; glioblastoma; stroke; traumatic brain injury; hepatic injury;
 KW psychiatric disorder; P-glycoprotein inhibitor; hepatic fibrosis.
 XX OS Synthetic.
 XX KW
 XX FH Key Location/Qualifiers
 FT Misc-difference 1..4 /note= "D-form residues"
 FT Modified-site 5
 FT /note= "D-form residue; optionally C-terminal amide
 FT which is particularly preferred"
 PN WO200158470-A2.
 XX PD 16-AUG-2001.
 XX PF 09-FEB-2001; 2001WO-US04178.
 XX PR 11-FEB-2000; 2000US-0181833.
 XX PR 11-FEB-2000; 2000US-0181943.
 XX PA (PRAE-) PRAECIS PHARM INC.
 XX PI Hayward NJ, Gefter ML;
 XX DR WPI; 2001-557599/62.
 XX PT Enhancing the bioavailability of a drug, for e.g. in the brain of a
 PT subject suffering from Alzheimer's disease, comprising administering a
 PT hydrophobic peptide (e.g. a beta-amyloid peptide derivative) with the
 PT drug -
 XX PS Disclosure; Page 27; 86pp; English.
 CC The invention relates to a method for enhancing bioavailability
 CC of a drug in a subject, comprising administering the drug with a
 CC hydrophobic peptide e.g. a beta-amyloid peptide derivative. The method
 CC is useful for enhancing bioavailability of a drug in subjects suffering
 CC from central nervous system (CNS) disorder, disorder characterised by
 CC multidrug resistance, cardiovascular disorder and neuromuscular disorder.
 CC The CNS disorder includes neurodegenerative disorder (e.g. Alzheimer's
 CC disease, Parkinson's disease, multiple sclerosis), cancer (e.g.
 CC glioblastoma), stroke, traumatic brain injury, and psychiatric disorder.
 CC The invention also relates to a method for treating or preventing hepatic
 CC injury using P-glycoprotein inhibitor. Examples of hepatic injury include
 CC hepatic fibrosis, cirrhosis, hepatic injury caused by a drug, injury due
 CC to prolonged ethanol uptake or due to carbon tetrachloride exposure.
 CC The present sequence is a beta-amyloid peptide derivative useful for
 CC enhancing bioavailability of a drug in a subject. The peptide is
 CC designed based on retro-inverso isomer of Abeta aggregation core domain
 CC (ACD, residues 17-21) of the beta-amyloid peptide.
 XX SQ Sequence 5 AA;
 Query Match 33.3%; Score 4; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PFLL 5
 ||||
 Db 1 PFLL 4

RESULT 46

AAE10005
 ID AAE10005 standard; peptide; 5 AA.
 XX AC AAE10005;
 XX DT 29-NOV-2001 (first entry)
 XX DE Beta-amyloid peptide derivative #20.
 XX KW Drug bioavailability; beta-amyloid peptide derivative; CNS disorder;
 KW central nervous system; multidrug resistance; liver cirrhosis;
 KW cardiovascular disorder; neuromuscular disorder; Parkinson's disease;
 KW neurodegenerative disorder; Alzheimer's disease; multiple sclerosis;
 KW cancer; glioblastoma; stroke; traumatic brain injury; hepatic injury;
 KW psychiatric disorder; P-glycoprotein inhibitor; hepatic fibrosis.
 XX OS Synthetic.
 XX KW
 XX FH Key Location/Qualifiers
 FT Misc-difference 1..4 /note= "D-form residues"
 FT Modified-site 5
 FT /note= "D-form residue; optionally C-terminal amide
 FT which is particularly preferred"
 PN WO200158470-A2.
 XX PD 16-AUG-2001.
 XX PF 09-FEB-2001; 2001WO-US04178.
 XX PR 11-FEB-2000; 2000US-0181833.
 XX PR 11-FEB-2000; 2000US-0181943.
 XX PA (PRAE-) PRAECIS PHARM INC.
 XX PI Hayward NJ, Gefter ML;
 XX DR WPI; 2001-557599/62.
 XX PT Enhancing the bioavailability of a drug, for e.g. in the brain of a
 PT subject suffering from Alzheimer's disease, comprising administering a
 PT hydrophobic peptide (e.g. a beta-amyloid peptide derivative) with the
 PT drug -
 XX PS Disclosure; Page 27; 86pp; English.
 CC The invention relates to a method for enhancing bioavailability
 CC of a drug in a subject, comprising administering the drug with a
 CC hydrophobic peptide e.g. a beta-amyloid peptide derivative. The method
 CC is useful for enhancing bioavailability of a drug in subjects suffering
 CC from central nervous system (CNS) disorder, disorder characterised by
 CC multidrug resistance, cardiovascular disorder and neuromuscular disorder.
 CC The CNS disorder includes neurodegenerative disorder (e.g. Alzheimer's
 CC disease, Parkinson's disease, multiple sclerosis), cancer (e.g.
 CC glioblastoma), stroke, traumatic brain injury, and psychiatric disorder.
 CC The invention also relates to a method for treating or preventing hepatic
 CC injury using P-glycoprotein inhibitor. Examples of hepatic injury include
 CC hepatic fibrosis, cirrhosis, hepatic injury caused by a drug, injury due
 CC to prolonged ethanol uptake or due to carbon tetrachloride exposure.
 CC The present sequence is a beta-amyloid peptide derivative useful for
 CC enhancing bioavailability of a drug in a subject. The peptide is
 CC designed based on retro-inverso isomer of Abeta aggregation core domain
 CC (ACD, residues 17-21) of the beta-amyloid peptide.
 XX SQ Sequence 5 AA;
 Query Match 33.3%; Score 4; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PFLL 5
 ||||

Db	2 FFFL 5	Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
RESULT 47											
AAE10006											
ID	AAE10006 standard; peptide; 5 AA.										
XX											
AC	AAE10006;										
XX											
DT	29-NOV-2001 (first entry)										
XX											
DE	Beta-amyloid peptide derivative #21.										
XX											
KW	Drug bioavailability; beta-amyloid peptide derivative; CNS disorder;										
KW	central nervous system; multidrug resistance; liver cirrhosis;										
KW	cardiovascular disorder; neuromuscular disorder; Parkinson's disease;										
KW	neurodegenerative disorder; Alzheimer's disease; multiple sclerosis;										
KW	cancer; glioblastoma; stroke; traumatic brain injury; hepatic injury;										
KW	psychiatric disorder; P-glycoprotein inhibitor; hepatic fibrosis.										
XX											
OS	Synthetic.										
XX											
FH	Key Location/Qualifiers										
FT	Misc-difference 1..4										
FT	Modified-site 5										
FT	/note= "D-form residues"										
FT	/note= "D-form residue; optionally C-terminal amide										
FT	which is particularly preferred"										
XX											
PN	WO200158470-A2.										
XX											
PD	16-AUG-2001.										
XX											
DF	09-FEB-2001; 2001WO-US04178.										
XX											
PR	11-FEB-2000; 2000US-0181833.										
PR	11-FEB-2000; 2000US-0181943.										
XX											
PA	(PRAE-) PRAECIS PHARM INC.										
XX											
PI	Hayward NJ, Geffer ML;										
XX											
DR	WPI; 2001-557599/62.										
XX											
PT	Enhancing the bioavailability of a drug, for e.g. in the brain of a										
PT	subject suffering from Alzheimer's disease, comprising administering a										
PT	hydrophobic peptide (e.g. a beta-amyloid peptide derivative) with the										
PT	drug -										
XX											
PS	Disclosure; Page 27; 86pp; English.										
XX											
CC	The invention relates to a method for enhancing bioavailability										
CC	of a drug in a subject, comprising administering the drug with a										
CC	hydrophobic peptide e.g. a beta-amyloid peptide derivative. The method										
CC	is useful for enhancing bioavailability of a drug in subjects suffering										
CC	from central nervous system (CNS) disorder, disorder characterised by										
CC	multidrug resistance, cardiovascular disorder and neuromuscular disorder.										
CC	The CNS disorder includes neurodegenerative disorder (e.g. Alzheimer's										
CC	disease, Parkinson's disease, multiple sclerosis), cancer (e.g.										
CC	glioblastoma), stroke, traumatic brain injury, and psychiatric disorder.										
CC	The invention also relates to a method for treating or preventing hepatic										
CC	injury using P-glycoprotein inhibitor. Examples of hepatic injury include										
CC	hepatic fibrosis, cirrhosis, hepatic injury caused by a drug, injury due										
CC	to prolonged ethanol uptake or due to carbon tetrachloride exposure.										
CC	The present sequence is a beta-amyloid peptide derivative useful for										
CC	enhancing bioavailability of a drug in a subject. The peptide is										
CC	designed based on retro-inverso isomer of Abeta. The peptide is										
CC	(ACD, residues 17-21) of the beta-amyloid peptide.										
XX											
SQ	Sequence 5 AA;										
Query Match	33.3%; Score 4; DB 22; Length 5;										
Best Local Similarity	100.0%; Pred. No. 9.3e+05;										

Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	2 FFFL 5								
Db	2 FFFL 5								
RESULT 48									
AAE26294									
ID	AAE26294 standard; peptide; 5 AA.								
XX									
AC	AAE26294;								
XX									
DT	14-NOV-2002 (first entry)								
XX									
DE	Peptide #16 capable of binding an amyloidogenic protein.								
XX									
KW	Amyloidogenic protein; Alzheimer's disease; Huntington's disease;								
KW	spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis;								
KW	Gerstmann-Strausler-Scheinker syndrome; spongiform encephalopathy; GSS;								
KW	Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytis; myeloma;								
KW	CJ.								
XX									
OS	Unidentified.								
XX									
FH	Key Location/Qualifiers								
FT	Misc-difference 1..5								
FT	/note= "D-form residues"								
XX									
PN	WO200242462-A2.								
XX									
PD	30-MAY-2002.								
XX									
PF	27-NOV-2001; 2001WO-US44581.								
XX									
PR	27-NOV-2000; 2000US-253302P.								
PR	29-NOV-2000; 2000US-250198P.								
PR	20-DEC-2000; 2000US-257186P.								
XX									
PA	(PRAE-) PRAECIS PHARM INC.								
XX									
PI	Geffer ML, Israel DI, Joyal JL, Gosselin M;								
XX									
DR	WPI; 2002-636427/68.								
XX									
PT	Novel therapeutic agent useful for treating an amyloidogenic disorder,								
PT	e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain								
PT	constant region linked to a peptide capable of binding amyloidogenic								
PT	protein -								
XX									
PS	Claim 18; Page 54; 79pp; English.								
XX									
CC	The invention relates to a compound comprising an immunoglobulin (Ig)								
CC	heavy chain constant region or its fragment that retains the ability								
CC	to bind an Fc receptor linked by a linker group or a direct bond to a								
CC	peptide capable of binding an amyloidogenic protein. The invention is								
CC	useful for clearing an amyloidogenic protein such as beta-amyloid,								
CC	transferrin (TTR), prion protein (PrP), islet amyloid polypeptide								
CC	(IAPP), atrial natriuretic factor (ANF), kappa light chain, lambda								
CC	light chain, amyloid A, procalsitonin, cystatin C, beta2-microglobulin,								
CC	ApoA-I, gelsolin, calcitonin, fibrinogen, Huntington, alpha-synuclein								
CC	and lysozyme from a subject and for treating an amyloidogenic disorder								
CC	such as Alzheimer's disease and spongiform encephalopathy. Disorders								
CC	treatable include those caused or characterised by deposits of TTR (eg.								
CC	familial amyloid cardiomyopathy), Prp (eg. spongiform encephalopathies,								
CC	including scrapie in sheep, bovine spongiform encephalopathy in cows								
CC	and Creutzfeldt-Jacob disease (CJ) and Gerstmann-Strausler-Scheinker								
CC	syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes),								
CC	ANF (eg. isolated atrial amyloid), kappa or lambda light chain (eg. A-I								
CC	idiopathic amyloidosis, myeloma), amyloid A (eg. amyloidosis), Apo A-I								
CC	(eg. hereditary non-neuropathic systemic amyloidosis), Gelsolin (eg.								
CC	familial amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal								
CC	amyloidosis), lysozyme (eg. hereditary systemic amyloidosis). Other								

CC examples of amyloidogenic disorders include Huntington's disease and
 CC inclusion body myocytis. The present sequence is a peptide capable of
 CC binding an amyloidogenic protein.
 XX
 SQ Sequence 5 AA;
 Query Match 33.3%; Score 4; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FFFL 5
 DB 1 FFFL 4
 RESULT 49
 AAE26295
 ID AAE26295 standard; peptide; 5 AA.
 AC
 XX AAE26295;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Peptide #17 capable of binding an amyloidogenic protein.
 XX
 KW Amyloidogenic protein; Alzheimer's disease; Huntington's disease;
 KW spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis;
 KW Gerstmann-Straussler-Scheinker syndrome; spongiform encephalopathy; GSS;
 KW Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytis; myeloma;
 KW CJ.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..5 /note= "D-form residues"
 FT
 XX WO200242462-A2.
 PN
 XX 30-MAY-2002.
 XX
 XX 27-NOV-2001; 2001WO-US44581.
 XX
 XX 27-NOV-2000; 2000US-253302P.
 PR
 XX 29-NOV-2000; 2000US-250198P.
 PR
 XX 20-DEC-2000; 2000US-257186P.
 XX
 XX (PRAE-) PRAECTIS PHARM INC.
 XX
 XX Geffer ML, Israel DI, Joyal JL, Gosselin M;
 XX WPI; 2002-636427/68.
 XX
 XX Novel therapeutic agent useful for treating an amyloidogenic disorder,
 PT e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain
 PT constant region linked to a peptide capable of binding amyloidogenic
 PT protein -
 XX
 XX Claim 18; Page 54; 79pp; English.
 XX
 XX The invention relates to a compound comprising an immunoglobulin (Ig)
 CC heavy chain constant region or its fragment that retains the ability
 CC to bind an FC receptor linked by a linker group or a direct bond to a
 CC peptide capable of binding an amyloidogenic protein. The invention is
 CC useful for clearing an amyloidogenic protein such as beta-amyloid,
 CC transthyretin (TTR), prion protein (PrP), Islet amyloid polypeptide
 CC (IAPP), atrial natriuretic factor (ANF), kappa light chain, lambda
 CC light chain, amyloid A, procainitonin, cystatin C, beta2-microglobulin,
 CC ApoA-I, gelsolin, calcitonin, fibrinogen, Huntington, alpha-synuclein
 CC and lysozyme from a subject and for treating an amyloidogenic disorder
 CC such as Alzheimer's disease and spongiform encephalopathy. Disorders
 CC treatable include those caused or characterised by deposits of TTR (eg.
 CC familial amyloid cardiomyopathy), PrP (eg. spongiform encephalopathies,

CC including scrapie in sheep, bovine spongiform encephalopathy in cows
 CC and Creutzfeldt-Jacob disease (CJ) and Gerstmann-Straussler-Scheinker
 CC syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes),
 CC ANP (eg. isolated atrial amyloid), kappa or lambda light chain (eg. A-I
 CC idiopathic amyloidosis, myeloma), amyloid A (eg. amyloidosis), Apo A-I
 CC (eg. hereditary non-neuropathic systemic amyloidosis), Gelsolin (eg.
 CC familial amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal
 CC amyloidosis), Lysozyme (eg. hereditary systemic amyloidosis). Other
 CC examples of amyloidogenic disorders include Huntington's disease and
 CC inclusion body myocytis. The present sequence is a peptide capable of
 CC binding an amyloidogenic protein.
 XX
 SQ Sequence 5 AA;
 Query Match 33.3%; Score 4; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FFFL 5
 DB 2 FFFL 5
 RESULT 50
 AAE26296
 ID AAE26296 standard; peptide; 5 AA.
 XX
 AC AAE26296;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Peptide #18 capable of binding an amyloidogenic protein.
 XX
 KW Amyloidogenic protein; Alzheimer's disease; Huntington's disease;
 KW spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis;
 KW Gerstmann-Straussler-Scheinker syndrome; spongiform encephalopathy; GSS;
 KW Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytis; myeloma;
 KW CJ.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..5 /note= "D-form residues"
 FT
 XX WO200242462-A2.
 PN
 XX 30-MAY-2002.
 XX
 XX 27-NOV-2001; 2001WO-US44581.
 XX
 XX 27-NOV-2000; 2000US-253302P.
 PR
 XX 29-NOV-2000; 2000US-250198P.
 PR
 XX 20-DEC-2000; 2000US-257186P.
 XX
 XX (PRAE-) PRAECTIS PHARM INC.
 XX
 XX Geffer ML, Israel DI, Joyal JL, Gosselin M;
 XX WPI; 2002-636427/68.
 XX
 XX Novel therapeutic agent useful for treating an amyloidogenic disorder,
 PT e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain
 PT constant region linked to a peptide capable of binding amyloidogenic
 PT protein -
 XX
 XX Claim 18; Page 54; 79pp; English.
 XX
 XX The invention relates to a compound comprising an immunoglobulin (Ig)
 CC heavy chain constant region or its fragment that retains the ability
 CC to bind an FC receptor linked by a linker group or a direct bond to a
 CC peptide capable of binding an amyloidogenic protein. The invention is
 CC useful for clearing an amyloidogenic protein such as beta-amyloid,
 CC transthyretin (TTR), prion protein (PrP), Islet amyloid polypeptide
 CC (IAPP), atrial natriuretic factor (ANF), kappa light chain, lambda
 CC light chain, amyloid A, procainitonin, cystatin C, beta2-microglobulin,
 CC ApoA-I, gelsolin, calcitonin, fibrinogen, Huntington, alpha-synuclein
 CC and lysozyme from a subject and for treating an amyloidogenic disorder
 CC such as Alzheimer's disease and spongiform encephalopathy. Disorders
 CC treatable include those caused or characterised by deposits of TTR (eg.
 CC familial amyloid cardiomyopathy), PrP (eg. spongiform encephalopathies,

CC transthyretin (TTR), prion protein (PrP), islet amyloid polypeptide (IAPP), atrial natriuretic factor (ANF), kappa light chain, lambda light chain, amyloid A, procalcitonin, cystatin C, beta2-microglobulin, ApoA-I, gelsolin, calcitonin, fibrinogen, Huntington, alpha-synuclein and lysozyme from a subject and for treating an amyloidogenic disorder such as Alzheimer's disease and spongiform encephalopathy. Disorders treatable include those caused or characterised by deposits of TTR (eg. familial amyloid cardiomyopathy), PrP (eg. spongiform encephalopathies, including scrapie in sheep, bovine spongiform encephalopathy in cows and Creutzfeldt-Jacob disease (CJ) and Gerstmann-Strausler-Scheinker syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes), ANF (eg. isolated atrial amyloid), kappa or lambda light chain (eg. A-I idiopathic amyloidosis, myeloma), amyloid A (eg. amyloidosis), Apo A-I (eg. hereditary non-neuropathic systemic amyloidosis), Gelsolin (eg. familial amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal amyloidosis), lysozyme (eg. hereditary systemic amyloidosis). Other examples of amyloidogenic disorders include Huntington's disease and inclusion body myocytis. The present sequence is a peptide capable of binding an amyloidogenic protein.

XX
SQ Sequence 5 AA;

Query Match 33.3%; Score 4; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5
Db 2 FFPL 5

RESULT 51
AAE15197
ID AAE15197 standard; peptide; 5 AA.
AC AAE15197;
XX
XX
DT 07-MAR-2002 (first entry)
DE Human HGF receptor chain analogue peptide #1.
XX
XX
KW Human; N-oxalyl peptide; therapeutic; prophylactic; treatment; psoriasis;
KW downstream signal transduction pathway; HGF receptor chain analogue;
XX tumour; Sem-5/Grb2 SH2 binding protein.
OS Homo sapiens.
XX
XX US6307090-B1.
PD 23-OCT-2001.
XX
PF 22-JAN-1999; 99US-0236160.
XX
PR 22-JAN-1999; 99US-0236160.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Burke TR, Yao Z, King CR;
XX
DR WPI; 2002-033269/04.
XX
PT New acylated oligopeptides having cell signal inhibiting activity are
PT useful in the treatment of e.g. psoriasis -
XX
PS Disclosure; Column 10; 42pp; English.
XX
CC The present invention relates to pharmaceutically active compounds comprising N-oxalyl peptide structure. The compounds of the invention are used in the therapeutic or prophylactic treatment of warm-blooded animal or human body e.g. tumour and psoriasis. They are useful in the diagnostic treatment of diseases depending on the downstream signal transduction pathway. The present peptide sequence is human HGF receptor chain analogue of Sem-5/Grb2 SH2 binding proteins. This

CC peptide is present in the compound of the invention.

XX
SQ Sequence 5 AA;

Query Match 33.3%; Score 4; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VNVL 11
Db 1 VNVL 4

RESULT 52
AAE15232
ID AAE15232 standard; peptide; 5 AA.
XX
AC AAE15232;
XX
DT 07-MAR-2002 (first entry)
DE Human HGF receptor chain analogue peptide #3.
XX
XX
KW Human; N-oxalyl peptide; therapeutic; prophylactic; treatment; psoriasis;
KW downstream signal transduction pathway; HGF receptor chain analogue;
XX tumour; SHPTP2 N-terminal SH2 binding protein.
OS Homo sapiens.
XX
XX US6307090-B1.
PD 23-OCT-2001.
XX
PF 22-JAN-1999; 99US-0236160.
XX
PR 22-JAN-1999; 99US-0236160.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Burke TR, Yao Z, King CR;
XX
DR WPI; 2002-033269/04.
XX
PT New acylated oligopeptides having cell signal inhibiting activity are
PT useful in the treatment of e.g. psoriasis -
XX
PS Disclosure; Column 11; 42pp; English.
XX
CC The present invention relates to pharmaceutically active compounds comprising N-oxalyl peptide structure. The compounds of the invention are used in the therapeutic or prophylactic treatment of warm-blooded animal or human body e.g. tumour and psoriasis. They are useful in the diagnostic treatment of diseases depending on the downstream signal transduction pathway. The present peptide sequence is an analogue of human HGF receptor chain of SHPTP2 N-terminal SH2 binding proteins. This peptide is present in the compound of the invention.

XX
SQ Sequence 5 AA;

Query Match 33.3%; Score 4; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VNVL 11
Db 1 VNVL 4

RESULT 53
AAE15324
ID AAE15324 standard; peptide; 5 AA.
XX
AC AAE15324;

XX 07-MAR-2002 (first entry)
 XX Peptide #5 related to pharmaceutical compounds of the invention.
 DE N-oxalyl peptide; therapeutic; prophylactic; treatment; psoriasis;
 XX downstream signal transduction pathway; tumour.
 KW Unidentified.
 XX OS US6307090-B1.
 PN 23-OCT-2001.
 XX 22-JAN-1999; 99US-0236160.
 XX 22-JAN-1999; 99US-0236160.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Burke TR, Yao Z, King CR;
 XX WPI; 2002-033269/04.
 XX New acylated oligopeptides having cell signal inhibiting activity are
 PT useful in the treatment of e.g. psoriasis -
 XX Disclosure; Column 63; 42pp; English.
 XX The present invention relates to pharmaceutically active compounds
 CC comprising N-oxalyl peptide structure. The compounds of the invention
 CC are used in the therapeutic or prophylactic treatment of warm-blooded
 CC animal or human body e.g. tumour and psoriasis. They are useful in the
 CC diagnostic treatment of diseases depending on the downstream signal
 CC transduction pathway. The present sequence is a peptide related to
 CC pharmaceutical compounds of the invention.
 XX SQ Sequence 5 AA;
 Query Match 33.3%; Score 4; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 VNVL 11
 Db 1 VNVL 4
 RESULT 54
 ABG73479
 ID ABG73479 standard; Peptide; 5 AA.
 XX AC ABG73479;
 XX 10-MAY-2003 (first entry)
 XX Natural beta-amyloid peptide modulator compound #22.
 DE Natural beta-amyloid peptide; aggregation inhibition; beta-amyloidosis;
 XX Alzheimer's disease; beta-amyloid deposition; Down's syndrome;
 KW hereditary cerebral haemorrhage with amyloidosis-Dutch-type; HCHWA-D;
 KW neurological impairment; neuroprotective; nootropic.
 XX Synthetic.
 XX OS US2002103134-A1.
 PN 01-AUG-2002.
 XX 29-JUN-2001; 2001US-0895443.
 XX 27-AUG-1997; 97US-0920162.
 PR 19-JUL-1999; 99US-0356931.

PR 27-OCT-1995; 95US-0548998.
 PR 14-MAR-1996; 96US-0616081.
 PR 27-AUG-1996; 96US-0703675.
 PR 21-JUL-1997; 97US-0897342.
 XX (PRAE-) PRAECIS PHARM INC.
 XX Findeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;
 PI Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;
 PI Arico-Muendel CC, Phillips K, Hayward NJ;
 XX WPI; 2003-298609/29.
 XX Novel compound that modulate natural beta-amyloid peptide aggregation,
 PT is useful for treating amyloidogenic diseases e.g. Alzheimer's disease
 XX Claim 1; Page 35; 42pp; English.
 XX The invention relates to a compound that modulates natural beta-amyloid
 CC peptide aggregation. The peptide is useful for inhibiting aggregation of
 CC natural beta-amyloid peptides and for treating a disorder associated with
 CC beta-amyloidosis, e.g. Alzheimer's disease. The compound is also useful
 CC for detecting the presence or absence of natural beta-amyloid peptides in
 CC a biological sample, by contacting the biological sample with the
 CC compound in vitro, where the compound is labelled with a detectable
 CC substance and detecting the compound bound to natural beta-amyloid
 CC peptides. The compound is preferably labelled with radioactive technetium
 CC or radioactive iodine and is administered to the subject. The compound is
 CC also useful for prophylactically or therapeutically treating other
 CC clinical occurrences of beta-amyloid deposition such as in Down's
 CC syndrome individuals and in patients with hereditary cerebral haemorrhage
 CC with amyloidosis-Dutch-type (HCHWA-D), and for therapeutically allowing
 CC for the sequestration of beta-amyloid proteins at sites that do not lead
 CC to neurological impairment. This sequence represents a natural
 CC beta-amyloid peptide modulator compound of the invention.
 XX SQ Sequence 5 AA;
 Query Match 33.3%; Score 4; DB 24; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 FFFL 5
 Db 1 FFFL 4
 RESULT 55
 ABG73480
 ID ABG73480 standard; Peptide; 5 AA.
 XX AC ABG73480;
 XX 10-MAY-2003 (first entry)
 XX Natural beta-amyloid peptide modulator compound #23.
 DE Natural beta-amyloid peptide; aggregation inhibition; beta-amyloidosis;
 XX Alzheimer's disease; beta-amyloid deposition; Down's syndrome;
 KW hereditary cerebral haemorrhage with amyloidosis-Dutch-type; HCHWA-D;
 KW neurological impairment; neuroprotective; nootropic.
 XX Synthetic.
 XX OS US2002103134-A1.
 PN 01-AUG-2002.
 XX 29-JUN-2001; 2001US-0895443.
 XX 27-AUG-1997; 97US-0920162.
 PR 19-JUL-1999; 97US-0920162.

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PR 19-JUL-1999; 99US-0356931.
PR 27-OCT-1995; 95US-0548998.
PR 14-MAR-1996; 96US-0616081.
PR 27-AUG-1996; 96US-0703675.
PR 21-JUL-1997; 97US-0897342.
XX (PRAE-) PRACIS PHARM INC.
XX
XX Findeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;
PI Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;
PI Arico-Muendel CC, Phillips K, Hayward NJ;
XX
XX WPI; 2003-298609/29.
XX
XX Novel compound that modulate natural beta-amyloid peptide aggregation,
PT is useful for treating amyloidogenic diseases e.g. Alzheimer's disease
PT
XX
XX Claim 1; Page 35; 42pp; English.
XX
XX The invention relates to a compound that modulates natural beta-amyloid
CC peptide aggregation. The peptide is useful for inhibiting aggregation of
CC natural beta-amyloid peptides and for treating a disorder associated with
CC beta-amyloidosis, e.g. Alzheimer's disease. The compound is also useful
CC for detecting the presence or absence of natural beta-amyloid peptides in
CC a biological sample, by contacting the biological sample with the
CC compound in vitro, where the compound is labelled with a detectable
CC substance and detecting the presence or absence of natural beta-amyloid
CC peptides to thus detect the presence or absence of natural beta-amyloid
CC peptides. The compound is preferably labelled with radioactive technetium
CC or radioactive iodine and is administered to the subject. The compound is
CC also useful for prophylactically or therapeutically treating other
CC clinical occurrences of beta-amyloid deposition such as in Down's
CC syndrome individuals and in patients with hereditary cerebral haemorrhage
CC with amyloidosis-Dutch-type (HCHWA-D), and for therapeutically allowing
CC for the sequestration of beta-amyloid proteins at sites that do not lead
CC to neurological impairment. This sequence represents a natural
CC beta-amyloid peptide modulator compound of the invention.
XX
XX SQ Sequence 5 AA;
XX
XX Query Match 33.3%; Score 4; DB 24; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 FFFL 5
XX ||||
XX Db 2 FFFL 5
XX
XX RESULT 56
XX ABG73481
XX ID ABG73481 standard; Peptide; 5 AA.
XX AC ABG73481;
XX
XX DT 10-MAY-2003 (first entry)
XX
XX DE Natural beta-amyloid peptide modulator compound #24.
XX
XX DE Natural beta-amyloid peptide; aggregation inhibition; beta-amyloidosis;
XX Alzheimer's disease; beta-amyloid deposition; Down's syndrome;
XX hereditary cerebral haemorrhage with amyloidosis-Dutch-type; HCHWA-D;
XX neurological impairment; neuroprotective; nootropic.
XX
XX OS Synthetic.
XX
XX PN US2002103134-A1.
XX
XX PD 01-AUG-2002.
XX
XX PF 29-JUN-2001; 2001US-0895443.
XX

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PR 27-AUG-1997; 97US-0920162.
PR 19-JUL-1999; 99US-0356931.
PR 27-OCT-1995; 95US-0548998.
PR 14-MAR-1996; 96US-0616081.
PR 27-AUG-1996; 96US-0703675.
PR 21-JUL-1997; 97US-0897342.
XX (PRAE-) PRACIS PHARM INC.
XX
XX Findeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;
PI Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;
PI Arico-Muendel CC, Phillips K, Hayward NJ;
XX
XX WPI; 2003-298609/29.
XX
XX Novel compound that modulate natural beta-amyloid peptide aggregation,
PT is useful for treating amyloidogenic diseases e.g. Alzheimer's disease
PT
XX
XX Claim 1; Page 35; 42pp; English.
XX
XX The invention relates to a compound that modulates natural beta-amyloid
CC peptide aggregation. The peptide is useful for inhibiting aggregation of
CC natural beta-amyloid peptides and for treating a disorder associated with
CC beta-amyloidosis, e.g. Alzheimer's disease. The compound is also useful
CC for detecting the presence or absence of natural beta-amyloid peptides in
CC a biological sample, by contacting the biological sample with the
CC compound in vitro, where the compound is labelled with a detectable
CC substance and detecting the presence or absence of natural beta-amyloid
CC peptides to thus detect the presence or absence of natural beta-amyloid
CC peptides. The compound is preferably labelled with radioactive technetium
CC or radioactive iodine and is administered to the subject. The compound is
CC also useful for prophylactically or therapeutically treating other
CC clinical occurrences of beta-amyloid deposition such as in Down's
CC syndrome individuals and in patients with hereditary cerebral haemorrhage
CC with amyloidosis-Dutch-type (HCHWA-D), and for therapeutically allowing
CC for the sequestration of beta-amyloid proteins at sites that do not lead
CC to neurological impairment. This sequence represents a natural
CC beta-amyloid peptide modulator compound of the invention.
XX
XX SQ Sequence 5 AA;
XX
XX Query Match 33.3%; Score 4; DB 24; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 FFFL 5
XX ||||
XX Db 2 FFFL 5
XX
XX RESULT 57
XX AAP40523
XX ID AAP40523 standard; peptide; 6 AA.
XX AC AAP40523;
XX
XX DT 16-AUG-2002 (updated)
XX DT 25-JAN-1992 (first entry)
XX
XX DE Sequence of substance P (a putative CNS neurotransmitter peptide)
XX agonist/antagonist.
XX
XX KW Analgesic; antihypertensive; neurotransmitter substance P.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX Modified-site 1 /label= H-Pro
XX Modified-site 2 /label= D-Phe
XX Modified-site 4
XX

```


CC DNA-binding domain to a library of DNA fragments and introducing this and
 CC a fusion of target protein and a polypeptide containing a region of Gal4
 CC which interacts with Gal4P into a cell containing Gal4P and identifying
 CC members of the library that interact with the target from activation of
 CC transcription. Such constructs are used to activate transcription in a
 CC cell, e.g. for controlling gene activity, particularly in gene therapy
 CC (e.g. recognizing a site close to a selected therapeutic gene).
 CC Transcription can be activated without blocking other transcriptional
 CC activators. They probably act by interacting with a component of the RNA
 CC polymerase II holoenzyme, Gal4, the strongest known yeast activator,
 CC which provides a more sensitive assay allowing detection of even weak
 CC protein-protein interactions. Such activators do not create toxicity
 CC problems even when overexpressed.

XX SQ Sequence 6 AA;

Query Match 33.3%; Score 4; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12
 ||||
 Db 3 NVLP 6

RESULT 60

AAB27043
 ID AAB27043 standard; Peptide; 6 AA.

AC AAB27043;

DT 02-FEB-2001 (first entry)

DE Beta-amyloid peptide modulator #21.

XX Beta-amyloid peptide; nootropic; neuroprotective; Alzheimer's disease;
 KW aggregation core domain.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Misc-difference 1.6 /note= "D-form residues"

FT Modified-site 3 /note= "[pF]Phe"

FT Modified-site 6 /note= "C-terminal amide"

XX PN WO200052048-A1.

XX PD 08-SEP-2000.

XX PF 03-MAR-2000; 2000WO-US05574.

XX PR 04-MAR-1999; 99US-0122736.

XX PA (PRAE-) PRAECIS PHARM INC.

XX PI Findeis MA, Phillips K, Olson GL, Self C;

XX DR WPI; 2000-594168/56.

XX Novel compounds that are useful as modulators of beta-amyloid peptide
 PT aggregation in treating amyloidosis, comprises D-amino acids -
 XX Claim 4; Page 76; 87pp; English.

XX The present invention relates to peptides (see AAB27023-B27046) that
 CC modulate beta-amyloid peptide aggregation, and hence inhibit the
 CC neurotoxicity of beta-amyloid peptide. The present sequence is one such
 CC peptide. The beta-amyloid peptide modulators would be useful for
 CC treating disorders associated with beta-amyloidosis for e.g. Alzheimer's
 CC disease. The present sequence was designed on the aggregation core domain

CC from beta-amyloid peptide (see AAB27021-B27022).

XX SQ Sequence 6 AA;

Query Match 33.3%; Score 4; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFP 4
 ||||
 Db 1 LFFP 4

RESULT 61

AAB27045

ID AAB27045 standard; Peptide; 6 AA.

AC AAB27045;

DT 02-FEB-2001 (first entry)

DE Beta-amyloid peptide modulator #23.

XX Beta-amyloid peptide; nootropic; neuroprotective; Alzheimer's disease;
 KW aggregation core domain.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Misc-difference 1.6 /note= "D-form residues"

FT Modified-site 1 /note= "N-methyl-Leu"

FT Modified-site 4 /note= "[FS]Phe"

FT Modified-site 6 /note= "C-terminal amide"

XX PN WO200052048-A1.

XX PD 08-SEP-2000.

XX PF 03-MAR-2000; 2000WO-US05574.

XX PR 04-MAR-1999; 99US-0122736.

XX PA (PRAE-) PRAECIS PHARM INC.

XX PI Findeis MA, Phillips K, Olson GL, Self C;

XX DR WPI; 2000-594168/56.

XX Novel compounds that are useful as modulators of beta-amyloid peptide
 PT aggregation in treating amyloidosis, comprises D-amino acids -
 XX Claim 4; Page 76; 87pp; English.

XX The present invention relates to peptides (see AAB27023-B27046) that
 CC modulate beta-amyloid peptide aggregation, and hence inhibit the
 CC neurotoxicity of beta-amyloid peptide. The present sequence is one such
 CC peptide. The beta-amyloid peptide modulators would be useful for
 CC treating disorders associated with beta-amyloidosis for e.g. Alzheimer's
 CC disease. The present sequence was designed on the aggregation core domain
 CC from beta-amyloid peptide (see AAB27021-B27022).

XX SQ Sequence 6 AA;

Query Match 33.3%; Score 4; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5
 ||||

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Db      3 PFPL 6

RESULT 62
AAB28963
ID AAB28963 standard; Peptide; 6 AA.
XX
AC AAB28963;
XX
DT 29-JAN-2001 (first entry)
XX
DE Peptide encoded by oligonucleotide C.
XX
KW Cat; allergy; human T cell reactive feline protein; hTRFP;
KW immunotherapy.
XX
OS Felis sp.
OS Synthetic.
XX
PN US6120769-A.
XX
PD 19-SEP-2000.
XX
PF 28-APR-1995; 95US-0431184.
XX
PR 02-SEP-1994; 94US-0300928.
PR 03-NOV-1989; 89US-0431565.
PR 28-FEB-1991; 91US-0662276.
PR 13-DEC-1991; 91US-0807529.
PR 25-MAR-1992; 92US-0857311.
PR 15-MAY-1992; 92US-0884718.
PR 15-JAN-1993; 93US-0006116.
XX
PA (IMMU-) IMMULOGIC PHARM CORP.
XX
PI Gefter ML, Garman RD., Greenstein JL, Bond JF;
XX
DR WPI; 2000-601477/57.
DR N-PSDB; AAC60128.
XX
XX Detecting, preventing and treating sensitivity to cat protein allergen
PT comprises combining a biological sample with a human T cell reactive
PT feline protein and determining the extent of binding that occurs -
XX
PS Example 25; Column 105-106; 106pp; English.
XX
CC The present invention relates to the detection of sensitivity to a cat
CC protein allergen by combining a blood sample from a subject with a
CC peptide of human T cell reactive feline protein (hTRFP). This method
CC and the hTRFP peptides are useful for diagnosing, preventing and
CC treating cat allergies by reducing or abolishing an individual's
CC allergic response to a cat allergen. DNA encoding the TRFP may be
CC used as probes to locate equivalent sequences present in other species.
CC These may further be used to study the mechanism of immunotherapy of
CC cat allergy, and to design modified derivatives, analogues or
CC functional equivalents useful in immunotherapy. The present
CC sequence was used in the invention.
XX
SQ Sequence 6 AA;
Query Match 33.3%; Score 4; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 LPVV 8
Db 3 LPVV 6
RESULT 63
AAY87707
ID AAY87707 standard; Protein; 6 AA.
XX
AC AAY87707;
XX
DT 22-AUG-2000 (first entry)
XX
DE Feline human TRFP oligonucleotide C derived peptide.
XX
KW T-cell reactive feline protein; TRFP; Fel d I; cat allergen; primer;
KW antiallergic; T cell stimulator; diagnostic; immunotherapy.
XX
OS Felis sp.
XX
PN US6048962-A.
XX
PD 11-APR-2000.
XX
PF 27-APR-1995; 95US-0430014.
XX
PR 02-SEP-1994; 94US-0300928.
PR 03-NOV-1989; 89US-0431565.
PR 28-FEB-1991; 91US-0662276.
PR 13-DEC-1991; 91US-0807529.
PR 25-MAR-1992; 92US-0857311.
PR 15-MAY-1992; 92US-0884718.
PR 15-JAN-1993; 93US-0006116.
XX
PA (IMMU-) IMMULOGIC PHARM CORP.
XX
PI Kuo M, Rogers BL, Gefter ML, Morgenstern JP, Brauer AW;
PI Greenstein JL, Griffith IJ, Garman RD;
XX
DR WPI; 2000-316905/27.
DR N-PSDB; AAA12266.
XX
XX New human T cell reactive feline protein useful for reducing or
PT abolishing individual's allergic response to cat allergen comprising
PT two different covalently linked peptide chains -
XX
PS Example 25; Column 105-106; 106pp; English.
XX
CC This invention describes a novel naturally occurring cat protein allergen
CC (I), human T cell reactive feline protein (TRFP), comprising two
CC different covalently linked peptide chains with a molecular weight of 20
CC kD, 40 kD or 130 kD under non-reducing conditions and 5 kD or 10-18 kD
CC under reducing conditions. The products of the invention have
CC antiallergic activity and act as human T cell stimulators. TRFP is useful
CC for reducing or preventing the adverse effects of cat allergens on cat
CC allergic individuals and in ex vivo diagnostic tests to determine which
CC peptides cause sensitivity so as to selectively use them to desensitize
CC a cat sensitive individual. Purified TRFP is also useful for studying
CC the mechanism of immunotherapy of cat allergy and to design modified
CC derivatives, analogs or functional equivalents that are more useful in
CC immunotherapy against cat allergy. DNA sequences encoding TRFP are
CC useful as probes to locate equivalent sequences present in other species
CC (goats, sheep, dogs, rabbits or horses) that may be useful in diagnostics
CC and/or therapeutics. Fully defined and characterized TRFP provides
CC complete and a very simple desensitization therapy. This sequence
CC represents a peptide fragment of TRFP used in the design of a primer
CC which is used in the construction and expression of peptides comprising
CC two or more regions of TRFP in a method described in the invention.
XX
SQ Sequence 6 AA;
Query Match 33.3%; Score 4; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 LPVV 8
Db 3 LPVV 6
RESULT 64
AAY90133

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ID AAY90133 standard; Peptide; 6 AA.
 AC AAY90133;
 XX
 DT 13-JUL-2000 (first entry)
 XX
 XX TRFP derived peptide, peptide C.
 DE
 XX
 KW Cat; TRFP; human T-cell reactive feline protein; cat protein allergen;
 KW house dust; Fel d I; cat allergy; Felis domesticus sensitivity; therapy;
 KW diagnosis; goat; sheep; horse; rabbit; dog.
 XX
 OS Felis domesticus.
 XX
 FN US6025162-A.
 XX
 XX 15-FEB-2000.
 PD
 XX
 XX 28-APR-1995; 95US-0430944.
 PF
 XX
 XX 02-SEP-1994; 94US-0300928.
 PR
 PR 03-NOV-1989; 89US-0431565.
 PR
 PR 28-FEB-1991; 91US-0662276.
 PR
 PR 13-DEC-1991; 91US-0807529.
 PR
 PR 25-MAR-1992; 92US-0857311.
 PR
 PR 15-MAY-1992; 92US-0884718.
 PR
 PR 15-JAN-1993; 93US-0006116.
 XX
 XX (IMMU-) IMMULOGIC PHARM CORP.
 PA
 XX Morgenstern JP, Griffith IJ, Rogers BL;
 PI
 XX WPI; 2000-181812/16.
 DR
 XX New human T cell reactive feline protein, useful for desensitizing cat
 PT allergic individuals to cat allergens -
 PT
 XX Example 25; Fig 28; 108pp; English.
 PS
 XX This sequence is a peptide derived from the human T cell reactive feline
 CC protein (TRFP) of the invention, and was used to design a PCR
 CC primer. The protein is a cat protein allergen,
 CC and was isolated from a vacuum bag extract obtained by affinity
 CC purification of house dust collected from several homes with cats. TRFP
 CC is composed of two covalently linked peptide chains, and is also referred
 CC to as Fel d I. TRFP and its peptides are useful for reducing or
 CC preventing the adverse effects that exposure to cat allergens normally
 CC has on cat allergic individuals (i.e. to desensitize individuals to cat
 CC allergens or block the effect of the allergens). TRFP is also used in
 CC methods of diagnosing sensitivity to Felis domesticus in an individual.
 CC DNA sequences encoding TRFP can be used as probes to locate equivalent
 CC sequences present in other species, e.g. goat, sheep, horse, rabbit and
 CC dog, that may be useful in diagnostic and/or therapeutic applications.
 XX
 SQ Sequence 6 AA;
 Query Match 33.3%; Score 4; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LPVV 8
 DB 3 LPVV 6
 RESULT 65
 AAY51504
 ID AAY51504 standard; Protein; 6 AA.
 XX
 XX AAY51504;
 AC
 XX
 DT 22-MAY-2000 (first entry)
 XX

DE Human TRFP derived peptide encoding oligonucleotide C.
 XX
 KW T-cell reactive feline protein; TRFP; T cell epitope; T cell receptor;
 KW down regulation; immune response; allergen; immunoglobulin E;
 KW sensitivity; cat protein allergen; human.
 XX
 OS Homo sapiens.
 XX
 FN US6019972-A.
 XX
 PD 01-FEB-2000.
 XX
 XX 02-SEP-1994; 94US-0300928.
 PF
 XX
 XX 03-NOV-1989; 89US-0431565.
 PR
 PR 28-FEB-1991; 91US-0662276.
 PR
 PR 13-DEC-1991; 91US-0807529.
 PR
 PR 25-MAR-1992; 92US-0857311.
 PR
 PR 15-MAY-1992; 92US-0884718.
 PR
 PR 15-JAN-1993; 93US-0006116.
 XX
 XX (IMMU-) IMMULOGIC PHARM CORP.
 PA
 XX Garman RD, Greenstein JL, Kuo M, Briner TJ, Morville M, Geffer ML;
 PI
 XX WPI; 2000-146862/13.
 DR
 DR N-FSDB; AAZ88639.
 XX
 XX Peptides of human T cell reactive feline protein for treating
 PT sensitivity to cat protein allergens comprise at least one T cell
 PT epitope recognized by a T cell receptor specific for the human T cell
 PT reactive feline protein -
 PT
 XX Example 25; Column 105-106; 105pp; English.
 PS
 XX This invention describes a novel peptide (I) of human T cell reactive
 CC feline protein (hTRFP) having at least one T cell epitope recognized
 CC by a T cell receptor specific for the human T cell reactive feline
 CC protein, the peptide consisting of at least 7-30 amino acids, and having
 CC an amino acid sequence derived from an amino acid sequence comprising
 CC 94, 96, 97, 109, or 111 residues, given in the specification. The
 CC peptides down regulate the immune response to the allergen. The peptides
 CC have reduced immunoglobulin E binding and reduce T cell responsiveness.
 CC The peptide (I) is useful in compositions for treating sensitivity to a
 CC cat protein allergen in a subject. AAY51504-Y51516 represent peptides
 CC used in the design of the oligonucleotides represented in AAZ88639-288650
 CC which are used to construct peptides comprising of two or more regions of
 CC human TRFP.
 XX
 SQ Sequence 6 AA;
 Query Match 33.3%; Score 4; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LPVV 8
 DB 3 LPVV 6
 RESULT 66
 AAR64963
 ID AAR64963 standard; peptide; 7 AA.
 XX
 XX AAR64963;
 AC
 XX
 XX 25-MAR-2003 (updated)
 DT
 DT 12-SEP-1995 (first entry)
 XX
 XX Peralkylated oligopeptide.
 DE
 XX Peralkylated oligopeptides; binding assays; hydrolysis resistance;
 KW antimicrobial drug design; S. aureus; S. sanguis.

```

XX OS Synthetic.
XX FH Key
XX FT Location/Qualifiers
FT Modified-site 1
FT Modified-site 7 /note= "trimethylammonium N-terminal nitrogen"
FT Modified-site 7 /note= "C-terminal carboxamide group"
FT Modified-site 1..7
FT Modified-site 1..7 /note= "A methyl group on each amido nitrogen of
FT the backbone and appropriately methylated
FT side chains."
XX PN WO9500539-A1.
XX PD 05-JAN-1995.
XX PF 10-JUN-1994; 94WO-US06554.
XX PR 17-JUN-1993; 93US-0079144.
XX PR 09-JUN-1994; 94US-0257782.
XX PA (HOUG-) HOUGHTEN PHARM INC.
XX PI Blondelle S, Houghten R, Ostresh JM, Houghten RA;
XX DR WPI; 1995-052001/07.
XX PT Sets and libraries of per-alkylated oligopeptide derivs. -
XX PT including new cpds., with selected amino acids at partic.
XX PT positions, used in binding assays to identify sequence with
XX PT optimum binding to e.g. cellular receptors.
XX PS Claim 33; Page 117; 162pp; English.
XX CC AAR78161-R78169 are peralkylated oligopeptides (POs), which
XX CC together comprise a PO library. This PO library can be used to
XX CC assay peptides for preferential binding to a S. aureus or a
XX CC S. sanguis acceptor, esp. for drug (specifically antimicrobial)
XX CC design. The POs are resistant to enzymatic hydrolysis, also POs
XX CC that are toxic to gram positive bacteria do not cause haemolysis
XX CC of human blood.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 7 AA;
XX Query Match 33.3%; Score 4; DB 16; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4
Db 2 LFFF 5

RESULT 67
AAR64966
ID AAR64966 standard; peptide; 7 AA.
XX AC AAR64966;
XX AC AAR64966;
XX DT 25-MAR-2003 (updated)
XX DT 12-SEP-1995 (first entry)
XX DE Peralkylated oligopeptide.
XX KW Peralkylated oligopeptides; binding assays; hydrolysis resistance;
XX KW antimicrobial drug design; S. aureus; S. sanguis.
XX OS Synthetic.
XX FH Key
XX FT Location/Qualifiers
FT Modified-site 1

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FT Modified-site 7 /note= "trimethylammonium N-terminal nitrogen"
FT Modified-site 7 /note= "C-terminal carboxamide group"
FT Modified-site 1..7
FT Modified-site 1..7 /note= "A methyl group on each amido nitrogen of
FT the backbone and appropriately methylated
FT side chains."
XX PN WO9500539-A1.
XX PD 05-JAN-1995.
XX PF 10-JUN-1994; 94WO-US06554.
XX PR 17-JUN-1993; 93US-0079144.
XX PR 09-JUN-1994; 94US-0257782.
XX PA (HOUG-) HOUGHTEN PHARM INC.
XX PI Blondelle S, Houghten R, Ostresh JM, Houghten RA;
XX DR WPI; 1995-052001/07.
XX PT Sets and libraries of per-alkylated oligopeptide derivs. -
XX PT including new cpds., with selected amino acids at partic.
XX PT positions, used in binding assays to identify sequence with
XX PT optimum binding to e.g. cellular receptors.
XX PS Claim 33; Page 117; 162pp; English.
XX CC AAR78161-R78169 are peralkylated oligopeptides (POs), which
XX CC together comprise a PO library. This PO library can be used to
XX CC assay peptides for preferential binding to a S. aureus or a
XX CC S. sanguis acceptor, esp. for drug (specifically antimicrobial)
XX CC design. The POs are resistant to enzymatic hydrolysis, also POs
XX CC that are toxic to gram positive bacteria do not cause haemolysis
XX CC of human blood.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 7 AA;
XX Query Match 33.3%; Score 4; DB 16; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4
Db 2 LFFF 5

RESULT 68
AAR64968
ID AAR64968 standard; peptide; 7 AA.
XX AC AAR64968;
XX AC AAR64968;
XX DT 25-MAR-2003 (updated)
XX DT 12-SEP-1995 (first entry)
XX DE Peralkylated oligopeptide.
XX KW Peralkylated oligopeptides; binding assays; hydrolysis resistance;
XX KW antimicrobial drug design; S. aureus; S. sanguis.
XX OS Synthetic.
XX FH Key
XX FT Location/Qualifiers
FT Modified-site 1
FT Modified-site 7 /note= "trimethylammonium N-terminal nitrogen"
FT Modified-site 7 /note= "C-terminal carboxamide group"
FT Modified-site 1..7
FT Modified-site 1..7 /note= "A methyl group on each amido nitrogen of

```

FT the backbone and appropriately methylated.
 FT side chains."
 PN WO9500539-A1.
 XX
 XX
 XX 05-JAN-1995.
 PD
 XX
 XX 10-JUN-1994; 94WO-US06554.
 PF
 XX 17-JUN-1993; 93US-0079144.
 XX
 PR 09-JUN-1994; 94US-0257782.
 XX
 XX (HOUG-) HOUGHTEN PHARM INC.
 PA
 XX Blondelle S, Houghten R, Ostresh JM, Houghten RA;
 XX WPI; 1995-052001/07.
 XX
 XX Sets and libraries of per-alkylated oligopeptide derivs. -
 PT including new cpds., with selected amino acids at partic.
 PT positions, used in binding assays to identify sequence with
 PT optimum binding to e.g. cellular receptors.
 XX
 PS Claim 33; Page 117; 162pp; English.
 XX
 CC AAR78161-R78169 are peralkylated oligopeptides (POs), which
 CC together comprise a PO library. This PO library can be used to
 CC assay peptides for preferential binding to a S. aureus or a
 CC S. sanguis acceptor, esp. for drug (specifically antimicrobial)
 CC design. The POs are resistant to enzymatic hydrolysis, also POs
 CC that are toxic to gram positive bacteria do not cause haemolysis
 CC of human blood.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 33.3%; Score 4; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LFFF 4
 Db 2 LFFF 5
 RESULT 69
 AAB23226
 ID AAB23226 standard; peptide; 7 AA.
 XX
 AC AAB23226;
 XX
 XX 29-JAN-2001 (first entry)
 XX
 DE Hsp47-binding phage display heptapeptide, SEQ ID NO:48.
 XX
 KW Hsp47-binding heptapeptide; phage display library;
 KW Hsp47 external domain; carcinoma; cancer; targeting molecule;
 KW therapy; diagnosis; detection; imaging; drug delivery; invasion;
 KW migration; metastasis; modulation; tumour; skin; basal cells; colon;
 KW large intestine; lung; breast; bladder; oral cancer;
 KW head and neck cancer; larynx; nasopharynx; adrenal cortex;
 KW apocrine gland; kidney; liver; pancreas; prostate.
 XX
 OS Synthetic.
 XX
 XX WO200054805-A1.
 PN
 XX 21-SEP-2000.
 PD
 XX 15-MAR-2000; 2000WO-US06588.
 PF
 XX 15-MAR-1999; 99US-0124481.
 PR
 XX

PA (UYMA-) UNIV MARYLAND BALTIMORE.
 XX
 XX Sauk JJ;
 XX
 DR WPI; 2000-655997/63.
 XX
 XX Treating, diagnosing or modulating a carcinoma cell, which expresses
 PT Heat shock protein 47 on its surface, involves administering an agent
 PT comprising targeting moiety which binds to Hsp47 external domain -
 XX
 XX Example 5; Page 9; 87pp; English.
 XX
 CC The invention relates to methods of treating and diagnosing carcinomas
 CC in which heat shock protein 47 (Hsp47) is expressed on the surface
 CC of the carcinoma cells, involving administering an agent comprising a
 CC targeting moiety which specifically binds to the external domain of
 CC Hsp47. The invention also relates to peptides (AAB23181-B23203) which
 CC specifically bind to external domains of such surface-localised Hsp47
 CC molecules and have sequences encompassed by the generic sequences
 CC XHYHYXXHXXHXXHy or HYXXHXXHXXHXX where X, independently, can be
 CC any amino acid and Hy, independently, can be any hydrophobic amino acid.
 CC The invention also encompasses methods of screening for agents which
 CC bind Hsp47 external domains. Hsp47-binding agents can be used to
 CC treat Hsp47-expressing carcinomas, and for modulating the activity of a
 CC tumour cell with respect to invasion, migration, motility or metastasis,
 CC or to its interaction with the extracellular matrix. The targeting
 CC moiety (such as an Hsp47-binding peptide, a toxin or an antibody) may be
 CC coupled with a therapeutic moiety (such as a cytotoxic agent or a
 CC therapeutic gene) for cancer treatment, or with a detectable moiety for
 CC imaging. Carcinomas which may be treated or diagnosed according to
 CC methods of the invention include those of the skin, basal cells, large
 CC intestine, lung, colon, breast, bladder, oral, head and neck, larynx,
 CC nasopharynx, adrenal cortex, apocrine glands, kidney, liver, pancreas, or
 CC prostate. Targeting carcinoma cells with Hsp47-binding agents results in
 CC efficient delivery of therapeutic agents, reduced doses, reduced side
 CC effects and sensitive detection or imaging of carcinoma cells. Sequences
 CC AAB23204-B23240 represent phage display library heptapeptides identified
 CC as being able to bind Hsp47 in an exmplication of the invention.
 XX
 SQ Sequence 7 AA;
 Query Match 33.3%; Score 4; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 FLPV 7
 Db 2 FLPV 5
 RESULT 70
 AAR61722
 ID AAR61722 standard; peptide; 8 AA.
 XX
 AC AAR61722;
 XX
 XX 25-MAR-2003 (updated)
 DT 11-MAY-1995 (first entry)
 XX
 DE PLP peptide 74, potential binder of HLA-A2.1.
 XX
 KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
 KW diagnostic; MHC class I molecule; major histocompatibility complex;
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
 KW algorithm prediction.
 XX
 OS Homo sapiens.
 XX
 PN WO9420127-A1.


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XX PD 15-SEP-1994.
XX PF 04-MAR-1994; 94WO-US02353.
XX PR 05-MAR-1993; 93US-0027146.
XX PR 04-JUN-1993; 93US-0073205.
XX PR 29-NOV-1993; 93US-0159184.
XX PA (CYTE-) CYTEL CORP.
XX PI Grey HM, Kast WM, Sette A, Sidney J;
XX PI WPI; 1994-302678/37.
XX DR Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
XX PT for treatment or prophylaxis of cancer, virus infection or
XX PT autoimmune diseases.
XX PS Disclosure; Page 115; 138pp; English.
XX CC AAR61714-837 are potential peptide binders of HLA-A2.1 motif. These
XX CC peptides are thus potentially immunogenic. They were predicted by
XX CC using an algorithm, which assigns a score for each amino acid, at
XX CC each position along a peptide. A peptide is scored in the 'Grouped
XX CC Ratio' algorithm as a product of the scores of each of its residues.
XX CC This value can then be used to predict a population of peptides with
XX CC the highest occurrence of good binders. The peptides of the invention
XX CC can induce cytotoxic T lymphocytes which can react with target cells.
XX CC They can be used for the treatment or prophylaxis of cancer, eg.
XX CC prostate cancer or lymphoma, etc.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX CC
XX SQ Sequence 8 AA;
    Query Match 33.3%; Score 4; DB 15; Length 8;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FFFL 5
DB 5 FFFL 8
    ||||
    ||||

RESULT 71
AAW39537
ID AAW39537 standard; peptide; 8 AA.
XX AC AAW39537;
XX DT 11-JUN-1998 (first entry)
XX DE HIV-1 pol peptide (pos. 306-313) capable of binding to HLA-A*0301.
XX KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
XX KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
XX KW disease; anti-tumour; anti-viral.
XX OS Human immunodeficiency virus type 1.
XX PN WO9741440-A1.
XX PD 06-NOV-1997.
XX PF 28-APR-1997; 97WO-NL00229.
XX PR 23-DEC-1996; 96EP-0203670.
XX PR 26-APR-1996; 96EP-0201145.
XX PA (UYLE-) RICKSUNIV LEIDEN.
XX PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
XX PI Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;

WPI; 1997-549891/50.
Method of selecting T cell peptide epitope(s) - by measuring the
stability of HLA class I-peptide complexes on intact B cells
Example 2; Page 62; 109pp; English.
Peptides AAW39430-W39734 are used in a novel method for the selection of
immunogenic T-cell peptide epitopes present in polypeptide antigens. The
method involves the identification of peptide sequences capable of
binding to an HLA (human leukocyte antigen) class I molecule and
measuring the binding of this epitope peptide to the HLA class I
peptide. The stability of binding of the peptide and MHC (major
histocompatibility complex) class I molecule is measured on intact human
B cells carrying the MHC molecule at their cell surfaces. The method can
be used to select peptide epitopes for generating vaccines against a
disease associated with the polypeptide, e.g. cancers or AIDS. The
peptide epitopes are especially T-cell peptide epitopes with strong
anti-tumour and anti-viral immune responses. Peptides AAW39528-W39547 are
conserved human immunodeficiency virus type 1 (HIV-1) pol sequences which
are compliant with the HLA-A*0301 binding motif.
Sequence 8 AA;
Query Match 33.3%; Score 4; DB 18; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 NVLP 12
DB 1 NVLP 4
    ||||
    ||||

RESULT 72
AAB37338
ID AAB37338 standard; Peptide; 8 AA.
XX AC AAB37338;
XX DT 19-FEB-2001 (first entry)
XX DE Peptide linker #23.
XX KW Cytostatic; antiproliferative; vascular endothelial growth factor;
XX KW VEGF; antibody; VEGF2 receptor; cancer; vascularised solid tumour;
XX KW peptide linker.
XX OS Rattus sp.
XX PN WO200064946-A2.
XX PD 02-NOV-2000.
XX PF 28-APR-2000; 2000WO-US11367.
XX PR 28-APR-1999; 99US-0131432.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Thorpe PE, Brekken RA;
XX PI WPI; 2000-687317/67.
XX DR Immunogenic composition for the treatment and diagnosis of cancer
XX PT comprises an anti-VEGF (vascular endothelial growth factor) antibody
XX PT binding the same epitope as the monoclonal antibody ARCC PTA 1595 -
XX PS Disclosure; Page 150; 298pp; English.
XX CC The present invention relates to anti-Vascular Endothelial Growth Factor
XX CC (VEGF) antibodies that bind to the same epitope as the monoclonal
XX CC antibody ARCC PTA 1595 and which significantly inhibit VEGF binding to

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CC the VEGF receptor VEGFR2, without inhibiting VEGF binding to the VEGF
 CC receptor VEGFR1. The present sequence is a peptide linker which can be
 CC used to link the antibodies of the present invention to anti-cellular or
 CC cytotoxic agents. The anti-VEGF antibodies of the present invention are
 CC useful for the treatment and diagnosis of cancer, especially vascularised
 CC solid tumours.

XX Sequence 8 AA;
 SQ Query Match 33.3%; Score 4; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LPVV 8
 ||||
 DB 3 LPVV 6

RESULT 73
 ABP14646
 ID ABP14646 standard; Peptide; 8 AA.

XX AC ABP14646;
 XX DT 15-JUL-2002 (first entry)
 XX DE HIV A03 super motif pol peptide #20.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -

XX Claim 32; Page 168; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

XX Sequence 8 AA;

XX Query Match 33.3%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 NVLP 12
 ||||
 DB 1 NVLP 4

RESULT 74
 ABP21858
 ID ABP21858 standard; Peptide; 8 AA.

XX AC ABP21858;

XX DT 15-JUL-2002 (first entry)

XX DE HIV A03 motif pol peptide #853.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -

XX Claim 32; Page 317; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

```
XX SQ Sequence 8 AA;
Query Match 33.3%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12
Db 1 NVLP 4

RESULT 75
ABP23685
ID ABP23685 standard; Peptide; 8 AA.
XX AC ABP23685;
XX DT 15-JUL-2002 (first entry)
XX DE HIV A11 motif pol peptide #627.
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US27766.
XX PR 05-OCT-1999; 99US-0412863.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-354887/37.
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX Claim 32; Page 354; 448pp; English.
XX The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP1501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX SQ Sequence 8 AA;
```

Query Match 33.3%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12
Db 1 NVLP 4

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Job time : 41.8723 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 23.8723 Seconds
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92.715 Million cell updates/sec

Title: US-09-641-801-4

Perfect score: 12

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- 13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	12	100.0	12	15	US-10-281-652-4
2	5	41.7	5	10	US-09-895-443-30
3	5	41.7	8	12	US-10-137-867-292
4	5	41.7	11	9	US-09-484-704-16
5	5	41.7	11	11	US-09-309-196-57
6	5	41.7	11	11	US-09-201-396-38
7	5	41.7	11	11	US-09-953-354-68
8	5	41.7	11	12	US-10-277-607-38
9	4	33.3	4	12	US-09-832-161-23
10	4	33.3	5	10	US-09-895-443-24
11	4	33.3	5	10	US-09-895-443-25
12	4	33.3	5	10	US-09-895-443-26
13	4	33.3	5	10	US-09-781-133-20
14	4	33.3	5	10	US-09-781-133-21
15	4	33.3	5	10	US-09-781-133-22
16	4	33.3	5	10	US-09-781-133-23
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25	4	33.3	5	10	US-09-781-133-32
26	4	33.3	5	10	US-09-781-133-33
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35	4	33.3	5	10	US-09-781-133-42
36	4	33.3	5	10	US-09-781-133-43
37	4	33.3	5	10	US-09-781-133-44
38	4	33.3	5	10	US-09-781-133-45
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85	4	33.3	5	10	US-09-781-133-92
86	4	33.3	5	10	US-09-781-133-93
87	4	33.3	5	10	US-09-781-133-94
88	4	33.3	5	10	US-09-781-133-95

16	4	33.3	6	8	US-08-464-363-13	Sequence 13, Appl
17	4	33.3	6	8	US-08-464-363-53	Sequence 53, Appl
18	4	33.3	7	9	US-09-833-067-26	Sequence 26, Appl
19	4	33.3	8	10	US-09-998-831-37	Sequence 37, Appl
20	4	33.3	8	12	US-10-373-561-37	Sequence 37, Appl
21	4	33.3	9	8	US-08-821-739A-43	Sequence 43, Appl
22	4	33.3	9	8	US-08-464-363-45	Sequence 45, Appl
23	4	33.3	9	11	US-09-865-548A-86	Sequence 86, Appl
24	4	33.3	9	12	US-09-932-165-283	Sequence 283, Appl
25	4	33.3	9	12	US-09-932-165-290	Sequence 290, Appl
26	4	33.3	9	12	US-09-932-165-452	Sequence 452, Appl
27	4	33.3	9	12	US-09-932-165-480	Sequence 480, Appl
28	4	33.3	9	12	US-09-932-165-660	Sequence 660, Appl
29	4	33.3	9	12	US-09-932-165-695	Sequence 695, Appl
30	4	33.3	9	12	US-09-932-165-876	Sequence 876, Appl
31	4	33.3	9	12	US-10-239-313A-655	Sequence 655, Appl
32	4	33.3	9	12	US-10-119-536A-183	Sequence 183, Appl
33	4	33.3	10	10	US-09-894-018-305	Sequence 305, Appl
34	4	33.3	10	11	US-09-572-404B-1033	Sequence 1033, Appl
35	4	33.3	10	11	US-09-572-404B-1035	Sequence 1035, Appl
36	4	33.3	10	11	US-09-572-404B-1109	Sequence 1109, Appl
37	4	33.3	10	11	US-09-895-298-138	Sequence 138, Appl
38	4	33.3	10	12	US-09-932-165-388	Sequence 388, Appl
39	4	33.3	10	12	US-09-932-165-553	Sequence 553, Appl
40	4	33.3	10	12	US-09-932-165-558	Sequence 558, Appl
41	4	33.3	10	12	US-09-932-165-751	Sequence 751, Appl
42	4	33.3	10	12	US-09-932-165-1369	Sequence 1369, Appl
43	4	33.3	10	12	US-09-833-039-129	Sequence 129, Appl
44	4	33.3	10	12	US-10-231-417-614	Sequence 614, Appl
45	4	33.3	10	12	US-10-200-708-295	Sequence 295, Appl
46	4	33.3	10	12	US-10-200-708-318	Sequence 318, Appl
47	4	33.3	10	12	US-10-177-277-129	Sequence 129, Appl
48	4	33.3	10	12	US-09-573-822C-403	Sequence 403, Appl
49	4	33.3	10	14	US-10-057-763-1	Sequence 1, Appl
50	4	33.3	11	10	US-09-828-708-79	Sequence 79, Appl
51	4	33.3	11	15	US-10-057-789-218	Sequence 218, Appl
52	4	33.3	12	15	US-10-212-628-218	Sequence 218, Appl
53	4	33.3	13	15	US-10-116-252-22	Sequence 22, Appl
54	4	33.3	14	9	US-09-853-080-32	Sequence 32, Appl
55	4	33.3	15	9	US-09-767-460-12	Sequence 12, Appl
56	4	33.3	15	10	US-09-981-876-224	Sequence 224, Appl
57	4	33.3	15	11	US-09-148-545-224	Sequence 224, Appl
58	4	33.3	15	12	US-10-336-491-6	Sequence 6, Appl
59	4	33.3	16	11	US-09-986-480-261	Sequence 261, Appl
60	4	33.3	17	10	US-09-071-838-88	Sequence 88, Appl
61	4	33.3	17	10	US-09-981-876-221	Sequence 221, Appl
62	4	33.3	17	11	US-09-148-545-221	Sequence 221, Appl
63	4	33.3	17	11	US-09-996-069-30	Sequence 30, Appl
64	4	33.3	17	11	US-09-996-069-31	Sequence 31, Appl
65	4	33.3	17	15	US-10-213-512-88	Sequence 88, Appl
66	4	33.3	18	15	US-10-084-813-248	Sequence 248, Appl
67	4	33.3	18	15	US-10-084-813-249	Sequence 249, Appl
68	4	33.3	18	15	US-10-084-813-250	Sequence 250, Appl
69	4	33.3	18	15	US-10-157-031-192	Sequence 192, Appl
70	4	33.3	19	15	US-10-106-698-7294	Sequence 7294, Appl
71	4	33.3	19	15	US-10-225-567A-1666	Sequence 1666, Appl
72	4	33.3	20	8	US-08-464-363-29	Sequence 29, Appl
73	4	33.3	20	9	US-09-864-761-35505	Sequence 35505, A
74	4	33.3	20	9	US-09-735-705-405	Sequence 405, Appl
75	4	33.3	20	9	US-09-841-132-156	Sequence 156, Appl
76	4	33.3	20	10	US-09-850-716A-405	Sequence 405, Appl
77	4	33.3	20	10	US-09-897-778-405	Sequence 405, Appl
78	4	33.3	20	10	US-09-731-449-27	Sequence 27, Appl
79	4	33.3	20	12	US-09-928-048A-8	Sequence 8, Appl
80	4	33.3	20	12	US-10-117-982-405	Sequence 405, Appl
81	4	33.3	20	12	US-10-267-730-27	Sequence 27, Appl
82	4	33.3	20	15	US-10-106-698-7129	Sequence 7129, Appl
83	4	33.3	20	15	US-10-106-698-7253	Sequence 7253, Appl
84	4	33.3	20	15	US-10-106-698-7391	Sequence 7391, Appl
85	4	33.3	20	15	US-10-254-426-27	Sequence 27, Appl
86	3	25.0	4	8	US-08-464-363-25	Sequence 25, Appl
87	3	25.0	4	9	US-09-803-126-34	Sequence 34, Appl
88	3	25.0	4	10	US-09-202-077-11	Sequence 11, Appl

89 Sequence 10, Appl
90 Sequence 12, Appl
91 Sequence 64, Appl
92 Sequence 3, Appl
93 Sequence 9, Appl
94 Sequence 178, Appl
95 Sequence 64, Appl
96 Sequence 10, Appl
97 Sequence 14, Appl
98 Sequence 2, Appl
99 Sequence 55, Appl
100 Sequence 2, Appl

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/895,443
FILING DATE: 29-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/356,931
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/897,342
FILING DATE: 21-JUL-1997
APPLICATION NUMBER: USSN 08/703,675
FILING DATE: 27-AUG-1996
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Jr., Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-016CP4CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION: 1-5
OTHER INFORMATION: /note= D amino acid
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-895-443-30

ALIGNMENTS

RESULT 1
US-10-281-652-4
Sequence 4, Application US/10281652
Publication No. US20030091606A1
GENERAL INFORMATION:
APPLICANT: STANTON, G. John
APPLICANT: HUGHES, Thomas K.
APPLICANT: BOLDOGH, Istvan
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
FILE REFERENCE: 265.00220101
CURRENT APPLICATION NUMBER: US/10/281,652
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/09/641,803
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 60/149,310
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 12
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-4

Query Match 100.0%; Score 12; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LFFFLPVNVLP 12
DB 1 LFFFLPVNVLP 12

RESULT 2
US-09-895-443-30
Sequence 30, Application US/09895443
Patent No. US20020103134A1
GENERAL INFORMATION:
APPLICANT: Findeis, M. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide
Aggregation Comprising D-Amino Acids
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1784
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

Query Match 41.7%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LFFFL 5
DB 1 LFFFL 5

RESULT 3
US-10-137-867-292
Sequence 292, Application US/10137867
Publication No. US20030207349A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C146
CURRENT APPLICATION NUMBER: US/10/137,867
CURRENT FILING DATE: 2002-05-03

; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 292
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-292

Query Match 41.7%; Score 5; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFEL 5
Db 1 LFFEL 5

RESULT 4
US-09-484-704-16
; Sequence 16, Application US/09484704
; Patent No. US20020081567A1
; GENERAL INFORMATION:
; APPLICANT: Henrickson, Kelly J.
; APPLICANT: Fan, Jiang (n.m.i.)
; TITLE OF INVENTION: VIRUS ASSAY METHOD
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/484.704
; FILING DATE:

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 650053.91126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-484-704-16

Query Match 41.7%; Score 5; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VVNVL 11
Db 7 VVNVL 11

RESULT 5
US-09-309-196-57
; Sequence 57, Application US/09309196
; Publication No. US20030008380A1
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M.

; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/309,196
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/322,137
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,328
; FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,431
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOLWKES=2C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-309-196-57

Query Match 41.7%; Score 5; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFELP 6
Db 6 FFELP 10

RESULT 6
US-09-201-396-38
; Sequence 38, Application US/09201396A
; Publication No. US20030009022A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; APPLICANT: Murphy, Andrew J.
; APPLICANT: Paul, Jeremy
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR
; TITLE OF INVENTION: EFFECTORS
; FILE REFERENCE: CPI-012CP9
; CURRENT APPLICATION NUMBER: US/09/201,396A
; CURRENT FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: 08/582,333

; EARLIER FILING DATE: 1996-01-17
; EARLIER APPLICATION NUMBER: 08/322,137
; EARLIER FILING DATE: 1994-10-13
; EARLIER APPLICATION NUMBER: 08/309,313
; EARLIER FILING DATE: 1994-09-20
; EARLIER APPLICATION NUMBER: 08/190,328
; EARLIER FILING DATE: 1994-01-31
; EARLIER APPLICATION NUMBER: 08/041,431
; EARLIER FILING DATE: 1993-03-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-201-396-38

Query Match 41.7%; Score 5; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6
| | | | |
Db 6 FFFLP 10

RESULT 7
US-09-953-354-68
; Sequence 68, Application US/09953354
; Publication No. US20030054402A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; MURPHY, Andrew J. M.
; TITLE OF INVENTION: Methods and Compositions for
; Identifying Receptor Effectors
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,354
; FILING DATE: 13-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/689,172
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: P41,106
; REFERENCE/DOCKET NUMBER: CPI-012CP7
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-953-354-68

Query Match 41.7%; Score 5; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6
| | | | |
Db 6 FFFLP 10

RESULT 8
US-10-277-607-38
; Sequence 38, Application US/10277607
; Publication No. US20030166143A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; MURPHY, Andrew J.
; APPLICANT: Paul, Jeremy I.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR
; TITLE OF INVENTION: EFFECTORS
; FILE REFERENCE: CPI-012CP9CN
; CURRENT APPLICATION NUMBER: US/10/277,607
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 09/201,396
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: 60/109,902
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: PCT/US98/21168
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 08/946,298
; PRIOR FILING DATE: 1997-10-07
; PRIOR APPLICATION NUMBER: 08/689,172
; PRIOR FILING DATE: 1996-08-06
; PRIOR APPLICATION NUMBER: 08/582,333
; PRIOR FILING DATE: 1996-01-17
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-10-277-607-38

Query Match 41.7%; Score 5; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6
| | | | |
Db 6 FFFLP 10

RESULT 9
US-09-832-161-23
; Sequence 23, Application US/09832161
; Publication No. US20030166587A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yinon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; TITLE OF INVENTION: NF-KB
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/09/832,161
; CURRENT FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: 09/210,060
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-161-23

Query Match 33.3%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VVNV 10
Db 1 VVNV 4

RESULT 10
US-09-895-443-24
; Sequence 24, Application US/09895443
; Patent No. US20020103134A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1784
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,443
; FILING DATE: 29-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/356,931
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/897,342
; FILING DATE: 21-JUL-1997
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Jr., Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-016CP4CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1-5
; OTHER INFORMATION: /note= D amino acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-895-443-24

Query Match 33.3%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFL 5
Db 1 FFFL 4

RESULT 11
US-09-895-443-25
; Sequence 25, Application US/09895443
; Patent No. US20020103134A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1784
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,443
; FILING DATE: 29-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/356,931
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/897,342
; FILING DATE: 21-JUL-1997
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Jr., Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-016CP4CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1-5
; OTHER INFORMATION: /note= D amino acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Query Match 33.3%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFL 5
Db 1 FFFL 4

Db 2 FFFL 5

RESULT 12

US-09-895-443-26
 ; Sequence 26, Application US/09895443
 ; Patent No. US20020103134A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fideis, M. et al.
 ; TITLE OF INVENTION: Modulators of -Amyloid Peptide
 ; Aggregation Comprising D-Amino Acids
 ;
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1784
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/895,443
 ; FILING DATE: 29-Jun-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/356,931
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: 08/897,342
 ; FILING DATE: 21-JUL-1997
 ; APPLICATION NUMBER: USN 08/703,675
 ; FILING DATE: 27-AUG-1996
 ; APPLICATION NUMBER: USN 08/616,081
 ; FILING DATE: 14-MAR-1996
 ; APPLICATION NUMBER: USN 08/548,998
 ; FILING DATE: 27-OCT-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DeConti, Jr., Giulio A.
 ; REGISTRATION NUMBER: 31,503
 ; REFERENCE/DOCKET NUMBER: PPI-016CP4CN
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified site
 ; LOCATION: 1-5
 ; OTHER INFORMATION: /note= D amino acid
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-895-443-26

Query Match 33.3%; Score 4; DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5
 ||||
 Db 2 FFFL 5

RESULT 13

US-09-781-133-20
 ; Sequence 20, Application US/09781133
 ; Patent No. US20020142950A1
 ; GENERAL INFORMATION:

; APPLICANT: Hayward, Neil J.
 ; APPLICANT: Gefter, Malcolm L.
 ; TITLE OF INVENTION: METHODS FOR ENHANCING THE BIOAVAILABILITY OF A DRUG
 ; FILE REFERENCE: PPI-064
 ; CURRENT APPLICATION NUMBER: US/09/781,133
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/181,833
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 60/181,943
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 20
 ; LENGTH: 5
 ; TYPE: PPT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Each protein is a D-amino acid
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptides
 US-09-781-133-20

Query Match 33.3%; Score 4; DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5
 ||||
 Db 1 FFFL 4

RESULT 14

US-09-781-133-21
 ; Sequence 21, Application US/09781133
 ; Patent No. US20020142950A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hayward, Neil J.
 ; APPLICANT: Gefter, Malcolm L.
 ; TITLE OF INVENTION: METHODS FOR ENHANCING THE BIOAVAILABILITY OF A DRUG
 ; FILE REFERENCE: PPI-064
 ; CURRENT APPLICATION NUMBER: US/09/781,133
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/181,833
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 60/181,943
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 21
 ; LENGTH: 5
 ; TYPE: PPT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Each protein is a D-amino acid
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptides
 US-09-781-133-21

Query Match 33.3%; Score 4; DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5
 ||||
 Db 2 FFFL 5

RESULT 15

US-09-781-133-22
 ; Sequence 22, Application US/09781133
 ; Patent No. US20020142950A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hayward, Neil J.

; APPLICANT: Gelter, Malcolm L.
; TITLE OF INVENTION: METHODS FOR ENHANCING THE BIOAVAILABILITY OF A DRUG
; FILE REFERENCE: PPI-064
; CURRENT APPLICATION NUMBER: US/09/781,133
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,833
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/181,943
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Each protein is a D-amino acid
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptides
US-09-781-133-22

Query Match 33.3%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFEL 5
|||
Db 2 FFEL 5

RESULT 16
US-08-464-363-13
; Sequence 13, Application US/08464363
; Publication No. US2003003581SAI
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,363
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-363-13

Query Match 33.3%; Score 4; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8
|||
Db 3 LPVV 6

RESULT 17
US-08-464-363-53
; Sequence 53, Application US/08464363
; Publication No. US2003003581SAI
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,363
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-464-363-53

Query Match 33.3%; Score 4; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8
|||

Db 3 LPVV 6

RESULT 18

US-09-833-067-26
; Sequence 26, Application US/09833067
; Patent No. US2002005488A1
; GENERAL INFORMATION:
; APPLICANT: O'HANLEY, PETER
; APPLICANT: DENICH, KENNETH
; TITLE OF INVENTION: DISSOCIATED PILL, THEIR PRODUCTION AND USE
; FILE REFERENCE: 050939/0102
; CURRENT APPLICATION NUMBER: US/09/833,067
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/196,493
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown Sequence
; FEATURE:
; OTHER INFORMATION: Description of Unknown Sequence: highly hydrophobic region
; OTHER INFORMATION: of amino acids
US-09-833-067-26

Query Match 33.3%; Score 4; DB 9; Length 7;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

Db 4 LFFF 7

RESULT 19

US-09-998-831-37
; Sequence 37, Application US/09998831
; Patent No. US20020119153A1
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
; TITLE OF INVENTION: INHIBITING VEGF
; FILE REFERENCE: 4001.002584
; CURRENT APPLICATION NUMBER: US/09/998,831
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/561,108
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-998-831-37

Query Match 33.3%; Score 4; DB 10; Length 8;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8

Db 3 LPVV 6

RESULT 20

US-10-373-561-37
; Sequence 37, Application US/10373561

Publication No. US20030175276A1
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF
; FILE REFERENCE: 4001.002582
; CURRENT APPLICATION NUMBER: US/10/373,561
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/561,499
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/131,432
; PRIOR FILING DATE: 1993-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-10-373-561-37

Query Match 33.3%; Score 4; DB 12; Length 8;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8

Db 3 LPVV 6

RESULT 21

US-08-821-739A-43
; Sequence 43, Application US/08821739A
; Publication No. US20020168374A1
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.005000A
; CURRENT APPLICATION NUMBER: US/08/821,739A
; CURRENT FILING DATE: 1999-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-821-739A-43

Query Match 33.3%; Score 4; DB 8; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5

Db 5 FFFL 8

RESULT 22
US-08-464-363-45
; Sequence 45, Application US/08464363
; Publication No. US2003005815A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,363
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-464-363-45

Query Match 33.3%; Score 4; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8

Db 6 LPVV 9

RESULT 23
US-09-865-548A-86
; Sequence 86, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon

; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-86

Query Match 33.3%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVNV 10

Db 6 VVNV 9

RESULT 24
US-09-932-165-283
; Sequence 283, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 283
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-283

Query Match 33.3%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

Db 5 LFFF 8

RESULT 25
US-09-932-165-290
; Sequence 290, Application US/09932165

/ Publication No. US20030134784A1

/ GENERAL INFORMATION:

/ APPLICANT: RAITANO, ARTHUR

/ APPLICANT: CHALLITA-EID, PIA M.

/ APPLICANT: FARIS, MARY

/ APPLICANT: SAFFRAN, DOUGLAS

/ APPLICANT: AFAR, DANIEL

/ APPLICANT: LEVIN, ELANA

/ APPLICANT: HUBERT, RENE

/ APPLICANT: GE, WANGMAO

/ APPLICANT: JAKOBOVITS, AYA

/ TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

/ 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND

/ TITLE OF INVENTION: DETECTION OF CANCER

/ FILE REFERENCE: 51158-20014.00

/ CURRENT APPLICATION NUMBER: US/09/932,165

/ CURRENT FILING DATE: 2001-08-17

/ PRIOR APPLICATION NUMBER: 60/226,329

/ PRIOR FILING DATE: 2000-08-17

/ NUMBER OF SEQ ID NOS: 1508

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 290

/ LENGTH: 9

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-932-165-290

Query Match

Best Local Similarity 33.3%; Score 4; DB 12; Length 9;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

Db 3 LFFF 6

RESULT 26

US-09-932-165-452

/ Sequence 452, Application US/09932165

/ Publication No. US20030134784A1

/ GENERAL INFORMATION:

/ APPLICANT: RAITANO, ARTHUR

/ APPLICANT: CHALLITA-EID, PIA M.

/ APPLICANT: FARIS, MARY

/ APPLICANT: SAFFRAN, DOUGLAS

/ APPLICANT: AFAR, DANIEL

/ APPLICANT: LEVIN, ELANA

/ APPLICANT: HUBERT, RENE

/ APPLICANT: GE, WANGMAO

/ APPLICANT: JAKOBOVITS, AYA

/ TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

/ 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND

/ TITLE OF INVENTION: DETECTION OF CANCER

/ FILE REFERENCE: 51158-20014.00

/ CURRENT APPLICATION NUMBER: US/09/932,165

/ CURRENT FILING DATE: 2001-08-17

/ PRIOR APPLICATION NUMBER: 60/226,329

/ PRIOR FILING DATE: 2000-08-17

/ NUMBER OF SEQ ID NOS: 1508

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 452

/ LENGTH: 9

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-932-165-452

Query Match

Best Local Similarity 33.3%; Score 4; DB 12; Length 9;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

Db 2 LFFF 5

RESULT 27

US-09-932-165-490

/ Sequence 490, Application US/09932165

/ Publication No. US20030134784A1

/ GENERAL INFORMATION:

/ APPLICANT: RAITANO, ARTHUR

/ APPLICANT: CHALLITA-EID, PIA M.

/ APPLICANT: FARIS, MARY

/ APPLICANT: SAFFRAN, DOUGLAS

/ APPLICANT: AFAR, DANIEL

/ APPLICANT: LEVIN, ELANA

/ APPLICANT: HUBERT, RENE

/ APPLICANT: GE, WANGMAO

/ APPLICANT: JAKOBOVITS, AYA

/ TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

/ 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND

/ TITLE OF INVENTION: DETECTION OF CANCER

/ FILE REFERENCE: 51158-20014.00

/ CURRENT APPLICATION NUMBER: US/09/932,165

/ CURRENT FILING DATE: 2001-08-17

/ PRIOR APPLICATION NUMBER: 60/226,329

/ PRIOR FILING DATE: 2000-08-17

/ NUMBER OF SEQ ID NOS: 1508

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 490

/ LENGTH: 9

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-932-165-490

Query Match

Best Local Similarity 33.3%; Score 4; DB 12; Length 9;

Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

Db 3 LFFF 6

RESULT 28

US-09-932-165-660

/ Sequence 660, Application US/09932165

/ Publication No. US20030134784A1

/ GENERAL INFORMATION:

/ APPLICANT: RAITANO, ARTHUR

/ APPLICANT: CHALLITA-EID, PIA M.

/ APPLICANT: FARIS, MARY

/ APPLICANT: SAFFRAN, DOUGLAS

/ APPLICANT: AFAR, DANIEL

/ APPLICANT: LEVIN, ELANA

/ APPLICANT: HUBERT, RENE

/ APPLICANT: GE, WANGMAO

/ APPLICANT: JAKOBOVITS, AYA

/ TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

/ 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND

/ TITLE OF INVENTION: DETECTION OF CANCER

/ FILE REFERENCE: 51158-20014.00

/ CURRENT APPLICATION NUMBER: US/09/932,165

/ CURRENT FILING DATE: 2001-08-17

/ PRIOR APPLICATION NUMBER: 60/226,329

/ PRIOR FILING DATE: 2000-08-17

/ NUMBER OF SEQ ID NOS: 1508

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 660

/ LENGTH: 9

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-660

Query Match      33.3%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LFFF 4
        ||||
Db      2 LFFF 5

RESULT 29
US-09-932-165-695
; Sequence 695, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AVA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2B11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 695
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-695

Query Match      33.3%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LFFF 4
        ||||
Db      3 LFFF 6

RESULT 30
US-09-932-165-876
; Sequence 876, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AVA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2B11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
```

```
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 876
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-876

Query Match      33.3%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LFFF 4
        ||||
Db      6 LFFF 9

RESULT 31
US-10-239-313A-655
; Sequence 655, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 655
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-655

Query Match      33.3%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 NVLP 12
        ||||
Db      3 NVLP 6

RESULT 32
US-10-119-536A-183
; Sequence 183, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacte
; FILE REFERENCE: 4305/LJ091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
```

```

; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 183
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CT841 immunogenic peptide
US-10-119-536A-183

```

```

Query Match      33.3%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 FFPL 5
Db      5 FFPL 8

```

RESULT 33

```

US-09-894-018-305
; Sequence 305, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Transgenic mouse
US-09-894-018-305

```

```

Query Match      33.3%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 LPVV 8
Db      7 LPVV 10

```

RESULT 34

```

US-09-572-404B-1033
; Sequence 1033, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0

```

```

; SEQ ID NO 1033
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in BMP1B at 63-72 and may interact with Sequ
; OTHER INFORMATION: in this patent.
US-09-572-404B-1033

```

```

Query Match      33.3%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 LPVV 8
Db      2 LPVV 5

```

RESULT 35

```

US-09-572-404B-1035
; Sequence 1035, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 1035
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in BMP1B at 62-71 and may interact with Sequ
; OTHER INFORMATION: in this patent.
US-09-572-404B-1035

```

```

Query Match      33.3%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 LPVV 8
Db      3 LPVV 6

```

RESULT 36

```

US-09-572-404B-1109
; Sequence 1109, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 1109
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in BONZO OR STRL33 OR TYMSTR at 197-206 and m
; OTHER INFORMATION: interact with Sequence 1110 in this patent.
US-09-572-404B-1109

```

```

Query Match      33.3%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 3 FFLP 6
 ||||
 Db 4 FFLP 7

RESULT 37

US-09-895-298-138
 ; Sequence 138, Application US/09895298
 ; Publication No. US20030078405A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 47 Human Secreted Proteins

; FILE REFERENCE: P2035P1

; CURRENT APPLICATION NUMBER: US/09/895,298

; CURRENT FILING DATE: 2001-07-02

; PRIOR APPLICATION NUMBER: 09/591,16

; PRIOR FILING DATE: 2000-06-09

; PRIOR APPLICATION NUMBER: PCT/US99/29950

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: 60/113,006

; PRIOR FILING DATE: 1998-12-18

; PRIOR APPLICATION NUMBER: 60/112,809

; PRIOR FILING DATE: 1998-12-17

; NUMBER OF SEQ ID NOS: 231

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 138

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-895-298-138

Query Match

33.3%; Score 4; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12

||||

Db 3 NVLP 6

RESULT 38

US-09-932-165-388

; Sequence 388, Application US/09932165

; Publication No. US20030134784A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA M.

; APPLICANT: FARIS, MARY

; APPLICANT: SAFFRAN, DOUGLAS

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITS, AYA

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

; 83P2H3 AND CATT2E11 USEFUL IN TREATMENT AND

; DETECTION OF CANCER

; FILE REFERENCE: 51158-20014.00

; CURRENT APPLICATION NUMBER: US/09/932,165

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/226,329

; PRIOR FILING DATE: 2000-08-17

; NUMBER OF SEQ ID NOS: 1508

; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 388

LENGTH: 10

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-932-165-388

Query Match

33.3%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

||||

Db 7 LFFF 10

RESULT 39

US-09-932-165-553

; Sequence 553, Application US/09932165

; Publication No. US20030134784A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA M.

; APPLICANT: FARIS, MARY

; APPLICANT: SAFFRAN, DOUGLAS

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITS, AYA

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

; 83P2H3 AND CATT2E11 USEFUL IN TREATMENT AND

; DETECTION OF CANCER

; FILE REFERENCE: 51158-20014.00

; CURRENT APPLICATION NUMBER: US/09/932,165

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/226,329

; PRIOR FILING DATE: 2000-08-17

; NUMBER OF SEQ ID NOS: 1508

; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 553

LENGTH: 10

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-932-165-553

Query Match

33.3%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

||||

Db 7 LFFF 10

RESULT 40

US-09-932-165-558

; Sequence 558, Application US/09932165

; Publication No. US20030134784A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA M.

; APPLICANT: FARIS, MARY

; APPLICANT: SAFFRAN, DOUGLAS

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITS, AYA

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

; 83P2H3 AND CATT2E11 USEFUL IN TREATMENT AND

; DETECTION OF CANCER

; FILE REFERENCE: 51158-20014.00

; CURRENT APPLICATION NUMBER: US/09/932,165

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/226,329

; PRIOR FILING DATE: 2000-08-17

; NUMBER OF SEQ ID NOS: 1508

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 558

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-558

Query Match

33.3%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred.No. 7.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

|||

Db 3 LFFF 6

RESULT 41

US-09-932-165-751

; Sequence 751, Application US/09932165

; Publication No. US20030134784A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA M.

; APPLICANT: FARIS, MARY

; APPLICANT: SAFFRAN, DOUGLAS

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITS, AVA

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND

; FILE REFERENCE: 51158-20014.00

; CURRENT APPLICATION NUMBER: US/09/932,165

; PRIOR FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/226,329

; PRIOR FILING DATE: 2000-08-17

; NUMBER OF SEQ ID NOS: 1508

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 751

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-751

Query Match

33.3%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred.No. 7.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

|||

Db 3 LFFF 6

RESULT 42

US-09-932-165-1369

; Sequence 1369, Application US/09932165

; Publication No. US20030134784A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA M.

; APPLICANT: FARIS, MARY

; APPLICANT: SAFFRAN, DOUGLAS

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITS, AVA

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND

; TITLE OF INVENTION: DETECTION OF CANCER

; FILE REFERENCE: 51158-20014.00

; CURRENT APPLICATION NUMBER: US/09/932,165

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/226,329

; PRIOR FILING DATE: 2000-08-17

; NUMBER OF SEQ ID NOS: 1508

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1369

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1369

Query Match

33.3%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred.No. 7.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

|||

Db 1 LFFF 4

RESULT 43

US-09-833-039-129

; Sequence 129, Application US/09833039

; Publication No. US20030175960A1

; GENERAL INFORMATION:

; APPLICANT: Tureci, Ozlem

; APPLICANT: Sahin, Ugur

; APPLICANT: Pfrendschuh, Michael

; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof

; FILE REFERENCE: LUD 5622.1

; CURRENT APPLICATION NUMBER: US/09/833,039

; CURRENT FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: US 09/409,455

; PRIOR FILING DATE: 1999-09-30

; PRIOR APPLICATION NUMBER: US 09/344,040

; PRIOR FILING DATE: 1999-06-25

; PRIOR APPLICATION NUMBER: US 09/105,839

; PRIOR FILING DATE: 1998-06-26

; PRIOR APPLICATION NUMBER: US 08/851,130

; PRIOR FILING DATE: 1997-05-05

; NUMBER OF SEQ ID NOS: 129

; SEQ ID NO 129

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-833-039-129

Query Match

33.3%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred.No. 7.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPV 7

|||

Db 5 FLPV 8

RESULT 44

US-10-231-417-614

; Sequence 614, Application US/10231417

; Publication No. US20030176681A1

; GENERAL INFORMATION:

; APPLICANT: Feng et al.

; TITLE OF INVENTION: 148 Human Secreted Proteins

; FILE REFERENCE: P2019P1

; CURRENT APPLICATION NUMBER: US/10/231,417

; CURRENT FILING DATE: 2002-08-30

; PRIOR APPLICATION NUMBER: US/09/296,622

; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 619
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 614
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-417-614

Query Match 33.3%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5
Db 5 FFFL 8

RESULT 45
US-10-200-708-295
; Sequence 295, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 295
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-295

Query Match 33.3%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12
Db 4 NVLP 7

RESULT 46
US-10-200-708-318
; Sequence 318, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 318
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-318

Query Match 33.3%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12
Db 6 NVLP 9

RESULT 47
US-10-177-277-129
; Sequence 129, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determining Expression of an Ssx Gene, Peptides Derived From Said Ssx Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 129
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-129

Query Match 33.3%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPV 7
Db 5 FLPV 8

RESULT 48
US-09-573-822C-403
; Sequence 403, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: Protpatent version 1.0
; SEQ ID NO 403
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG130 at 207-216 and may interact with Seq
; OTHER INFORMATION: in this patent.
US-09-573-822C-403

Query Match 33.3%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VNVL 11
|
|
|
|
Db 4 VNVL 7

RESULT 49

US-10-057-763-1

; Sequence 1, Application US/10057763

; Publication No. US20020155184A1

; GENERAL INFORMATION:

; APPLICANT: IZEVIGIE, ERNEST B.

; TITLE OF INVENTION: PHYTOCHEMOTHERAPY FOR CANCER

; FILE REFERENCE: 11428.0003.NFUS01 (JASU003)

; CURRENT APPLICATION NUMBER: US/10/057,763

; CURRENT FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: 60/264,035

; PRIOR FILING DATE: 2001-01-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Vernonia amygdalina

US-10-057-763-1

Query Match 33.3%; Score 4; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VNVV 10
|
|
|
|
Db 5 VNVV 8

RESULT 50

US-09-828-708-79

; Sequence 79, Application US/09828708

; Patent No. US20020146753A1

; GENERAL INFORMATION:

; APPLICANT: Ditzel, H.

; APPLICANT: Burton, D.

; APPLICANT: Schaller, M.

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici

; TITLE OF INVENTION: autoimmune disease

; FILE REFERENCE: 1361.005US1

; CURRENT APPLICATION NUMBER: US/09/828,708

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 123

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 79

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-828-708-79

Query Match 33.3%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VNVV 10
|
|
|
|
Db 6 VNVV 9

RESULT 51

US-10-057-789-218

; Sequence 218, Application US/10057789

; Publication No. US20030082522A1

; GENERAL INFORMATION:
; APPLICANT: Paul Haynes
; APPLICANT: Jing Wei
; APPLICANT: John Yates
; APPLICANT: Nancy Andon
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE
; TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES
; FILE REFERENCE: NAD11.022A
; CURRENT APPLICATION NUMBER: US/10/057,789
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/264,576
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/305,232
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 218
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 9
; OTHER INFORMATION: Xaa = Modified Cysteine
US-10-057-789-218

Query Match 33.3%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFLP 6
|
|
|
|
Db 5 FFLP 8

RESULT 52

US-10-212-628-218

; Sequence 218, Application US/10212628

; Publication No. US20030087329A1

; GENERAL INFORMATION:

; APPLICANT: Paul Haynes

; APPLICANT: Jing Wei

; APPLICANT: John Yates

; APPLICANT: Nancy Andon

; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE

; TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES

; FILE REFERENCE: NAD11.022CP1

; CURRENT APPLICATION NUMBER: US/10/212,628

; CURRENT FILING DATE: 2002-08-01

; PRIOR APPLICATION NUMBER: US 60/264,576

; PRIOR FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: US 60/305,232

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 10/057,789

; NUMBER OF SEQ ID NOS: 311

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 218

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: 9

; OTHER INFORMATION: Xaa = Modified Cysteine

US-10-212-628-218

Query Match 33.3%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFLP 6
|
|
|
|

Db 5 FFLP 8

RESULT 53

US-10-116-252-22
; Sequence 22, Application US/10116252
; Publication No. US20030028008A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Seven Transmembrane Receptor Polynucleotides,
; Polypeptides, and Antibodies
; FILE REFERENCE: P7007P1
; CURRENT APPLICATION NUMBER: US/10/116,252
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US/09/711,909
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: PCT/US00/13737
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 60/135,167
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/143,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: 60/152,934
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/189,029
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-252-22

Query Match

Best Local Similarity 33.3%; Score 4; DB 15; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6

Db 4 FFLP 7

RESULT 54

US-09-853-080-32
; Sequence 32, Application US/09853080
; Patent No. US20020068303A1
; GENERAL INFORMATION:
; APPLICANT: Laub, Ruth
; TITLE OF INVENTION: ANTIGENIC POLYPEPTIDE SEQUENCES OF FACTOR
; VIII, FRAGMENTS AND/OR EPITOPES OF THESE SEQUENCES
; FILE REFERENCE: VANMA48.001CP1
; CURRENT APPLICATION NUMBER: US/09/853,080
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 08/765,837
; PRIOR FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: PCT/BE95/00068
; PRIOR FILING DATE: 1995-07-14
; PRIOR APPLICATION NUMBER: BE 9400666
; PRIOR FILING DATE: 1994-07-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: epitope Pro 2292 to Tyr 2305 of C domain of Factor
; OTHER INFORMATION: VIII
US-09-853-080-32

Query Match

33.3%; Score 4; DB 9; Length 14;

Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVVN 9

Db 1 PVVN 4

RESULT 55

US-09-767-460-12
; Sequence 12, Application US/09767460
; Patent No. US20020009756A1
; GENERAL INFORMATION:
; APPLICANT: Mandell, Arnold
; APPLICANT: Seiz, Karen
; APPLICANT: Shlesinger, Michael
; TITLE OF INVENTION: Algorithms Design of Peptides for Binding and/or Modulation o:
; TITLE OF INVENTION: Functions of Receptors and/or Other Proteins
; FILE REFERENCE: 01561-0002-CPUS01
; CURRENT APPLICATION NUMBER: US/09/767,460
; CURRENT FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-767-460-12

Query Match

Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VNVL 11

Db 10 VNVL 13

RESULT 56

US-09-981-876-224
; Sequence 224, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525
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; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 224
; LENGTH: 15

Query Match      33.3%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FFFL 5
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Db       8 FFFL 11

RESULT 57
US-09-148-545-224
; Sequence 224, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
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; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,492
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
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; EARLIER APPLICATION NUMBER: 60/056,872
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; EARLIER APPLICATION NUMBER: 60/056,864
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; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599
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; EARLIER APPLICATION NUMBER: 60/047,588
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
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; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
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; EARLIER APPLICATION NUMBER: 60/056,881
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; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 224
; LENGTH: 15

Query Match 33.3%; Score 4; DB 11; Length 15;

Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPFL 5
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Db 8 FPFL 11

RESULT 58

US-10-336-491-6
; Sequence 6, Application US/10336491
; Publication No. US20030148464A1
; GENERAL INFORMATION:
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Pedersen, Henrik
; TITLE OF INVENTION: Oxaloacetate Hydrolase Deficient Fungal Host Cells
; FILE REFERENCE: 5789.200-US
; CURRENT APPLICATION NUMBER: US/10/336,491
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US/09/501,612
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-336-491-6

Query Match 33.3%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVVN 9
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Db 6 PVVN 9

RESULT 59

US-09-986-480-261
; Sequence 261, Application US/09986480
; Publication No. US20030027999A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 143 Human Secreted Proteins
; FILE REFERENCE: PS500P1
; CURRENT APPLICATION NUMBER: US/09/986,480
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/12788
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/134,068
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 456
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 261

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; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-480-261

Query Match      33.3%; Score 4; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LFFP 4
Db      10 LFFP 13

RESULT 60
US-09-071-838-88
; Sequence 88, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Ydegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-086100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-071-838-88

Query Match      33.3%; Score 4; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 FFLP 6
Db      10 FFLP 13

RESULT 61
US-09-981-876-221
; Sequence 221, Application US/09981876
; Patent No. US20020164669A1
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
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; PRIOR FILING DATE: 1997-03-07
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; PRIOR APPLICATION NUMBER: 60/043,580
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; PRIOR APPLICATION NUMBER: 60/048,974
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 05-Sep-1997
; PRIOR APPLICATION NUMBER: 60/047,599
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; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 17

Query Match 33.3%; Score 4; DB 10; Length 17;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 LFFF 4
Db 6 LFFF 9

RESULT 62

US-09-148-545-221
; Sequence 221, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482

[illegible]

; EARLIER FILING DATE: 1997-05-23
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 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,664
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,876
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,881
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,909
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,875
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,862
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,887
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,908
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/048,964
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/057,650
 ; EARLIER FILING DATE: 1997-09-05
 ; EARLIER APPLICATION NUMBER: 60/056,884
 ; EARLIER FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 280
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 221
 ; LENGTH: 17

Query Match 33.3%; Score 4; DB 11; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFF 4
 DB 6 LPFF 9

RESULT 63

US-09-996-069-30
 ; Sequence 30, Application US/09996069
 ; Publication No. US20030036199A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bamdad, Cynthia
 ; APPLICANT: Bamdad, R. Shoshana
 ; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBI
 ; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER
 ; FILE REFERENCE: M01015/70071
 ; CURRENT APPLICATION NUMBER: US/09/996,069
 ; CURRENT FILING DATE: 2001-11-27
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 30
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-996-069-30

Query Match 33.3%; Score 4; DB 11; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12
 DB 5 NVLP 8

RESULT 64

US-09-996-069-31
 ; Sequence 31, Application US/09996069
 ; Publication No. US20030036199A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bamdad, Cynthia
 ; APPLICANT: Bamdad, R. Shoshana
 ; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INH
 ; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER
 ; FILE REFERENCE: M01015/70071
 ; CURRENT APPLICATION NUMBER: US/09/996,069
 ; CURRENT FILING DATE: 2001-11-27
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 31
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-996-069-31

Query Match 33.3%; Score 4; DB 11; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12
 DB 5 NVLP 8

RESULT 65

US-10-213-512-88
 ; Sequence 88, Application US/10213512
 ; Publication No. US20030110536A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischer, Robert L.
 ; APPLICANT: Ohad, Nir
 ; APPLICANT: Kiyosue, Tomohiro
 ; APPLICANT: Yadegari, Ramin
 ; APPLICANT: Margossian, Linda
 ; APPLICANT: Harada, John
 ; APPLICANT: Goldberg, Robert B.
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
 ; TITLE OF INVENTION: Fruit Development in Plants
 ; FILE REFERENCE: 023070-086110US
 ; CURRENT APPLICATION NUMBER: US/10/213,512
 ; CURRENT FILING DATE: 2002-08-06
 ; PRIOR APPLICATION NUMBER: US/09/177,206
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: US 09/071,838
 ; PRIOR FILING DATE: 1998-05-01
 ; NUMBER OF SEQ ID NOS: 324
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO 88
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis sp.
 US-10-213-512-88

Query Match 33.3%; Score 4; DB 15; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6
|
|
|
|
Db 10 FFLP 13

RESULT 66

US-10-084-813-248
; Sequence 248, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 248
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-248

Query Match 33.3%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-10-084-813-248

QY 3 FFLP 6
|
|
|
|
Db 12 FFLP 15

RESULT 67

US-10-084-813-249
; Sequence 249, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 249
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-249

Query Match 33.3%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-10-084-813-249

QY 3 FFLP 6
|
|
|
|
Db 8 FFLP 11

RESULT 68

US-10-084-813-250
; Sequence 250, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 250
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-250

Query Match 33.3%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-10-084-813-250

QY 3 FFLP 6
|
|
|
|
Db 4 FFLP 7

RESULT 69

US-10-157-031-192
; Sequence 192, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequenc
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-192

Query Match 33.3%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-10-157-031-192

QY 8 VNVL 11
|
|
|
|
Db 3 VNVL 6

RESULT 70

US-10-106-698-7294
; Sequence 7294, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
US-10-106-698-7294

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; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 7294
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (12)_
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (14)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (17)_
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (18)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-10-106-698-7294

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Query Match          33.3%; Score 4; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 FFFL 5
        ||||
Db      6 FFFL 9

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RESULT 71
US-10-225-567A-1666
; Sequence 1666, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1666
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1666

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Query Match          33.3%; Score 4; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      7 VVNV 10
        ||||
Db      6 VVNV 9

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RESULT 72
US-08-464-363-29

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; Sequence 29, Application US/08464363
; Publication No. US20030035815A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,363
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-464-363-29

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Query Match          33.3%; Score 4; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      5 LPVV 8
        ||||
Db      15 LPVV 18

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RESULT 73
US-09-864-761-35505
; Sequence 35505, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312

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; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35505
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF146367.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 7.8
; OTHER INFORMATION: EST_HUMAN HIT: A1820784.1, EVALUE 9.00e-06
US-09-864-761-35505

Query Match 33.3%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPV 7
|||
Db 8 FLPV 11

RESULT 74
US-09-735-705-405
; Sequence 405, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Panger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Panger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 405
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-405
Query Match 33.3%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Qy 7 VVNV 10
|||
Db 2 VVNV 5
|||
RESULT 75
US-09-841-132-156
; Sequence 156, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 156
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-841-132-156
Query Match 33.3%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Qy 3 FFLP 6
|||
Db 10 FFLP 13

Search completed: November 25, 2003, 20:25:29
Job time : 24.8723 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 13.0851 Seconds
(without alignments)
38.802 Million cell updates/sec

Title: US-09-641-801-4
Perfect score: 12
Sequence: 1 LFFFLPVNVLP 12

Scoring table: OLIGO
Gapex 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

- Database :
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	100.0	12	4	US-09-641-803-4
2	5	41.7	5	2	US-08-920-162A-30
3	5	41.7	5	3	US-09-356-931-30
4	5	41.7	11	1	US-08-552-907-16
5	5	41.7	11	1	US-08-464-531-57
6	5	41.7	11	2	US-08-461-598-57
7	5	41.7	11	3	US-08-691-045-16
8	5	41.7	11	3	US-08-322-137-57
9	5	41.7	11	3	US-08-582-333A-68
10	5	41.7	20	1	US-08-468-543-23
11	5	41.7	20	2	US-08-469-692-23
12	5	41.7	20	2	US-08-398-046-23
13	4	33.3	5	2	US-08-920-162A-24
14	4	33.3	5	2	US-08-920-162A-25
15	4	33.3	5	2	US-08-920-162A-26
16	4	33.3	5	3	US-09-356-931-24
17	4	33.3	5	3	US-09-356-931-25
18	4	33.3	5	3	US-09-356-931-26
19	4	33.3	5	4	US-08-703-675C-24
20	4	33.3	5	4	US-08-703-675C-25
21	4	33.3	5	4	US-08-703-675C-26
22	4	33.3	5	4	US-08-236-160-17
23	4	33.3	5	4	US-09-236-160-52
24	4	33.3	6	1	US-08-257-782-28
25	4	33.3	6	1	US-08-257-782-31
26	4	33.3	6	1	US-08-257-782-33
27	4	33.3	6	1	US-07-807-529A-13

ALIGNMENTS

RESULT 1
US-09-641-803-4
; Sequence 4, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-4

Query Match 100.0%; Score 12; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVNVLP 12
|||||
Db 1 LFFFLPVNVLP 12

RESULT 2
US-08-920-162A-30
; Sequence 30, Application US/08920162A
; Patent No. 5985242
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide
; TITLE OF INVENTION: Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162A
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/703,675

; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 21-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1-5
; OTHER INFORMATION: /note= D amino acid
US-08-920-162A-30
Query Match 41.7%; Score 5; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LFFFL 5
|||||
Db 1 LFFFL 5
RESULT 3
US-09-356-931-30
; Sequence 30, Application US/09356931
; Patent No. 6277826
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; TITLE OF INVENTION: Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1784
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/356,931
; FILING DATE: 19-JUL-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/920,162
; FILING DATE: 27-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/897,342
; FILING DATE: 21-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Jr., Giulio A.
 REGISTRATION NUMBER: 31,503
 REFERENCE/DOCKET NUMBER: PFI-016CP4CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 1-5
 OTHER INFORMATION: /note= D amino acid
 US-09-356-931-30

Query Match 41.7%; Score 5; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFL 5
 Db 1 LFFFL 5

RESULT 4

US-08-552-907-16
 Sequence 16, Application US/08552907
 Patent No. 5744299
 GENERAL INFORMATION:
 APPLICANT: Henrickson, Kelly J.
 APPLICANT: Fan, Jiang (n.m.i.)
 TITLE OF INVENTION: HUMAN PARAINFLUENZA VIRUS-1 ASSAY
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: U.S.A.
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/552,907
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Baker, Jean C.
 REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 650053.91037
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 277-5000
 TELEFAX: (414) 271-3552
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-552-907-16

Query Match 41.7%; Score 5; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVNVL 11

Db 7 VVNVL 11

RESULT 5

US-08-464-531-57
 Sequence 57, Application US/08464531
 Patent No. 5789184
 GENERAL INFORMATION:
 APPLICANT: FOWLKES, Dana M.
 APPLICANT: BROACH, Jim
 APPLICANT: MANFREDI, John
 APPLICANT: KLEIN, Christine
 APPLICANT: MURPHY, Andrew J.
 APPLICANT: PAUL, Jeremy
 APPLICANT: TRUEHEART, Joshua
 TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
 TITLE OF INVENTION: PHERMON SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
 NUMBER OF SEQUENCES: 119
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,531
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/322,137
 FILING DATE: 13-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/309,313
 FILING DATE: 20-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/190,328
 FILING DATE: 31-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/041,431
 FILING DATE: 31-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, Iver P.
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: FOLWKS=2G
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-464-531-57

Query Match 41.7%; Score 5; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6
 Db 6 FFFLP 10

RESULT 6

```

US-08-461-598-57
; Sequence 57, Application US/08461598
; Patent No. 5876951
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,598
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/322,137
; FILING DATE: 13-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/309,313
; FILING DATE: 20-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,328
; FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,431
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOLWKES=2F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-461-598-57
Query Match 41.7%; Score 5; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFFLP 6
Db 6 PFFLP 10

RESULT 7
US-08-691-045-16
; Sequence 16, Application US/08691045
; Patent No. 6015664
; GENERAL INFORMATION:
; APPLICANT: Henrickson, Kelly J.

```

```

; APPLICANT: Fan, Jiang (n.m.i.)
; TITLE OF INVENTION: VIRUS ASSAY METHOD
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,045
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 650053.91037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-691-045-16
Query Match 41.7%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VNVNL 11
Db 7 VNVNL 11

RESULT 8
US-08-322-137-57
; Sequence 57, Application US/08322137
; Patent No. 6100042
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/322,137

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; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/309,313
;   FILING DATE: 20-SEP-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/190,328
;   FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/041,431
;   FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: COOPER, Iver P.
;   REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOLWKES=2C
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-628-5197
;   TELEFAX: 202-737-3528
;   TELEX: 248633
; INFORMATION FOR SEQ ID NO: 57:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 11 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
; US-08-322-137-57

Query Match      41.7%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FFFLP 6
Db      6 FFFLP 10

RESULT 9
US-08-582-333A-68
; Sequence 68, Application US/08582333A
; Patent No. 625059
; GENERAL INFORMATION:
;   APPLICANT: Klein, Christine A.
;   TITLE OF INVENTION: Methods and Compositions for
;   IDENTIFYING RECEPTOR EFFECTORS
;   NUMBER OF SEQUENCES: 98
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: LAHIVE & COCKFIELD
;     STREET: 28 State Street
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: USA
;     ZIP: 02109-1875
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/582,333A
;   FILING DATE: 17-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Catherine J. Kara
;   REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: CPI-012CP5
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617)227-7400
;   TELEFAX: (617)227-4214
; INFORMATION FOR SEQ ID NO: 68:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 11 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-582-333A-68

Query Match      41.7%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FFFLP 6
Db      6 FFFLP 10

RESULT 10
US-08-468-543-23
; Sequence 23, Application US/08468543
; Patent No. 5726153
; GENERAL INFORMATION:
;   APPLICANT: Lees, Robert S. et al.
;   TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR ARTERIAL IMAGING
;   NUMBER OF SEQUENCES: 27
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fish & Richardson P.C.
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: MA
;     COUNTRY: USA
;     ZIP: 02110-2804
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/468,543
;   FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/398,046
;   FILING DATE: 02-MAR-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/201,057
;   FILING DATE: 24-FEB-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/048,569
;   FILING DATE: 16-APR-1993
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/694,929
;   FILING DATE: 02-MAY-1991
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/518,215
;   FILING DATE: 03-MAY-1990
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/518,142
;   FILING DATE: 03-MAY-1990
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/189,130
;   FILING DATE: 02-MAY-1988
; ATTORNEY/AGENT INFORMATION:
;   NAME: Clark, Paul T.
;   REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04547/002003
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/542-5070
;   TELEFAX: 617/542-8906
;   TELEX: 200154
; INFORMATION FOR SEQ ID NO: 23:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 20
;     TYPE: amino acid
;     STRANDEDNESS:
;     TOPOLOGY: linear
;   MOLECULE TYPE: linear
; US-08-468-543-23
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Query Match 41.7%; Score 5; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVNVV 10
 Db 11 PVNVV 15

RESULT 11
 US-08-469-692-23
 ; Sequence 23, Application US/08469692
 ; Patent No. 5955055
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Robert S. et al.
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR ARTERIAL IMAGING
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/469,692
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/398,046
 ; FILING DATE: 02-MAR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/201,057
 ; FILING DATE: 24-FEB-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/048,569
 ; FILING DATE: 16-APR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/694,929
 ; FILING DATE: 02-MAY-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/518,215
 ; FILING DATE: 03-MAY-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/518,142
 ; FILING DATE: 03-MAY-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/189,130
 ; FILING DATE: 02-MAY-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 04547/002002
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-469-692-23

Query Match 41.7%; Score 5; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 38;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PVNVV 10
 Db 11 PVNVV 15

RESULT 12
 US-08-398-046-23
 ; Sequence 23, Application US/08398046
 ; Patent No. 5972890
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Robert S. et al.
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR
 ; TITLE OF INVENTION: ARTERIAL IMAGING
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX
 ; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
 ; SOFTWARE: WordPerfect (Version 5.0)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/398,046
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/201,057
 ; FILING DATE:
 ; APPLICATION NUMBER: US/08/048,569
 ; FILING DATE:
 ; APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/694,929
 ; FILING DATE: May 3, 1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/517,215
 ; FILING DATE: May 3, 1990
 ; APPLICATION NUMBER: 07/518,142
 ; FILING DATE: May 3, 1990
 ; APPLICATION NUMBER: 07/189,130
 ; FILING DATE: May 2, 1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 04547/002001
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-398-046-23

Query Match 41.7%; Score 5; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVNVV 10
 Db 11 PVNVV 15

RESULT 13

```
US-08-920-162A-24
; Sequence 24, Application US/08920162A
; Patent No. 5985242
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162A
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 21-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1-5
; OTHER INFORMATION: /note= D amino acid
US-08-920-162A-24

Query Match 33.3%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5
Db 1 FFFL 4

RESULT 14
US-08-920-162A-25
; Sequence 25, Application US/08920162A
; Patent No. 5985242
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 21-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1-5
; OTHER INFORMATION: /note= D amino acid
US-08-920-162A-24

Query Match 33.3%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5
Db 1 FFFL 4

RESULT 15
US-08-920-162A-26
; Sequence 26, Application US/08920162A
; Patent No. 5985242
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162A
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 21-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1-5
; OTHER INFORMATION: /note= D amino acid
US-08-920-162A-25

Query Match 33.3%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5
Db 2 FFFL 5
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162A
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/703,675
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 21-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1-5
; OTHER INFORMATION: /note= D amino acid
; US-08-920-162A-26

Query Match 33.3%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5
Db 2 FFPL 5

RESULT 16
US-09-356-931-24
; Sequence 24, Application US/09356931
; Patent No. 6277826
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; TITLE OF INVENTION: Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1784
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/356,931
; FILING DATE: 19-JUL-1999
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/920,162
; FILING DATE: 27-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/897,342
; FILING DATE: 21-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/703,675
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Jr., Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-016CP4CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1-5
; OTHER INFORMATION: /note= D amino acid
; US-09-356-931-24

Query Match 33.3%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5
Db 1 FFPL 4

RESULT 17
US-09-356-931-25
; Sequence 25, Application US/09356931
; Patent No. 6277826
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; TITLE OF INVENTION: Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1784
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/356,931
; FILING DATE: 19-JUL-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/920,162
; FILING DATE: 27-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/897,342

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; FILING DATE: 21-JUL-1997
; PRIORITY APPLICATION NUMBER: USN 08/703,675
; FILING DATE: 27-AUG-1996
; PRIORITY APPLICATION DATA:
; FILING DATE: 27-AUG-1996
; APPLICATION NUMBER: USN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Jr., Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-016CP4CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1-5
; OTHER INFORMATION: /note= D amino acid
; US-09-356-931-25

Query Match 33.3%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5
Db 2 FFPL 5

RESULT 18
US-09-356-931-26
; Sequence 26, Application US/09356931
; Patent No. 6277826
; GENERAL INFORMATION:
; APPLICANT: Findex, M. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1784
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/356,931
; FILING DATE: 19-JUL-1999
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USN 08/920,162
; FILING DATE: 27-AUG-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/897,342
; FILING DATE: 21-JUL-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USN 08/703,675
; FILING DATE: 27-AUG-1996
; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: USN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Jr., Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-016CP4CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1-5
; OTHER INFORMATION: /note= D amino acid
; US-09-356-931-26

Query Match 33.3%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5
Db 2 FFPL 5

RESULT 19
US-08-703-675C-24
; Sequence 24, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findex, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION: 1-5
OTHER INFORMATION: /note= D amino acid
US-08-703-675C-24

Query Match 33.3%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFPL 5
Db 1 PFPL 4

RESULT 20

US-08-703-675C-25
Sequence 25, Application US/08703675C
Patent No. 6303567

GENERAL INFORMATION:
APPLICANT: Findex, Mark A. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703.675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

Aggregation Comprising D-

FEATURE:
NAME/KEY: Modified site
LOCATION: 1-5
OTHER INFORMATION: /note= D amino acid
US-08-703-675C-25

Query Match 33.3%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFPL 5
Db 2 PFPL 5

RESULT 21

US-08-703-675C-26
Sequence 26, Application US/08703675C
Patent No. 6303567

GENERAL INFORMATION:
APPLICANT: Findex, Mark A. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703.675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION: 1-5
OTHER INFORMATION: /note= D amino acid
US-08-703-675C-26

Aggregation Comprising

Query Match 33.3%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY      2 FFPL 5
Db      2 FFPL 5

RESULT 22
US-09-236-160-17
; Sequence 17, Application US/09236160A
; Patent No. 6307090
; GENERAL INFORMATION:
; APPLICANT: BURKE Jr., Terrence R.
; TITLE OF INVENTION: ACYLATED OLIGOPEPTIDE DERIVATIVES HAVING CELL SIGNAL
; TITLE OF INVENTION: INHIBITING ACTIVITY
; FILE REFERENCE: 175895
; CURRENT APPLICATION NUMBER: US/09/236,160A
; CURRENT FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 5
; TYPE: PRT
; ORGANISM: mammalian
US-09-236-160-17

Query Match      33.3%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VNVL 11
Db      1 VNVL 4

RESULT 23
US-09-236-160-52
; Sequence 52, Application US/09236160A
; Patent No. 6307090
; GENERAL INFORMATION:
; APPLICANT: BURKE Jr., Terrence R.
; TITLE OF INVENTION: ACYLATED OLIGOPEPTIDE DERIVATIVES HAVING CELL SIGNAL
; TITLE OF INVENTION: INHIBITING ACTIVITY
; FILE REFERENCE: 175895
; CURRENT APPLICATION NUMBER: US/09/236,160A
; CURRENT FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 5
; TYPE: PRT
; ORGANISM: mammalian
US-09-236-160-52

Query Match      33.3%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VNVL 11
Db      1 VNVL 4

RESULT 24
US-08-257-782-28
; Sequence 28, Application US/08257782
; Patent No. 5480971
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard A.
; APPLICANT: Ostrech, John M.
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: PERALKYLATED OLIGOPEPTIDE MIXTURES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 135 South LaSalle Street, Suite 1625
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,782
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/079,144
; FILING DATE: 13-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-781-9470
; TELEFAX: 312-781-9548
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "This is a permethylated
; OTHER INFORMATION: peptide."
US-08-257-782-28

Query Match      33.3%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LFFF 4
Db      1 LFFF 4

RESULT 25
US-08-257-782-31
; Sequence 31, Application US/08257782
; Patent No. 5480971
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard A.
; APPLICANT: Ostrech, John M.
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: PERALKYLATED OLIGOPEPTIDE MIXTURES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 135 South LaSalle Street, Suite 1625
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,782
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/079,144
FILING DATE: 13-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-781-9470
TELEFAX: 312-781-9548
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..6
OTHER INFORMATION: /note= "This is a permethylated peptide."
US-08-257-782-31

Query Match 33.3%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF 4
Db 1 LFFF 4

RESULT 26
US-08-257-782-33
Sequence 33, Application US/08257782
Patent No. 5480971
GENERAL INFORMATION:
APPLICANT: Houghten, Richard A.
APPLICANT: Ostreich, John M.
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: PERALKYLATED OLIGOPEPTIDE MIXTURES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 135 South LaSalle Street, Suite 1625
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,782
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/079,144
FILING DATE: 13-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-781-9470
TELEFAX: 312-781-9548
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide

LOCATION: 1..6
OTHER INFORMATION: /note= "This is a permethylated peptide."
US-08-257-782-33

Query Match 33.3%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF 4
Db 1 LFFF 4

RESULT 27
US-07-807-529A-13
Sequence 13, Application US/07807529A
Patent No. 5547669
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
APPLICANT: Morgenstern, Jay
APPLICANT: Bond, Julian F.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: One Kendall Square, Building 600
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,529A
FILING DATE: 19911213
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Channing, Stacey L.
REGISTRATION NUMBER: 31,095
REFERENCE/DOCKET NUMBER: IPC-027/imi-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 494-0060
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-807-529A-13

Query Match 33.3%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 3 LPVV 6

RESULT 28

US-07-807-529A-53
; Sequence 53, Application US/07807529A
; Patent No. 5547669
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Wei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: One Kendall Square, Building 600
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/807,529A
; FILING DATE: 19911213
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Channing, Stacey L.
; REGISTRATION NUMBER: 31,095
; REFERENCE/DOCKET NUMBER: IPC-027/imi-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 494-0060
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-07-807-529A-53

Query Match 33.3%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8
|||
Db 3 LPVV 6

RESULT 29
US-08-577-846-28
; Sequence 28, Application US/08577846
; Patent No. 5763193
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard A.
; APPLICANT: Ostrech, John M.
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: PERALKYLATED OLIGOPEPTIDE MIXTURES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 135 South Lasalle Street, Suite 1625
; CITY: Chicago
; STATE: Illinois

; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/577,846
; FILING DATE: 22-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,782
; FILING DATE: 09-JUN-1994
; APPLICATION NUMBER: US 08/079,144
; FILING DATE: 13-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-781-9470
; TELEFAX: 312-781-9548
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "this is a permethylated
; OTHER INFORMATION: peptide."
US-08-577-846-28

Query Match 33.3%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4
|||
Db 1 LFFF 4

RESULT 30
US-08-577-846-31
; Sequence 31, Application US/08577846
; Patent No. 5763193
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard A.
; APPLICANT: Ostrech, John M.
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: PERALKYLATED OLIGOPEPTIDE MIXTURES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 135 South Lasalle Street, Suite 1625
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/577,846
; FILING DATE: 22-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,782
; FILING DATE: 09-JUN-1994

```
; APPLICATION NUMBER: US 08/079,144
; FILING DATE: 13-JUN-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: Gamson, Edward P.
;   REGISTRATION NUMBER: 29,381
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 312-781-9470
;     TELEFAX: 312-781-9548
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 6 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "This is a permethylated
;   OTHER INFORMATION: peptide."
US-08-577-846-31

Query Match 33.3%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF 4
Db 1 LFFF 4

RESULT 31
US-08-577-846-33
; Sequence 33, Application US/08577846
; Patent No. 5763193
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard A.
; APPLICANT: Ostreich, John M.
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: PERALKYLATED OLIGOPEPTIDE MIXTURES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 135 South LaSalle Street, Suite 1625
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/577,846
; FILING DATE: 22-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,782
; FILING DATE: 09-JUN-1994
; APPLICATION NUMBER: US 08/079,144
; FILING DATE: 13-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-781-9470
; TELEFAX: 312-781-9548
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 6 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
```

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; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "This is a permethylated
;   OTHER INFORMATION: peptide."
US-08-577-846-33

Query Match 33.3%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF 4
Db 1 LFFF 4

RESULT 32
US-08-300-928C-62
; Sequence 62, Application US/08300928C
; Patent No. 6019972
; GENERAL INFORMATION:
; APPLICANT: GEFTER, Malcolm L. et al.
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
;   TITLE OF INVENTION: PROTEIN (TRPP)
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/300,928C
; FILING DATE: September 2, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,529
; FILING DATE: December 13, 1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: AMY E. MANDRAGOURAS
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 6 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-300-928C-62

Query Match 33.3%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 3 LPVV 6

RESULT 33
US-08-430-944D-62
; Sequence 62, Application US/08430944D
; Patent No. 6025162
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,944D
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-430-944D-62

Query Match 33.3%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 3 LPVV 6

RESULT 34
US-08-430-014-62
; Sequence 62, Application US/08430014
; Patent No. 6048962
; GENERAL INFORMATION:
; APPLICANT: GEFTER, Malcolm L. et al.
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,014
```

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;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/300,928
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 002.6US(IMI-044)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-430-014-62

Query Match 33.3%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 3 LPVV 6

RESULT 35
US-08-431-184-62
; Sequence 62, Application US/08431184
; Patent No. 6120769
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,184
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-431-184-62

Query Match 33.3%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 3 LPVV 6

RESULT 36

US-08-559-492-10
; Sequence 10, Application US/08559492
; Patent No. 5843884
; GENERAL INFORMATION:
; APPLICANT: Sims, Peter J.
; TITLE OF INVENTION: C9 Complement Inhibitor
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,492
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-559-492-10

Query Match 33.3%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFPL 5
Db 1 PFPL 4

RESULT 37

US-09-561-500-37
; Sequence 37, Application US/09561500
; Patent No. 6342219
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
; FILE REFERENCE: 4001.002500
; CURRENT APPLICATION NUMBER: US/09/561,500
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/131,432

; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-561-500-37

Query Match 33.3%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 3 LPVV 6

RESULT 38

US-09-561-108-37
; Sequence 37, Application US/09561108
; Patent No. 6342221
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VE
; FILE REFERENCE: 4001.002584
; CURRENT APPLICATION NUMBER: US/09/561,108
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/131,432
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-561-108-37

Query Match 33.3%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 3 LPVV 6

RESULT 39

US-09-561-526-37
; Sequence 37, Application US/09561526
; Patent No. 6416758
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF
; FILE REFERENCE: 4001.002586
; CURRENT APPLICATION NUMBER: US/09/561,526
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/131,432
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-561-526-37

Query Match      33.3%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 3 LPVV 6

RESULT 40
US-09-561-499-37
; Sequence 37, Application US/09561499
; Patent No. 6524583
; GENERAL INFORMATION:
; APPLICANT: Philip B. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF
; FILE REFERENCE: 4001.002582
; CURRENT APPLICATION NUMBER: US/09/561,499
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/131,432
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-561-499-37

Query Match      33.3%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 3 LPVV 6

RESULT 41
US-07-807-529A-45
; Sequence 45, Application US/07807529A
; Patent No. 5547669
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: One Kendall Square, Building 600
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/807,529A
; FILING DATE: 19911213
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Channing, Stacey L.
; REGISTRATION NUMBER: 31,095
; REFERENCE/DOCKET NUMBER: IPC-027/imi-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 494-0060
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-07-807-529A-45

Query Match      33.3%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 6 LPVV 9

RESULT 42
US-08-934-222-106
; Sequence 106, Application US/08934222
; Patent No. 5928896
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interact
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,222
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
```

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-222-106

Query Match 33.3%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12
|
|
|
|
Db 5 NVLP 8

RESULT 43
US-08-933-402-106
; Sequence 106, Application US/08933402
; Patent No. 5948887
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,402
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-402-106

Query Match 33.3%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12
|
|
|
|
Db 5 NVLP 8

RESULT 44
US-09-207-621-106
; Sequence 106, Application US/09207621

; Patent No. 5952465
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interact
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,621
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-207-621-106

Query Match 33.3%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12
|
|
|
|
Db 5 NVLP 8

RESULT 45
US-08-532-818-106
; Sequence 106, Application US/08532818
; Patent No. 5965698
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interact
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-532-818-106

Query Match 33.3%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 9 NVLP 12
DB 5 NVLP 8

RESULT 46
US-08-942-819-9
Sequence 9, Application US/08942819
Patent No. 5965707
GENERAL INFORMATION:
APPLICANT: Tam, See-Ying
APPLICANT: Tsai, Mindy
APPLICANT: Galli, Stephen J.
TITLE OF INVENTION: RIN2, A NOVEL INHIBITOR OF
TITLE OF INVENTION: RAS-MEDIATED SIGNALING
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,819
FILING DATE: 02-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/058,520
FILING DATE: 11-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: BIH96-13pA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-9540
TELEFAX:

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-942-819-9

Query Match 33.3%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 4 FLPV 7
DB 5 FLPV 8

RESULT 47
US-08-159-339A-652
Sequence 652, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 652:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-652

Query Match 33.3%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 FFFL 5
 ||||
 Db 5 FFFL 8

RESULT 48

US-08-159-339A-694
 ; Sequence 694, Application US/08159339A
 ; Patent No. 6037135
 ; GENERAL INFORMATION:
 ; APPLICANT: Kubo, Ralph T.
 ; APPLICANT: Grey, Howard M.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Celis, Esteban
 ; TITLE OF INVENTION: HLA Binding peptides and Their
 ; NUMBER OF SEQUENCES: 1254
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/159,339A
 ; FILING DATE: 29-NOV-1993
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/926,666
 ; FILING DATE: 07-AUG-1992
 ; APPLICATION NUMBER: US 08/027,746
 ; FILING DATE: 05-MAR-1993
 ; APPLICATION NUMBER: US 08/103,396
 ; FILING DATE: 06-AUG-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weber, Ellen Lauver
 ; REGISTRATION NUMBER: 32,762
 ; REFERENCE/DOCKET NUMBER: 018623-005030US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 694:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-159-339A-694

Query Match 33.3%; Score 4; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred.No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 FFFL 5
 ||||
 Db 2 FFFL 5

RESULT 49

US-08-159-339A-695
 ; Sequence 695, Application US/08159339A
 ; Patent No. 6037135
 ; GENERAL INFORMATION:
 ; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Celis, Esteban
 ; TITLE OF INVENTION: HLA Binding peptides and Their
 ; NUMBER OF SEQUENCES: 1254
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/159,339A
 ; FILING DATE: 29-NOV-1993
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/926,666
 ; FILING DATE: 07-AUG-1992
 ; APPLICATION NUMBER: US 08/027,746
 ; FILING DATE: 05-MAR-1993
 ; APPLICATION NUMBER: US 08/103,396
 ; FILING DATE: 06-AUG-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weber, Ellen Lauver
 ; REGISTRATION NUMBER: 32,762
 ; REFERENCE/DOCKET NUMBER: 018623-005030US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 695:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-159-339A-695

Query Match 33.3%; Score 4; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred.No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 FFFL 5
 ||||
 Db 1 FFFL 4

RESULT 50

US-09-231-797-106
 ; Sequence 106, Application US/09231797
 ; Patent No. 6084066
 ; GENERAL INFORMATION:
 ; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha
 ; TITLE OF INVENTION: Polypeptides That Include Conformation-
 ; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interactio-
 ; NUMBER OF SEQUENCES: 153
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: Suite 500, 3000 K Street NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20007

; COMPUTER READABLE FORM:

;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/231,797
;/ FILING DATE:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/532,818
;/ FILING DATE: 03-MAY-1996
;/ APPLICATION NUMBER: PCT/US94/04294
;/ FILING DATE: 21-APR-1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: U.S. 08/143,364
;/ FILING DATE: 29-OCT-1993
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: U.S. 08/051,741
;/ FILING DATE: 23-APR-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Isaacson, John P.
;/ REGISTRATION NUMBER: 33,751
;/ REFERENCE/DOCKET NUMBER: 040433/0148
;/ INFORMATION FOR SEQ ID NO: 106:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 9 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ US-09-231-797-106

Query Match 33.3%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12
Db ||||
5 NVLP 8

RESULT 51
US-08-934-224-106
;/ Sequence 106, Application US/08934224
;/ Patent No. 6100044
;/ GENERAL INFORMATION:
;/ APPLICANT: EVANS, Herbert J.
;/ TITLE OF INVENTION: Polypeptides That Include Conformation-
;/ TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
;/ TITLE OF INVENTION: Site
;/ NUMBER OF SEQUENCES: 153
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Foley & Lardner
;/ STREET: Suite 500, 3000 K Street NW
;/ CITY: Washington
;/ STATE: DC
;/ COUNTRY: USA
;/ ZIP: 20007
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/934,224
;/ FILING DATE:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/532,818
;/ FILING DATE: 03-MAY-1996
;/ APPLICATION NUMBER: PCT/US94/04294
;/ FILING DATE: 21-APR-1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: U.S. 08/143,364
;/ FILING DATE: 29-OCT-1993
;/ PRIOR APPLICATION DATA:

;/ APPLICATION NUMBER: U.S. 08/051,741
;/ FILING DATE: 23-APR-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Isaacson, John P.
;/ REGISTRATION NUMBER: 33,751
;/ REFERENCE/DOCKET NUMBER: 040433/0148
;/ INFORMATION FOR SEQ ID NO: 106:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 9 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ US-08-934-224-106

Query Match 33.3%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12
Db ||||
5 NVLP 8

RESULT 52
US-08-933-843-106
;/ Sequence 106, Application US/08933843
;/ Patent No. 6111069
;/ GENERAL INFORMATION:
;/ APPLICANT: EVANS, Herbert J.
;/ APPLICANT: KINI, R. Manjunatha
;/ TITLE OF INVENTION: Polypeptides That Include Conformation-
;/ TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interact
;/ TITLE OF INVENTION: Site
;/ NUMBER OF SEQUENCES: 153
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Foley & Lardner
;/ STREET: Suite 500, 3000 K Street NW
;/ CITY: Washington
;/ STATE: DC
;/ COUNTRY: USA
;/ ZIP: 20007
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/933,843
;/ FILING DATE: 19-SEPT-1997
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/532,818
;/ FILING DATE: 03-MAY-1996
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: U.S. 08/143,364
;/ FILING DATE: 29-OCT-1993
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: U.S. 08/051,741
;/ FILING DATE: 23-APR-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Isaacson, John P.
;/ REGISTRATION NUMBER: 33,751
;/ REFERENCE/DOCKET NUMBER: 040433/0148
;/ INFORMATION FOR SEQ ID NO: 106:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 9 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ US-08-933-843-106

Query Match 33.3%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12

```
Db          5 NVLP 8
|||||
RESULT 53
US-08-934-223-106
; Sequence 106, Application US/08934223
; Patent No. 6147189
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,223
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-223-106

Query Match          33.3%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          9 NVLP 12
|||||
Db          5 NVLP 8

RESULT 54
US-09-413-492-106
; Sequence 106, Application US/09413492
; Patent No. 6258550
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/413,492
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-413-492-106

Query Match          33.3%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          9 NVLP 12
|||||
Db          5 NVLP 8

RESULT 55
US-09-522-955A-9
; Sequence 9, Application US/09522955A
; Patent No. 650942
; GENERAL INFORMATION:
; APPLICANT: Tam, See-Ying
; APPLICANT: Tsai, Mindy
; APPLICANT: Galli, Stephen J.
; TITLE OF INVENTION: RIN2, A NOVEL INHIBITOR OF RAS-MEDICATED
; TITLE OF INVENTION: SIGNALING
; FILE REFERENCE: 1440.1089-004
; CURRENT APPLICATION NUMBER: US/09/522,955A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: PCT/US98/19056
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: US 08/942,819
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: US 60/058,520
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(9)
```

; OTHER INFORMATION: Xaa = Any Amino Acid
; OTHER INFORMATION: GTPase binding homology motif II
US-09-522-955A-9

Query Match 33.3%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPV 7
Db 5 FLPV 8

RESULT 56
US-08-159-339A-717
; Sequence 717, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esceban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 717:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-717

Query Match 33.3%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5
Db 7 FFPL 10

RESULT 57
US-08-159-339A-718
; Sequence 718, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esceban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 718:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-718

Query Match 33.3%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5
Db 2 FFPL 5

RESULT 58
US-08-159-339A-719
; Sequence 719, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esceban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 719:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-719

;
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 719:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-719

Query Match 33.3%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 2 PFFL 5
Db 1 PFFL 4

RESULT 59
US-09-101-886B-56
; Sequence 56, Application US/09101886B
; Patent No. 6197507
; GENERAL INFORMATION:
; APPLICANT: BERG, THOMAS
; APPLICANT: TOLLERSRUD, OLE K
; APPLICANT: NILSEN, OLIVIND
; TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BARBARA G. ERNST
; STREET: 555 13TH STREET, NW SUITE 701E
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

;
; APPLICATION NUMBER: US/09/101,886B
; FILING DATE: 29-JANUARY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/00109
; FILING DATE: 12-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1181-240
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: not relevant
; ANTI-SENSE: not relevant
; FRAGMENT TYPE: internal
US-09-101-886B-56

Query Match 33.3%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 5 LPVV 8
Db 3 LPVV 6

RESULT 60
US-09-344-040C-129
; Sequence 129, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Dete
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Ge
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 129
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-129

Query Match 33.3%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 4 FLPV 7
Db 5 FLPV 8

RESULT 61
US-09-347-926-16
; Sequence 16, Application US/09347926

; Patent No. 6440386
; GENERAL INFORMATION:
; APPLICANT: LEUNG, SHUI-ON
; TITLE OF INVENTION: STABILIZED RADIOPHOSPHATE-LABELED PROTEINS
; FILE REFERENCE: 018733/0936
; CURRENT APPLICATION NUMBER: US/09/347,926
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-347-926-16

Query Match 33.3%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPV 7
Db 1 FLPV 4

RESULT 62
US-08-194-981E-16
; Sequence 16, Application US/08194981E
; Patent No. 5886157
; GENERAL INFORMATION:
; APPLICANT: GUENGERICH, F. Peter
; APPLICANT: GUO, Zuyu
; APPLICANT: SANDHU, Punam
; APPLICANT: GILLAM, Elizabeth M. J.
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF
; TITLE OF INVENTION: HUMAN
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street, NE
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,981E
; FILING DATE: February 10, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Selby
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 22000.0022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; FRAGMENT TYPE: N-terminal
US-08-194-981E-16

Query Match 33.3%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 FLPV 7
Db 8 FLPV 11

RESULT 63
US-09-501-612A-6
; Sequence 6, Application US/09501612A
; Patent No. 6544765
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Henrik
; APPLICANT: Hjord, Carsten M.
; TITLE OF INVENTION: Oxaloacetate Hydrolase Deficient Fungal Host Cells
; FILE REFERENCE: 5789-200-US
; CURRENT APPLICATION NUMBER: US/09/501.612A
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-501-612A-6

Query Match 33.3%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PVVN 9
Db 6 PVVN 9

RESULT 64
US-09-490-702B-12
; Sequence 12, Application US/09490702B
; Patent No. 6560542
; GENERAL INFORMATION:
; APPLICANT: Mandell, Arnold
; APPLICANT: Selz, Karen
; APPLICANT: Shlesinger, Michael
; TITLE OF INVENTION: Algorithmic Design of Peptides for Binding and/or Modulation o
; TITLE OF INVENTION: Functions of Receptors and/or Other Proteins
; FILE REFERENCE: 01561-0002-000S00
; CURRENT APPLICATION NUMBER: US/09/490,702B
; CURRENT FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: synthetic
US-09-490-702B-12

Query Match 33.3%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VNVL 11
Db 10 VNVL 13

RESULT 65
US-09-009-953-15
; Sequence 15, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:

```
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; REACTIVE DR Restricted Epitopes
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,953
; FILING DATE: 21-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,713
; FILING DATE: 23-JAN-1997
; APPLICATION NUMBER: US 60/037,432
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-011520US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-009-953-15

Query Match 33.3%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6
Db 5 FFLP 8

RESULT 66
US-09-009-953-25
; Sequence 25, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; REACTIVE DR Restricted Epitopes
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,953
; FILING DATE: 21-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,713
; FILING DATE: 23-JAN-1997
; APPLICATION NUMBER: US 60/037,432
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-011520US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-009-953-25

Query Match 33.3%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6
Db 13 FFLP 16

RESULT 67
US-09-177-249-88
; Sequence 88, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-88

Query Match 33.3%; Score 4; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6
Db 10 FFLP 13
```



```
RESULT 68
US-08-392-828C-28
; Sequence 28, Application US/08392828C
; Patent No. 5795962
; GENERAL INFORMATION:
; APPLICANT: IWANAGA, SADAOKI
; APPLICANT: MUTA, TATSUSHI
; APPLICANT: SEKI, NORIAKI
; APPLICANT: ODA, TOSHIO
; TITLE OF INVENTION: NOVEL POLYPEPTIDE AND DNA ENCODING
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 28-FEB-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FUN-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "TABLE 2, PEPTIDE 7"
US-08-392-828C-28

Query Match 33.3%; Score 4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8
Db 8 LPVV 11

RESULT 69
US-09-330-945-28
; Sequence 28, Application US/09330945
; Patent No. 6077946
; GENERAL INFORMATION:
; APPLICANT: IWANAGA, SADAOKI
; APPLICANT: MUTA, TATSUSHI
; APPLICANT: SEKI, NORIAKI
; APPLICANT: ODA, TOSHIO
; TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
; TITLE OF INVENTION: AMEBOCYTE LYSATE FACTOR G SUBUNIT A
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT, LLP
```

```
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09330,945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: FUN-032DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "TABLE 2, PEPTIDE 7"
US-09-330-945-28

Query Match 33.3%; Score 4; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8
Db 8 LPVV 11

RESULT 70
US-08-918-288-59
; Sequence 59, Application US/08918288
; Patent No. 6238890
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,288
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

; APPLICATION NUMBER: 09/282,357
; FILING DATE: 09/282,357
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-918-288-59

Query Match 33.3%; Score 4; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFEL 5
Db 6 FFEL 9

RESULT 71
US-09-282-357-59
; Sequence 59, Application US/09282357
; Patent No. 6242580
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/282,357
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/918,289
; FILING DATE: 25 AUG-1997
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-282-357-59

Query Match 33.3%; Score 4; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFEL 5
Db 6 FFEL 9

RESULT 72
US-07-807-529A-29
; Sequence 29, Application US/07807529A
; Patent No. 5547669
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Wei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: One Kendall Square, Building 600
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/807,529A
; FILING DATE: 19911213
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Channing, Stacey L.
; REGISTRATION NUMBER: 31,095
; REFERENCE/DOCKET NUMBER: IPC-027/Imi-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 494-0060
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
US-07-807-529A-29

Query Match 33.3%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVW 8
Db 15 LPVW 18

RESULT 73
US-08-743-553-1
; Sequence 1, Application US/08743553
; Patent No. 5824636
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, B.B.
; TITLE OF INVENTION: NOVEL ANTIPROLIFERATIVE PROTEIN FROM
; TITLE OF INVENTION: BACILLUS THURINGIENSIS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler, GILBRETH & ADLER, P.C.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,553
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,636
; FILING DATE: 05/31/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Dr. Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5789
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: No
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
US-08-743-553-1
Query Match 33.3%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 VNV 10
Db 4 VNV 7
RESULT 74
US-08-300-928C-78
; Sequence 78, Application US/08300928C
; Patent No. 6019972
; GENERAL INFORMATION:
; APPLICANT: GEFTER, Malcolm L. et al.
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
; TITLE OF INVENTION: PROTEIN (TRFP)

NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AMT E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-300-928C-78
Query Match 33.3%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 LPV 8
Db 15 LPV 18
RESULT 75
US-08-430-944D-78
; Sequence 78, Application US/08430944D
; Patent No. 6025162
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,944D
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-430-944D-78

Query Match 33.3%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred.No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 LPV 8
Db 15 LPV 18

Search completed: November 25, 2003, 20:16:00
Job time : 14.0851 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 13.8032 Seconds
(without alignments)
104.507 Million cell updates/sec

Title: US-09-641-801-5
Perfect score: 15
Sequence: 1 DLBMPVLPVEPPFFV 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	26.7	16	PC4371	telomeric and tetr
2	4	26.7	17	JQ2030	hypothetical 1.9K
3	3	20.0	6	A61049	halo-toxin - Pseud
4	3	20.0	6	I51317	bHLH transcription
5	3	20.0	8	A39308	glycine reductase
6	3	20.0	9	A61620	locustamyotropin I
7	3	20.0	9	S66635	alpha-2-macroglobu
8	3	20.0	9	FD0443	3-oxoacid CoA-tran
9	3	20.0	10	B33710	ornithine decarbox
10	3	20.0	10	A44646	neurotoxin-associa
11	3	20.0	10	I44644	neurotoxin-associa
12	3	20.0	11	S32575	ribosomal protein
13	3	20.0	11	P58501	43.5K bile stone p
14	3	20.0	11	A55149	tetracenomycin A2
15	3	20.0	11	PA0028	protein QA300042 -
16	3	20.0	11	C61497	seed protein ws-18
17	3	20.0	11	P50257	31K protein 3208 -
18	3	20.0	11	A54348	N-acetylglucosamin
19	3	20.0	12	PA0037	plascocyanin 2 - A
20	3	20.0	13	S09395	hypothetical prote
21	3	20.0	13	PL0157	Ig kappa chain V-I
22	3	20.0	13	PH1772	T cell receptor al
23	3	20.0	13	S01904	H+-transporting tw
24	3	20.0	14	A60737	pollen allergen Lo
25	3	20.0	14	C33098	223K exoantigen -
26	3	20.0	14	A23996	beta-granin - rat
27	3	20.0	15	T09463	ribosomal protein
28	3	20.0	15	PA0024	protein QA300050 -
29	3	20.0	15	P50452	32K protein 3306 -

30	3	20.0	15	2	PA0059	protein QF200021 -
31	3	20.0	15	2	PA0088	protein QF200051 -
32	3	20.0	15	2	B61457	alpha-glucosidase
33	3	20.0	15	2	C61511	milk band B protei
34	3	20.0	15	2	PT0205	insulin-like growt
35	3	20.0	15	2	I46909	voltage-dependent
36	3	20.0	15	2	A31902	bone acidic glycop
37	3	20.0	15	2	A45096	thyrotropin-releas
38	3	20.0	16	1	A49761	locustapyrokinin -
39	3	20.0	16	2	S03405	hydrogenase (EC 1.
40	3	20.0	16	2	C45133	casein kinase II (
41	3	20.0	16	2	T37075	hypothetical prote
42	3	20.0	16	2	S09732	photosystem I prot
43	3	20.0	16	2	C61414	chymotrypsin (EC 3
44	3	20.0	16	2	S68730	bleomycin-binding
45	3	20.0	17	2	I65274	glutathione S-tran
46	3	20.0	17	2	S05033	photosystem II pro
47	3	20.0	17	2	S50742	proteinase inhibit
48	3	20.0	17	2	B61414	chymotrypsin (EC 3
49	3	20.0	17	2	A60570	Ig mu heavy chain
50	3	20.0	17	2	B31769	T-cell receptor de
51	3	20.0	17	2	I55612	thyroid hormone re
52	3	20.0	17	2	G85956	hypothetical prote
53	3	20.0	18	2	B24735	glutathione transf
54	3	20.0	18	2	S29264	ovohemerythrin - d
55	3	20.0	18	2	S48863	cyclin C - mouse (
56	3	20.0	18	2	I40062	shikimate 5-dehydr
57	3	20.0	18	2	S46241	NAD(P)H-flavin oxi
58	3	20.0	18	2	S71592	serine proteinase
59	3	20.0	18	2	I46653	T-cell receptor de
60	3	20.0	19	2	C56049	superoxide dismuta
61	3	20.0	19	2	S59485	hydroxyproline-rich
62	3	20.0	19	2	I40063	shikimate 5-dehydr
63	3	20.0	19	2	S43641	carboxylesterase (
64	3	20.0	19	2	A61144	probable flagellar
65	3	20.0	19	2	S69153	Neb-colloostatin -
66	3	20.0	19	2	A39504	octamer-binding pr
67	3	20.0	19	2	I46654	T-cell receptor de
68	3	20.0	19	2	S68394	H+-transporting tw
69	3	20.0	20	2	C54052	phosphoribosyl-AMP
70	3	20.0	20	2	S50741	probable trypsin i
71	3	20.0	20	2	B44581	bombinin H Met-8 -
72	3	20.0	20	2	S06466	T-cell receptor al
73	3	20.0	20	2	PL0145	carbon-monoxide de
74	3	20.0	20	2	B30208	hypothetical prote
75	3	20.0	20	2	B60365	chymotrypsin inhib
76	3	20.0	20	2	S77989	cytochrome-c oxida
77	3	20.0	20	2	A61414	chymotrypsin (EC 3
78	3	20.0	20	2	S46479	retinoid-X-recepto
79	3	20.0	20	2	S58382	hypothetical prote
80	3	20.0	20	2	I46652	T-cell receptor de
81	3	20.0	20	2	A48406	annexin VI homolog
82	3	20.0	20	2	A61526	major milk gland p
83	3	20.0	20	2	A85659	hypothetical prote
84	3	13.3	3	3	A33802	thyrotropin-releas
85	2	13.3	3	3	I78890	tyrosine protein k
86	2	13.3	4	2	S53508	starvation-induced
87	2	13.3	4	2	I54357	schwannomin - mous
88	2	13.3	4	2	A26209	protein-glutamine
89	2	13.3	5	1	HOR0HA	proctolin - Americ
90	2	13.3	5	2	JN0862	peptidyl-dipeptida
91	2	13.3	5	2	JN0860	peptidyl-dipeptida
92	2	13.3	5	2	E42364	flagellar protein
93	2	13.3	5	2	FQ0009	angiotensin-conver
94	2	13.3	5	2	T14908	hypothetical prote
95	2	13.3	5	2	S55237	zinc-binding prote
96	2	13.3	5	2	B37988	acid proteinase li
97	2	13.3	5	2	A44692	fulcin - giant Af
98	2	13.3	5	2	A60411	proctolin - Atlant
99	2	13.3	5	2	JS0319	subesophageal gang
100	2	13.3	5	2	S53595	hypothetical prote

ALIGNMENTS

```

RESULT 1
PC4371
telomeric and tetraplex DNA binding protein qTBP42 I - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C:Accession: PC4371
R:Sarig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A:Title: Telomeric and tetraplex DNA binding properties of the CA
A:Reference number: PC4371; MUID:97445086; PMID:9299414
A:Accession: PC4371
A:Molecule type: protein
A:Residues: 1-16 <SAR>
C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match      26.7%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 PVEP 11
      ||||
Db      5 PVEP 8

RESULT 2
JQ2030
hypothetical 1.9K protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus
N:Alternate names: ORF2 mini gene protein
C:Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNVP
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C:Accession: JQ2030
R:Russell, R.L.Q.; Rohmann, G.F.
J. Gen. Virol. 74, 1191-1195, 1993
A:Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia pseudotsug
A:Reference number: PQ0633; MUID:93286576; PMID:8389803
A:Accession: JQ2030
A:Molecule type: DNA
A:Residues: 1-17 <RUS>
A:Cross-references: DDBJ:DL3375; NID:g222217; PID:BAA02640.1; PID:d1003144; PID:g2222222

Query Match      26.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VLPV 9
      ||||
Db      2 VLPV 5

RESULT 3
A61049
halo-toxin - Pseudomonas syringae pv. mori
C:Species: Pseudomonas syringae pv. mori
A:Note: host mulberry tree
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
C:Accession: A61049
R:Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.;
Chem. Lett. 00, 679-680, 1989
A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri
A:Reference number: A61049
A:Accession: A61049
A:Molecule type: protein
A:Residues: 1-6 <KAJ>
A:Note: sequence confirmed by synthesis
C:Comment: This toxin is one of the etiological agents of halo bright disease in mulberry
C:Keywords: toxin

Query Match      20.0%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      11 PFP 13
      |||
Db      1 PFP 3

RESULT 4
I51317
bHLH transcription factor inhibitor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51317
R:Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G.
Mech. Dev. 50, 119-130, 1995
A:Title: Id gene activity during Xenopus embryogenesis.
A:Reference number: I51316; MUID:95344988; PMID:7619724
A:Accession: I51317
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-6 <ZHA>
A:Cross-references: GB:S79038; NID:gl042006; PIDN:AAD14294.1; PID:g4261994
C:Genetics:
A:Gene: Xidib

Query Match      20.0%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 EPF 12
      |||
Db      4 EPF 6

RESULT 5
A39308
glycine reductase (EC 1.4.99.-) sulphydryl protein C, alpha chain - Clostridium stick
C:Species: Clostridium sticklandii
C>Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 15-Aug-1997
C:Accession: A39308
R:Stadtman, T.C.; Davis, J.N.
J. Biol. Chem. 266, 22147-22153, 1991
A:Title: Glycine reductase protein C. Properties and characterization of its role in
A:Reference number: A39308; MUID:92042141; PMID:1939235
A:Accession: A39308
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <STA>
C:Function:
A:Description: glycine reductase complex catalyzes the reductive deamination of glyci
C:Keywords: ATP; oxidoreductase

Query Match      20.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PVL 7
      |||
Db      3 PVL 5

RESULT 6
A61620
locustamytropin III - migratory locust
C:Species: locusta migratoria (migratory locust)
C>Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
C:Accession: A61620
R:Schooft, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
Insect Biochem. Mol. Biol. 22, 447-452, 1992
A:Title: Isolation, identification and synthesis of locustamytropin III and IV, two
A:Reference number: A61620
A:Accession: A61620
A>Status: preliminary
A:Molecule type: protein

```

A;Residues: 1-9 <SCH>
A;Keywords: amidated carboxyl end; neuropeptide
F;9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15
Db 4 PFV 6

RESULT 7

S66635

alpha-2-macroglobulin isoform 1 - bovine (fragment)

C;Species: Bos primigenius indicus (zebu cattle)

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S66635

R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottrup

FEB5 Lett. 372, 93-95, 1995

A;Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain of

A;Reference number: S66634; MUID:96032553; PMID:7556651

A;Accession: S66635

A;Status: preliminary

A;Molecule type: Protein

A;Residues: 1-9 <DOL>

Query Match 20.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FPF 14
Db 4 FPF 6

RESULT 8

PD0443

3-oxoacid CoA-transferase (EC 2.8.3.5) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999

C;Accession: PD0443

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.

submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Contents: Striatum

A;Accession: PD0443

A;Molecule type: protein

A;Residues: 1-9 <KAW>

C;Keywords: CoA-transferase

Query Match 20.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10
Db 7 PVE 9

RESULT 9

B33710

ornithine decarboxylase leader peptide - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 24-Sep-1999

C;Accession: B33710

R;Wen, L.; Huang, J.K.; Blackshear, P.J.

J. Biol. Chem. 264, 9016-9021, 1989

A;Title: Rat ornithine decarboxylase gene. Nucleotide sequence, potential regulatory ele

A;Reference number: A33710; MUID:89255378; PMID:2722815

A;Accession: B33710

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual t
A;Molecule type: mRNA
A;Residues: 1-10 <WEN>
A;Cross-references: GB:J04791; NID:G205807; PIDN:AAA66163.1; PID:G806309
C;Superfamily: unassigned leader peptides

Query Match 20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
Db 8 PVL 10

RESULT 10

A44646

neurotoxin-associated protein type A Hn+ 57K chain - Clostridium botulinum (fragment)

C;Species: Clostridium botulinum

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C;Accession: A44646

R;Somers, E.; DasGupta, B.R.

J. Protein Chem. 10, 415-425, 1991

A;Title: Clostridium botulinum types A, B, Cl, and E produce proteins with or without

A;Reference number: A44644; MUID:92143938; PMID:1781887

A;Contents: type A

A;Accession: A44646

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <SOM>

A;Note: sequence extracted from NCBI backbone (NCBIP:83774)

A;Note: 6-Trp was also found

C;Keywords: hemagglutinin

Query Match 20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db 7 VLP 9

RESULT 11

I44644

neurotoxin-associated protein type B Hn+ 57K chain - Clostridium botulinum (fragment)

C;Species: Clostridium botulinum

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C;Accession: I44644

R;Somers, E.; DasGupta, B.R.

J. Protein Chem. 10, 415-425, 1991

A;Title: Clostridium botulinum types A, B, Cl, and E produce proteins with or without

A;Reference number: A44644; MUID:92143938; PMID:1781887

A;Contents: type B

A;Accession: I44644

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <SOM>

A;Note: sequence extracted from NCBI backbone (NCBIP:83783)

C;Keywords: hemagglutinin

Query Match 20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db 7 VLP 9

RESULT 12

S32575

ribosomal protein S2, plastid - squawroot plastid (fragment)

C;Species: plastid *Concopholis americana* (squawroot)
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 13-Aug-1999
 C;Accession: S32575
 R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; depamphilis, C.W.; Palmer, J.D.
 Curr. Genet. 20, 515-518, 1991
 A;Title: Lack of a functional plastid tRNA (Cys) gene is associated with loss of photosynthesis in *Concopholis americana*
 A;Reference number: S32575; PMID:92145776; PMID:1723664
 A;Accession: S32575
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-11 <TAY>
 A;Cross-references: ENBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276
 C;Genetics:
 A;Gene: rps2
 A;Genome: plastid
 C;Superfamily: Escherichia coli ribosomal protein S2
 C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 20.0%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLE 3
 ||||
 Db 9 DLE 11

RESULT 13
 F58501
 43.5K bile stone protein - unidentified bacterium (fragment)
 C;Species: unidentified bacterium
 C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
 C;Accession: F58501
 R;Binette, J.P.; Binette, M.B.
 submitted to the Protein Sequence Database, October 1996
 A;Description: The proteins of kidney and gallbladder stones.
 A;Reference number: A58501
 A;Accession: F58501
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-11 <BIN>
 A;Experimental source: human bile with stones
 A;Note: 6-Asn and 8-Ala were also found

Query Match 20.0%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10
 ||||
 Db 9 PVE 11

RESULT 14
 A55149
 tetraacenomycin A2 oxygenase (EC 1.11.1.1) - Streptomyces glaucescens (fragment)
 N;Alternate names: tcmA2 oxygenase; tcmG
 C;Species: Streptomyces glaucescens
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Mar-1996
 C;Accession: A55149
 R;Shen, B.; Hutchinson, C.R.
 J. Biol. Chem. 269, 30726-30733, 1994
 A;Title: Triple hydroxylation of tetraacenomycin A2 to tetraacenomycin C in Streptomyces glaucescens
 A;Reference number: A55149; PMID:95074090; PMID:7982994
 A;Accession: A55149
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-11 <SHE>
 C;Genetics:
 A;Start codon: TTG
 C;Keywords: antibiotic biosynthesis; FAD; monomer; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
 ||||
 Db 7 PVL 9

RESULT 15
 PA0028
 protein QA300042 - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C;Accession: PA0028
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
 A;Reference number: PA0001
 A;Accession: PA0028
 A;Molecule type: protein
 A;Residues: 1-11 <KAM>
 A;Experimental source: seed
 C;Keywords: seed

Query Match 20.0%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFP 13
 ||||
 Db 6 PFP 8

RESULT 16
 C61497
 seed protein wa-18 - winged bean (fragment)
 C;Species: Psophocarpus tetragonolobus (winged bean)
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
 C;Accession: C61497
 R;Hirano, H.
 J. Protein Chem. 8, 115-130, 1989
 A;Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gel electrophoresis
 A;Reference number: A61491; PMID:89351606; PMID:2765119
 A;Accession: C61497
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-11 <HIR>
 C;Keywords: glycoprotein; seed

Query Match 20.0%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
 ||||
 Db 7 PVL 9

RESULT 17
 PS0257
 31K protein 3208 - rice (strain Nihonbare) (fragment)
 C;Species: Oryza sativa (rice)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
 C;Accession: PS0257
 R;Tsugita, A.; Kamo, M.
 submitted to JIPID, April 1993
 A;Reference number: PS0209
 A;Accession: PS0257
 A;Molecule type: protein
 A;Residues: 1-11 <TSU>
 A;Experimental source: callus, strain Nihonbare
 C;Comment: molecular weight 31K, pI 5.9.

Query Match 20.0%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLE 3
 |||
 Db 5 DLE 7

RESULT 18

A54348
 N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
 C;Accession: A54348
 R;Shilatifard, A.; Cummings, R.D.
 Biochemistry 33, 4273-4282, 1994
 A;Title: Purification and characterization of N-acetylglucosamine-6-sulfate sulfatase from *Bos primigenius*
 A;Reference number: A54348; PMID:94206936; PMID:8155645
 A;Accession: A54348
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-11 <SH1>
 C;Keywords: sulfuric ester hydrolase

Query Match 20.0%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPP 12
 |||
 Db 2 EPP 4

RESULT 19

PA0037
 plastocyanin 2 - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
 C;Accession: PA0037
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 Submitted to JIPD, July 1994
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
 A;Reference number: PA0001
 A;Accession: PA0037
 A;Molecule type: protein
 A;Residues: 1-12 <KAM>
 A;Experimental source: stem

Query Match 20.0%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
 |||
 Db 5 VLP 7

RESULT 20

S09395
 hypothetical protein - fruit fly (Drosophila melanogaster) (fragment)
 C;Species: Drosophila melanogaster
 C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
 C;Accession: S09395
 R;Gasselmann, G.; Sewing, S.; Madsen, B.W.; Mallart, A.; Angaut-Petit, D.; Mueller-Holtkamp, J.
 EMBO J. 8, 2359-2364, 1989
 A;Title: The interference of truncated with normal potassium channel subunits leads to a novel type of potassium channel
 A;Reference number: S09395; PMID:90005442; PMID:2551680
 A;Accession: S09395
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-13 <GIS>

Query Match 20.0%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
 |||
 Db 5 LPV 7

RESULT 21

PL0157
 Ig kappa chain V-II region (anti-myelin-associated glycoprotein, PFC) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Feb-1997
 C;Accession: PL0157; C61458
 R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
 J. Exp. Med. 170, 1551-1558, 1989
 A;Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-associated glycoprotein (P0157)
 A;Reference number: A61458; PMID:90039128; PMID:2478651
 A;Accession: PL0157
 A;Molecule type: protein
 A;Residues: 1-13 <BRO>
 A;Accession: C61458
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-13 <BR2>

C;Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycoprotein (P0157)
 C;Keywords: glycoprotein; heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
 |||
 Db 11 LPV 13

RESULT 22

PH1772
 T cell receptor alpha chain V region (clone 2V alpha 23-3) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C;Accession: PH1772
 R;Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
 J. Exp. Med. 178, 1-16, 1993
 A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood lymphocytes
 A;Reference number: PH1754; PMID:93301585; PMID:8391057
 A;Accession: PH1772
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-13 <POR>

Query Match 20.0%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11
 |||
 Db 4 VEP 6

RESULT 23

S01904
 H+transporting two-sector ATPase (EC 3.6.3.14) beta chain - Arabidopsis thaliana chl
 C;Species: Chloroplast Arabidopsis thaliana (mouse-ear cress)
 C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 03-Jun-2002
 C;Accession: S01904
 R;Chen, H.C.; Wintz, H.; Weil, J.H.; Pillay, D.T.N.
 Nucleic Acids Res. 16, 10372, 1988
 A;Title: Nucleotide sequence of chloroplast CFI-ATPase epsilon-subunit and elongator

A;Reference number: S01903; MUID:89057486; PMID:2904134
A;Accession: S01904
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-13 <CHE>
A;Cross-references: EMBL:X12889; NID:g11332; PIDN:CAA31380.1; PID:g829297
C;Genetics:
A;Gene: atpB
A;Genome: chloroplast
C;Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match 20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
|||
Db 5 LEM 7

RESULT 24
A60737
pollen allergen Lol p IV - perennial ryegrass (fragments)
C;Species: Lolium perenne (perennial ryegrass)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 17-Mar-1999
C;Accession: A60737
R;Jaggi, K.S.; Ekramoddoullah, A.K.M.; Kisil, F.T.
Int. Arch. Allergy Appl. Immunol. 89, 342-348, 1989
A;Title: Allergenic fragments of ryegrass (Lolium perenne) pollen allergen Lol p IV.
A;Reference number: A60737; MUID:90007726; PMID:2793222
A;Accession: A60737
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <JAG>
C;Keywords: pollen

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
|||
Db 4 PVL 6

RESULT 25
C33098
223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: C33098
R;Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
A;Accession: C33098
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <NIC>

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
|||
Db 1 VLP 3

RESULT 26
A23996
beta-granin - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Jun-1993

C;Accession: A23996
R;Hutton, J.C.; Hansen, F.; Peshavaria, M.
FEBS Lett. 188, 336-340, 1985
A;Title: Beta-granins: 21 kDa co-secreted peptides of the insulin granule closely related to the insulin B-chain
A;Reference number: A23996; MUID:85285598; PMID:3896848
A;Accession: A23996
A;Molecule type: protein
A;Residues: 1-14 <HUT>

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
|||
Db 1 LPV 3

RESULT 27
T09463
ribosomal protein S14 - brown alga (Pylaiella littoralis) mitochondrion (fragment)
C;Species: mitochondrion Pylaiella littoralis
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C;Accession: T09463
R;Rousvoal, S.; Oudot, M.; Fontaine, J.; Kloareg, B.; Goer, S.L.
J. Mol. Biol. 277, 1047-1057, 1998
A;Title: Witnessing the evolution of transcription in mitochondria: The mitochondrial ribosomal protein S14
A;Reference number: Z16681; MUID:98239704; PMID:9571021
A;Accession: T09463
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-15 <ROU>
A;Cross-references: EMBL:AF034976; NID:g3243103; PID:g3243104
A;Experimental source: strain Roscoff
C;Genetics:
A;Gene: rps14
A;Genome: mitochondrion
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
|||
Db 6 VLP 8

RESULT 28
PA0024
protein QA300050 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0024
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
A;Reference number: PA0001
A;Accession: PA0024
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Experimental source: seed

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFP 13
|||
Db 6 PFP 8

RESULT 29

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PS0452
32K protein 3306 - rice (strain Nihonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C;Accession: PS0452
R;Tsugita, A.; Miyatake, N.
submitted to JIPID, April 1993
A;Reference number: PS0208
A;Accession: PS0452
A;Molecule type: protein
A;Residues: 1-15 <TSU>
A;Experimental source: bran, strain Nihonbare
C;Comment: molecular weight 32K, pI 5.3.

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 PFP 13
      |||
Db      6 PFP 8

RESULT 30
PA0059
protein QF200021 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0059
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PA0051
A;Accession: PA0059
A;Molecule type: protein
A;Residues: 1-15 <CHO>

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DLE 3
      |||
Db      3 DLE 5

RESULT 31
PA0088
protein QF200051 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0088
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PA0051
A;Accession: PA0088
A;Molecule type: protein
A;Residues: 1-15 <CHO>

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PVL 7
      |||
Db     13 PVL 15

RESULT 32
B61457
alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)
C;Species: Tetrahymena pyriformis

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999
C;Accession: B61457
R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
J. Protozool. 36, 562-567, 1989
A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification and characterization
A;Reference number: A61457; MUID:90095988; PMID:2689637
A;Accession: B61457
A;Molecule type: protein
A;Residues: 1-15 <BAN>
C;Genetics:
A;Genetic code: SGCS
A;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; moi

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 VLP 8
      |||
Db      1 VLP 3

RESULT 33
C61511
milk band B protein - Australian echidna (fragment)
C;Species: Tachyglossus aculeatus (Australian echidna)
C;Date: 09-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000
C;Accession: C61511
R;Teahan, C.G.; McKenzie, H.A.; Griffiths, M.
Comp. Biochem. Physiol. B 99, 99-118, 1991
A;Title: Some monotreme milk "whey" and blood proteins.
A;Reference number: A61511; MUID:92070088; PMID:1959333
A;Accession: C61511
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <GRI>
C;Keywords: glycoprotein

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy     12 PFP 14
      |||
Db     13 PFP 15

RESULT 34
PT0205
insulin-like growth factor-binding protein, bone - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 08-Dec-1994
C;Accession: PT0205; A33175
R;Bautista, C.M.; Baylink, D.J.; Mohan, S.
Biochem. Biophys. Res. Commun. 176, 756-763, 1991
A;Title: Isolation of a novel insulin-like growth factor (IGF) binding protein from human
A;Reference number: PT0205; MUID:91222244; PMID:1709017
A;Accession: PT0205
A;Molecule type: protein
A;Residues: 1-15 <BAU>

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 VEP 11
      |||
Db      7 VEP 9

RESULT 35
I46909
voltage-dependent dihydropyridine-sensitive calcium channel alpha 1 subunit 155 kda i:

```

C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
 C:Accession: I46909
 R:Malouf, N.N.; McMahon, D.K.; Hainsworth, C.N.; Kay, B.K.
 Neuron 8, 899-906, 1992
 A:Title: A two-motif isoform of the major calcium channel subunit in skeletal muscle.
 A:Reference number: I46909; MUID:92265303; PMID:1316766
 A:Accession: I46909
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-15 <MAL>
 A:Cross-references: GB:S36895; NID:G249481; PIDN:AAB22180.1; PID:G249482

Query Match 20.0%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
 |||
 Db 13 LEM 15

RESULT 36
 A31902
 bone acidic glycoprotein-75 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 31-Dec-1993
 C:Accession: A31902
 R:Gorski, J.P.; Shimizu, K.
 J. Biol. Chem. 263, 15938-15945, 1988

A:Title: Isolation of new phosphorylated glycoprotein from mineralized phase of bone
 A:Reference number: A31902; MUID:89034045; PMID:2846530
 A:Accession: A31902
 A:Molecule type: protein
 A:Residues: 1-15 <GOR>
 A>Note: 14-Glu and 15-Glu were also found
 C:Keywords: Glycoprotein

Query Match 20.0%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
 |||
 Db 1 LPV 3

RESULT 37
 A45096
 thyrotropin-releasing hormone receptor, splice form 387 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A45096
 R:de la Peña, F.; Delgado, L.M.; del Camino, D.; Barros, F.
 J. Biol. Chem. 267, 25703-25708, 1992

A:Title: Two isoforms of the thyrotropin-releasing hormone receptor generated by alternative splicing
 A:Reference number: A45096; MUID:93100278; PMID:1334485
 A:Accession: A45096
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-15
 A:Cross-references: GB:S51512; NID:G261982; PIDN:AAB24549.1; PID:G261983
 A:Experimental source: GH3 anterior pituitary cells
 A>Note: sequence extracted from NCBI backbone (NCBIP:120927)

Query Match 20.0%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
 |||
 Db 7 PVL 9

RESULT 38
 A49761

locustapyrokinin - migratory locust
 C:Species: Locusta migratoria (migratory locust)
 C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 08-Dec-1995
 C:Accession: A49761
 R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.
 Gen. Comp. Endocrinol. 81, 97-104, 1991
 A:Title: Isolation, primary structure, and synthesis of locustapyrokinin: a myotropic
 A:Reference number: A49761; MUID:91224474; PMID:2026322
 A:Accession: A49761

A:Molecule type: protein
 A:Residues: 1-16 <SCH>
 C:Comment: This neuropeptide stimulates contractions in an isolated cockroach hindgut
 C:Superfamily: pyrokinin
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:16/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 20.0%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15
 |||
 Db 11 PFV 13

RESULT 39
 S03405

hydrogenase (EC 1.18.99.1) small chain - Alcaligenes eutrophus (fragment)
 C:Species: Alcaligenes eutrophus
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Sep-1998
 C:Accession: S03405
 R:Lorenz, B.; Schneider, K.; Kratzin, H.; Schlegel, H.G.
 Biochim. Biophys. Acta 995, 1-9, 1989
 A:Title: Immunological comparison of subunits isolated from various hydrogenases of a
 A:Reference number: S03404; MUID:89166625; PMID:2493816
 A:Accession: S03405

A:Molecule type: protein
 A:Residues: 1-16 <LOR>
 A:Experimental source: strain H16, DMS 541
 C:Superfamily: hydrogenase (NiFe) small chain
 C:Keywords: hydrogen metabolism; iron-sulfur protein; membrane bound; metalloprotein;

Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
 |||
 Db 8 PVL 10

RESULT 40
 C45133

casein kinase II (EC 2.7.1.1-) alpha chain - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 03-Jun-1996
 C:Accession: C45133
 R:Ou, W.J.; Thomas, D.Y.; Bell, A.W.; Bergeron, J.J.
 J. Biol. Chem. 267, 23789-23796, 1992
 A:Title: Casein kinase II phosphorylation of signal sequence receptor alpha and the a:
 A:Reference number: A45133; MUID:93054738; PMID:1331100
 A:Accession: C45133

A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-16 <OU1>
 A:Experimental source: endoplasmic reticulum, pancreas
 A>Note: sequence extracted from NCBI backbone (NCBIP:118799)
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; heterotetramer; phosphotransferase; serine/threonine-specific protein;

Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EPF 12
 |||
 Db 6 EPF 8

RESULT 41

T37075
 hypothetical protein SCJ30.08 - Streptomyces coelicolor
 C;Species: Streptomyces coelicolor
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C;Accession: T37075
 R;Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, August 1999
 A;Reference number: Z21621
 A;Accession: T37075
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-16 <SAN>
 A;Cross-references: EMBL:AL109973; PIDN:CAB53303.1; GSPDB:GN00070; SCOEDB:SCJ30.08
 A;Experimental source: strain A3(2)
 C;Genetics:
 A;Gene: SCOEDB:SCJ30.08

Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPV 6
 |||
 Db 1 MPV 3

RESULT 42

S09732
 photosystem I protein psaJ - spinach chloroplast (fragment)
 C;Species: chloroplast Spinacia oleracea (spinach)
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Feb-1997
 C;Accession: S09732
 R;Ikemuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.
 FEBS Lett. 263, 274-278, 1990
 A;Title: Polypeptide composition of higher plant photosystem I complex. Identification of
 A;Reference number: S09730; MUID:90242987; PMID:2185953
 A;Accession: S09732
 A;Molecule type: protein
 A;Residues: 1-16 <IKE>
 C;Genetics:
 A;Gene: psaJ
 A;Genome: chloroplast
 C;Keywords: chloroplast; photosynthesis; photosystem I; transmembrane protein

Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVL 7
 |||
 Db 12 PVL 14

RESULT 43

C61414
 chymotrypsin (EC 3.4.21.1) - slider turtle (fragment)
 C;Species: Pseudemys scripta (slider)
 C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
 C;Accession: C61414
 R;Bhargava, A.K.; Barnard, E.A.
 J. Mol. Evol. 2, 187-198, 1973
 A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determi

A;Reference number: A61414; MUID:76146602; PMID:4807189

A;Accession: C61414
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-16 <BHA>
 C;Keywords: hydrolase; protein digestion; serine proteinase

Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVL 7
 |||
 Db 8 PVL 10

RESULT 44

S68730
 bleomycin-binding protein - Streptomyces verticillus (fragment)
 C;Species: Streptomyces verticillus
 C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999
 C;Accession: S68730
 R;Sugiyama, M.; Kumagai, T.; Matsuo, H.; Bhuiyan, M.Z.A.; Ueda, K.; Mochizuki, H.; Na
 FEBS Lett. 362, 80-84, 1995
 A;Title: Overproduction of the bleomycin-binding proteins from bleomycin-producing St.
 ai characterisation.
 A;Reference number: S68730; MUID:95212588; PMID:7535252
 A;Accession: S68730
 A;Molecule type: protein
 A;Residues: 1-16 <SUG>
 A;Experimental source: ATCC 15003
 C;Keywords: antibiotic resistance

Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVL 7
 |||
 Db 9 PVL 11

RESULT 45

I65274
 glutathione S-transferase Ya subunit (put.) - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Jun-1999
 C;Accession: I65274
 R;Rothkopf, G.S.; Telakowski-Hopkins, C.A.; Stotish, R.L.; Pickett, C.B.
 Biochemistry 25, 993-1002, 1986
 A;Title: Multiplicity of glutathione S-transferase genes in the rat and association w
 A;Reference number: I52395; MUID:8618772; PMID:2421763
 A;Accession: I65274
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-17 <RES>
 A;Cross-references: GB:M12894; NID:G204504; PIDN:AAA41289.1; PID:G204505
 C;Superfamily: glutathione transferase

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPV 9
 |||
 Db 1 LPV 3

RESULT 46

S05033
 photosystem II protein psbL - Synechococcus sp. (strain Copeland) (fragment)
 N;Alternate names: photosystem II 5K protein
 C;Species: Synechococcus sp.

C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C;Accession: S05033
R;Ikemuchi, M.; Koike, H.; Inoue, Y.
FEBS Lett. 251, 155-160, 1989
A;Title: Identification of psbI and psbL gene products in cyanobacterial photosystem II
A;Reference number: S05030
A;Accession: S05033
A;Molecule type: protein
A;Residues: 1-17 <IKS>
A;Note: the source is designated as Synechococcus vulcanus
C;Genetics:
A;Gene: psbL
C;Keywords: photosynthesis; photosystem II; thylakoid

Query Match 20.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10
|||
Db 9 PVE 11
|||

RESULT 47

S50742
proteinase inhibitor (Kunitz-type) 1-related protein - potato (fragment)
N;Alternate names: PKPI minor protein
C;Species: Solanum tuberosum (potato)
C;Date: 14-Jul-1995 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996
C;Accession: S50742
R;Mitsumori, C.; Yamagishi, K.; Fujino, K.; Kikuta, Y.
Plant Mol. Biol. 26, 961-969, 1994
A;Title: Detection of immunologically related Kunitz and Bowman-Birk proteinase inhibitors
A;Reference number: S50741; MUID:95093035; PMID:8000008
A;Accession: S50742
A;Molecule type: protein
A;Residues: 1-17 <MIT>

Query Match 20.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
|||
Db 7 PVL 9
|||

RESULT 48

B61414
chymotrypsin (EC 3.4.21.1) - painted turtle (fragment)
C;Species: Chrysemys picta (painted turtle)
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
C;Accession: B61414
R;Bhargava, A.K.; Barnard, E.A.
J. Mol. Evol. 2, 187-198, 1973
A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determined
A;Reference number: A61414; MUID:76146602; PMID:4807189
A;Accession: B61414
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <BHA>
C;Keywords: hydrolase; serine proteinase

Query Match 20.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
|||
Db 8 PVL 10
|||

RESULT 49

A60570

Ig mu heavy chain disease extra sequence - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 16-Aug-1996
C;Accession: A60570
R;Mihesco, C.; Ferrara, P.; Guillemot, J.C.; Congy, N.; Gendron, M.C.; Roy, J.P.; Si Mol. Immunol. 27, 771-776, 1990
A;Title: A new extra sequence at the amino terminal of a mu heavy chain disease protein
A;Reference number: A60570; MUID:90384486; PMID:2119480
A;Accession: A60570
A;Molecule type: protein
A;Residues: 1-17 <MIH>
C;Comment: This sequence is derived from the amino terminus of an abnormal immunoglobulin
C;Keywords: immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
|||
Db 6 PVL 8
|||

RESULT 50

B31769
T-cell receptor delta-2 chain J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 05-Nov-1999
C;Accession: B31769
R;Loeh, E.V.; Swirla, S.; Serafini, A.T.; Phillips, J.H.; Lanier, L.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 9714-9718, 1988
A;Title: Human T-cell-receptor delta chain: genomic organization, diversity, and expression
A;Reference number: A94221; MUID:89071766; PMID:2974163
A;Accession: B31769
A;Molecule type: DNA
A;Residues: 1-17 <LOH>
A;Cross-references: GB:L36386; MID:g540455; PIDN:AAA61108.1; PID:g540456
C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11
|||
Db 15 VEP 17
|||

RESULT 51

I55612
thyroid hormone receptor beta - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I55612
R;Adams, M.; Matthews, C.; Collingwood, T.N.; Tone, Y.; Beck-Peccoz, P.; Chatterjee, J. Clin. Invest. 94, 506-515, 1994
A;Title: Genetic analysis of 29 kindreds with generalized and pituitary resistance to thyroid hormone
A;Reference number: I55612; MUID:94314950; PMID:8040303
A;Accession: I55612
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-17 <RES>
A;Cross-references: GB:S72623; MID:g633779; PIDN:AAB31420.1; PID:g633780
C;Genetics:
A;Gene: TRbeta

Query Match 20.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PVL 15
|||

Db 7 PFV 9

RESULT 52

G85956
hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain EDL956)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: G85956
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85956
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-17 <STO>
A:Cross-references: GB:AE005174; NID:g12517539; PIDN:AAG58115.1; GSPDB:GN00145; UWGP:Z43
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z4331

Query Match 20.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFV 13
Db 6 PFV 8

RESULT 53

B24735
glutathione transferase (EC 2.5.1.18) 1-2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993
C:Accession: B24735
R:Mannervik, B.; Alin, P.; Guthenberg, C.; Jonsson, H.; Tahir, M.K.; Warholm, M.; Jornva
Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985
A:Title: Identification of three classes of cytosolic glutathione transferase common to
A:Reference number: A24735; MUID:86042634; PMID:3864155
A:Accession: B24735
A:Molecule type: protein
A:Residues: 1-18 <MAN>
C:Superfamily: glutathione transferase
C:Keywords: transferase

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
Db 4 PVL 6

RESULT 54

S29264
ovoheemerythrin - duck leech (fragment)
N:Alternate names: 14K yolk protein
C:Species: Theromyzon tessulatum (duck leech)
C>Date: 19-Mar-1997 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: S29264
R:Baert, J.L.; Britel, M.; Sautiere, P.; Malecha, J.
Eur. J. Biochem. 209, 563-569, 1992
A:Title: Ovoheemerythrin, a major 14-kDa yolk protein distinct from vitellogenin in leech
A:Reference number: S29264; MUID:93049299; PMID:1425663
A:Accession: S29264
A:Molecule type: protein
A:Residues: 1-18 <BAE>
A:Cross-references: PIDN:AB23969.1; PID:g258980
C:Superfamily: hemerythrin

C:Keywords: egg yolk; oxygen carrier

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPF 12
Db 5 EPF 7

RESULT 55

S48863
cyclin C - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: S48863
R:Wu, L.; Hall, P.L.
submitted to the EMBL Data Library, October 1994
A:Reference number: S48863
A:Accession: S48863
A:Molecule type: mRNA
A:Residues: 1-18 <WUL>
A:Cross-references: EMBL:X82403; NID:g563901; PIDN:CAA57797.1; PID:g563902

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
Db 10 PVL 12

RESULT 56

I40062
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C:Species: Buchnera aphidicola
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999
C:Accession: I40062
R:Roubbakhsh, D.; Baumann, P.
Gene 155, 107-112, 1995
A:Title: Characterization of a putative 238-5S rRNA operon of Buchnera aphidicola (enc
A:Reference number: I40061; MUID:95212914; PMID:7535281
A:Accession: I40062
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18 <RES>
A:Cross-references: EMBL:U10496; NID:g854711; PIDN:AAA79125.1; PID:g854712
C:Genetics:
A:Gene: aroE
C:Keywords: oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db 8 VLP 10

RESULT 57

S46241
NAD(P)H-flavin oxidoreductase (EC 1.-.-.-) - Vibrio fischeri
C:Species: Vibrio fischeri
C>Date: 10-Dec-1994 #sequence_revision 12-May-1995 #text_change 16-Oct-1998
C:Accession: S46241
R:inouye, S.
FEBS Lett. 347, 163-168, 1994
A:Title: NAD(P)H-flavin oxidoreductase from the bioluminescent bacterium, Vibrio fisch
A:Reference number: S46241; MUID:94307374; PMID:8033996
A:Accession: S46241

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <INO>
C;Keywords: NAD; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLE 3
|||
Db 7 DLE 9

RESULT 58

serine proteinase inhibitor, 31K - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998
C;Accession: S71592
R;Rao, C.N.; Liu, Y.Y.; Peavey, C.L.; Woodley, D.T.
Arch. Biochem. Biophys. 317, 311-314, 1995
A;Title: Novel extracellular matrix-associated serine proteinase inhibitors from human s

A;Reference number: S71592; MUID:95177668; PMID:7872799
A;Accession: S71592
A;Molecule type: protein
A;Residues: 1-18 <RAO>

C;Function:

A;Description: involved in turnover of connective tissues

C;Keywords: serine proteinase inhibitor

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EPF 12
|||
Db 5 EPF 7

RESULT 59

T-cell receptor delta-chain J-delta-2 - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 30-May-1997

C;Accession: I46653

R;Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.

J. Immunol. 155, 1981-1993, 1995

A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old

A;Reference number: I46623; MUID:95363165; PMID:7636249

A;Accession: I46653

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-18 <YAN>

A;Cross-references: GB:D49561; NID:g1041174; PID:g1041175

C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEP 11
|||
Db 16 VEP 18

RESULT 60

superoxide dismutase (EC 1.15.1.1) (Fe/Mn) [similarity] - unidentified organism (fragment)
C;Species: unidentified organism

C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 20-Apr-2000

C;Accession: C56049

R;Binette, J.P.; Binette, M.B.

Scanning Microsc. 8, 233-239, 1994
A;Title: Sequencing of proteins extracted from stones.
A;Reference number: A56049; MUID:95215817; PMID:7701298
A;Accession: C56049
A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-19 <BIN>

A;Experimental source: urate-calcium oxalate kidney stones

A;Note: the source is designated as Homo sapiens, however the true source probably or

C;Superfamily: superoxide dismutase (Mn)

C;Keywords: metalloprotein; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLP 8
|||
Db 4 VLP 6

RESULT 61

hydroxyproline-rich cell wall glycoprotein (42K and others) - kidney bean (fragment)
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 05-Dec-1998

C;Accession: S59485; S59484; S59483

R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A;Title: Specificity in the immobilisation of cell wall proteins in response to diffe

A;Reference number: S59481; MUID:96011753; PMID:7548825

A;Accession: S59485

A;Molecule type: protein

A;Residues: 1-19 <WOJ>

A;Note: hydroxyproline-rich cell wall glycoprotein, 42K

A;Accession: S59484

A;Molecule type: protein

A;Residues: 1-15 <WOW>

A;Note: hydroxyproline-rich cell wall glycoprotein, 84K

A;Accession: S59483

A;Molecule type: protein

A;Residues: 1-14 <WOP>

A;Note: hydroxyproline-rich cell wall glycoprotein, 136K, minor component

C;Superfamily: proline-rich protein 3

C;Keywords: Glycoprotein; hydroxyproline

F;6.11.16/Modified site: hydroxyproline (Pro) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVE 10
|||
Db 6 PVE 8

RESULT 62

shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C;Species: Buchnera aphidicola
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999

C;Accession: I40063

R;Roubakshin, D.; Baumann, P.

Gene 155, 107-112, 1995

A;Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (en

A;Reference number: I40061; MUID:95212914; PMID:7535281

A;Accession: I40063

A;Status: preliminary; translated from GB/EMBL/DDJ

A;Molecule type: DNA

A;Residues: 1-19 <RES>

A;Cross-references: EMBL:U10497; NID:g854713; PIDN:AAA79126.1; PID:g854714

C;Genetics:

A;Gene: aroE

C;Keywords: oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
|||
Db 8 VLP 10

RESULT 63

S43641
carboxylesterase (EC 3.1.1.1), thermostable - Alicyclobacillus acidocaldarius (fragment)
C;Species: Alicyclobacillus acidocaldarius
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
C;Accession: S43641
R;Manco, G.; di Gennaro, S.; de Rosa, M.; Rossi, M.
Eur. J. Biochem. 221, 965-972, 1994
A;Title: Purification and characterization of a thermostable carboxylesterase from the
A;Reference number: S43641; MUID:94237161; PMID:8181479
A;Accession: S43641
A;Molecule type: protein
A;Residues: 1-19 <MAN>
A;Experimental source: strain MT3
A;Note: the source is designated as Bacillus acidocaldarius
C;Keywords: carboxylic ester hydrolase; monomer

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10
|||
Db 4 PVE 6

RESULT 64

A61144
Probable flagellar protein (clone FCH-P8-4) - Trypanosoma cruzi (fragment)
C;Species: Trypanosoma cruzi
C;Date: 10-Mar-1994 #sequence_revision 07-Apr-1994 #text_change 24-Feb-1995
C;Accession: A61144
R;Bua, J.; Bontempi, E.J.; Levin, M.; Orn, A.; Velasco, D.; Moreno, M.; Levi-Yeyati, P.;
Exp. Parasitol. 72, 54-62, 1991
A;Title: Trypanosoma cruzi: cellular and antibody response against the parasite in mice
A;Reference number: A61144; MUID:91130571; PMID:1993465
A;Accession: A61144
A;Molecule type: mRNA
A;Residues: 1-19 <BUA>

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11
|||
Db 17 VEP 19

RESULT 65

S69153
Neb-colloostatin - flesh fly (Sarcophaga bullata)
C;Species: Sarcophaga bullata
C;Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 19-May-2000
C;Accession: S69153
R;Byllemans, D.; Proost, P.; Samijn, B.; Borovsky, D.; Grauwels, L.; Huybrechts, R.; van
Eur. J. Biochem. 228, 45-49, 1995
A;Title: Neb-colloostatin, a second folliculastatin of the grey fleshfly, Neobellieria bu
A;Reference number: S69153; MUID:95188911; PMID:7883009
A;Accession: S69153
A;Molecule type: protein
A;Residues: 1-19 <BYL>

Query Match

20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
|||
Db 7 LPV 9

RESULT 66

A39504
octamer-binding protein, Ku-like, 72K chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C;Accession: A39504
R;May, G.; Sutton, C.; Gould, H.
J. Biol. Chem. 266, 3052-3059, 1991
A;Title: Purification and characterization of Ku-2, an octamer-binding protein relate
A;Reference number: A39504; MUID:91131605; PMID:1993678
A;Accession: A39504
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <MAY>

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
|||
Db 11 LEM 13

RESULT 67

I46654
T-cell receptor delta-chain J-delta-3 - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C;Accession: I46654
R;Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-c
A;Reference number: I46623; MUID:95363165; PMID:7636249
A;Accession: I46654
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-19 <YAN>
A;Cross-references: GB:D49562; NID:G1041176; PIDN:BAA08506.1; PID:G1041177
C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11
|||
Db 17 VEP 19

RESULT 68

S68394
H+-transporting two-sector ATPase (EC 3.6.3.14) chain G - Chlamydomonas reinhardtii (C
N;Alternate names: ATP synthase chain G
C;Species: Chlamydomonas reinhardtii
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 03-Jun-2002
C;Accession: S68394
R;Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.
FEBS Lett. 377, 163-166, 1995
A;Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-termin
A;Reference number: S68398; MUID:96128220; PMID:8543042
A;Accession: S68394
A;Molecule type: protein

A;Residues: 1-19 <PIE>
 A;Experimental source: strain CW15
 C;Genetics:
 A;Genome: nuclear
 C;Keywords: chloroplast; hydrolase

Query Match 20.0%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
 ||||
 DB 11 LPV 13

RESULT 69

CS4052

Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / phosphoribosyl-ATP diphosphatase (EC 3

C;Species: Klebsiella pneumoniae
 C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2002
 C;Accession: CS4052

R;Rieder, G.; Merrick, M.J.; Castorff, H.; Kleiner, D.

J. Biol. Chem. 269, 14386-14390, 1994

A;Title: Function of hisP and hisH gene products in histidine biosynthesis.

A;Reference number: A54052; MUID:94237842; PMID:8182043

A;Accession: CS4052

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-20 <RIE>

A;Experimental source: MSal

A;Note: sequence extracted from NCBI backbone (NCBIN:148607, NCBIPI:148610)

C;Genetics:

A;Gene: hisIE

C;Superfamily: hisI bifunctional enzyme; hisI bifunctional enzyme homology; hisI protein

C;Keywords: histidine biosynthesis; hydrolase; multifunctional enzyme

Query Match 20.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPV 6
 ||||
 DB 15 MPV 17

RESULT 70

S50741

probable trypsin inhibitor - potato (fragment)

N;Alternate names: PKPI major protein

C;Species: Solanum tuberosum (potato)

C;Date: 14-Jul-1995 #sequence_revision 12-Apr-1996 #text_change 11-Jan-2000

C;Accession: S50741

R;Mitsumori, C.; Yamagishi, K.; Fujino, K.; Kikuta, Y.

Plant Mol. Biol. 26, 961-969, 1994

A;Title: Detection of immunologically related Kunitz and Bowman-Birk proteinase inhibitors

A;Reference number: S50741; MUID:95093035; PMID:8000008

A;Accession: S50741

A;Molecule type: protein

A;Residues: 1-20 <MIT>

C;Superfamily: cathepsin D inhibitor

Query Match 20.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
 ||||
 DB 2 VLP 4

RESULT 71

B44581

bombinin H Met-8 - yellow-bellied toad

Query Match 20.0%; Score 3; DB 2; Length 20;

C;Species: Bombina variegata (yellow-bellied toad)
 C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 11-Jan-2000
 C;Accession: B44581
 R;Mignogna, G.; Simmaco, M.; Kreil, G.; Barra, D.
 EMBO J. 12, 4829-4832, 1993
 A;Title: Antibacterial and haemolytic peptides containing D-alloisoleucine from the
 A;Reference number: S39612; MUID:94039967; PMID:8223431
 A;Accession: B44581
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <MIG>
 C;Superfamily: bombinin H precursor
 C;Keywords: amidated carboxyl end; D-amino acid
 F;2/Modified site: D-allo-isoleucine (Ile) #status experimental
 F;20/Modified site: amidated carboxyl end (Ile) #status predicted

Query Match 20.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
 ||||
 DB 4 PVL 6

RESULT 72

S06466

T-cell receptor alpha chain J segment (DO) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 06-Jun-1997

C;Accession: S06466

R;Yague, J.; Blackman, M.; Born, W.; Marrack, P.; Kappler, J.; Palmer, E.

Nucleic Acids Res. 16, 11355-11364, 1988

A;Title: The structure of V-alpha and J-alpha segments in the mouse.

A;Reference number: S06466; MUID:89083566; PMID:2849763

A;Accession: S06466

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-20 <YAG>

A;Experimental source: strain Balb/c

C;Genetics:

A;Map position: 14

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: glycoprotein; heterodimer; T-cell receptor

F;1-18/Domain: J segment <USE>

F;19-20/Domain: C region (fragment) <CRE>

Query Match 20.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11
 ||||
 DB 16 VEP 18

RESULT 73

PL0145

carbon-monoxide dehydrogenase (EC 1.2.99.2) small chain - Pseudomonas carboxydoflava

C;Species: Pseudomonas carboxydoflava

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993

C;Accession: PL0145

R;Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.

Arch. Microbiol. 152, 335-341, 1989

A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydot

A;Reference number: PL0138; MUID:90055678; PMID:2818128

A;Accession: PL0145

A;Molecule type: protein

A;Residues: 1-20 <KRA>

C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large,

C;Keywords: oxidoreductase

Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11
|||
DB 18 VEP 20

RESULT 74

B30208
hypothetical protein 1 (cpc-1 5' region) - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C:Accession: B30208
R:Patel, J.L.; Obach, M.J.; Legerton, T.L.; Yanofsky, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 3728-3732, 1988
A:Title: The cross-pathway control gene of Neurospora crassa, cpc-1, encodes a protein s
A:Reference number: A30208; MUID:88234499; PMID:2967496
A:Accession: B30208
A:Molecule type: DNA
A:Residues: 1-20 <PAL>
A:Cross-references: GB:J03262

Query Match 20.0%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFP 13
|||
DB 6 PFP 8

RESULT 75

B60365
chymotrypsin inhibitor 2 - tobacco hornworm (fragment)
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 03-Feb-1994
C:Accession: B60365
R:Kanost, M.R.
Insect Biochem. 20, 141-147, 1990
A:Title: Isolation and characterization of four serine proteinase inhibitors (serpins) f
A:Reference number: A60365
A:Accession: B60365
A:Molecule type: protein
A:Residues: 1-20 <KAN>
C:Keywords: hemolymph; monomer; serine proteinase inhibitor

Query Match 20.0%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15
|||
DB 6 PFV 8

Search completed: November 25, 2003, 18:28:17

Job time : 14.8032 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 7.26064 Seconds
(without alignments)
97.154 Million cell updates/sec

Title: US-09-641-801-5

Perfect score: 15

Sequence: 1 DLEMPVLVBPFFV 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	26.7	12	1	TM2A_METMA
2	3	20.0	9	1	LMT3_LOCM1
3	3	20.0	9	1	ULAH_HUMAN
4	3	20.0	10	1	FAR6_PANRE
5	3	20.0	10	1	UHA3_HUMAN
6	3	20.0	11	1	R22_CONAM
7	3	20.0	13	1	FIBB_RABIT
8	3	20.0	13	1	PEDI_HYDAT
9	3	20.0	13	1	TENE_RANTE
10	3	20.0	13	1	UHA3_CANFA
11	3	20.0	13	1	YPE2_LACLC
12	3	20.0	14	1	UC15_MAIZE
13	3	20.0	15	1	UC16_MAIZE
14	3	20.0	15	1	UC25_MAIZE
15	3	20.0	16	1	LPK1_LOCM1
16	3	20.0	17	1	PSBL_SYNVU
17	3	20.0	18	1	AL12_CYDPO
18	3	20.0	18	1	HEMH_THETS
19	3	20.0	19	1	COOT_SABSU
20	3	20.0	20	1	COXN_THUOB
21	3	20.0	20	1	MAX7_BOMMX
22	3	20.0	20	1	MAX8_BOMMX
23	3	20.0	20	1	PSAL_SYNVU
24	3	20.0	20	1	SB60_MAIZE
25	3	20.0	20	1	TRYL_STREX
26	2	13.3	5	1	E103_LITRU
27	2	13.3	5	1	PAP2_PARMA
28	2	13.3	5	1	PRCT_PERAM
29	2	13.3	5	1	SUGA_ACHDO
30	2	13.3	5	1	TPIS_CANFA
31	2	13.3	6	1	ACPH_RABIT
32	2	13.3	6	1	CIP1_MYTED
33	2	13.3	6	1	CIP2_MYTED

34	2	13.3	6	1	E101_LITRU
35	2	13.3	6	1	TRPI_PSEPU
36	2	13.3	7	1	ALL3_CARMA
37	2	13.3	7	1	CARP_MYTED
38	2	13.3	7	1	CCF1_ENTFA
39	2	13.3	7	1	E105_LITRU
40	2	13.3	7	1	FAR1_HELTI
41	2	13.3	7	1	PH2_LYCES
42	2	13.3	7	1	UNW6_PINPS
43	2	13.3	7	1	WWA1_ACHFU
44	2	13.3	7	1	WWA3_ACHFU
45	2	13.3	8	1	ALL6_CYDPO
46	2	13.3	8	1	ANG2_BORJA
47	2	13.3	8	1	CAD1_ENTFA
48	2	13.3	8	1	CUP_THICU
49	2	13.3	8	1	COM2_CONPU
50	2	13.3	8	1	PR2_PERAM
51	2	13.3	8	1	PR3_PERAM
52	2	13.3	8	1	UC26_MAIZE
53	2	13.3	8	1	UF06_MOUSE
54	2	13.3	9	1	B43_SERPL
55	2	13.3	9	1	CCAP_CARMA
56	2	13.3	9	1	COXE_THUOB
57	2	13.3	9	1	FAR5_PENMO
58	2	13.3	9	1	FIBB_ERYPA
59	2	13.3	9	1	KNL3_BOMVA
60	2	13.3	9	1	LMP1_LOCM1
61	2	13.3	9	1	OXVA_SCYCA
62	2	13.3	9	1	OXIF_SCYCA
63	2	13.3	9	1	OXIT_EISFO
64	2	13.3	9	1	OXIV_SQUAC
65	2	13.3	9	1	PRSP_BOMMO
66	2	13.3	9	1	SAMP_MUSCA
67	2	13.3	9	1	ULAE_HUMAN
68	2	13.3	9	1	UN19_CLOPA
69	2	13.3	9	1	UPA3_HUMAN
70	2	13.3	10	1	ANG1_BOTJA
71	2	13.3	10	1	ANGT_BOVIN
72	2	13.3	10	1	ANGT_CHICK
73	2	13.3	10	1	CATE_SHEEP
74	2	13.3	10	1	COXA_ONCMY
75	2	13.3	10	1	ESL_LACCA
76	2	13.3	10	1	GAJU_HUMAN
77	2	13.3	10	1	GON1_PETMA
78	2	13.3	10	1	GON3_ONCKE
79	2	13.3	10	1	GONL_SQUAC
80	2	13.3	10	1	ODP2_BOVIN
81	2	13.3	10	1	PNEU_HUMAN
82	2	13.3	10	1	PNEU_RAT
83	2	13.3	10	1	PVK_LOCM1
84	2	13.3	10	1	Q2OB_COMTE
85	2	13.3	10	1	RL16_ACHLA
86	2	13.3	10	1	RT02_BOVIN
87	2	13.3	10	1	SLAP_BACTG
88	2	13.3	10	1	TEMK_RANTE
89	2	13.3	10	1	TKNB_CHICK
90	2	13.3	10	1	TKNB_ONCMY
91	2	13.3	10	1	TKNK_PIG
92	2	13.3	10	1	TKUL_URRIN
93	2	13.3	10	1	TPIS_NICPL
94	2	13.3	10	1	UPAS_HUMAN
95	2	13.3	10	1	URE3_MORMO
96	2	13.3	10	1	UXB1_YEAST
97	2	13.3	10	1	XNBN_DICB4
98	2	13.3	11	1	ANGT_CRIGE
99	2	13.3	11	1	BPBP_AKSHA
100	2	13.3	11	1	BRK_MEGFL

ALIGNMENTS

RESULT 1

TM2A METWA
ID TM2A METWA STANDARD; PRT; 12 AA.
AC P80652;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin-coenzyme M
DE methyltransferase 28 kDa subunit) [Fragment].
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE.
RX STRAIN=Goe1 / Goe1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=96370840; PubMed=8774736;
RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RA "Sodium ion translocation by N5-methyltetrahydromethanopterin;
RT coenzyme M methyltransferase from Methanosarcina mazei Goe1
RT reconstituted in ether lipid liposomes.";
RL Eur. J. Biochem. 239:857-864(1996).
CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN
CC METHANOGENESIS. THE FORMATION OF METHYL-COENZYME M AND
CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
CC TETRAHYDROMETHANOPTERIN.
CC -!- CATALYTIC ACTIVITY: S-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC mercaptoethanesulfonate = S-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC (methylthio)ethanesulfonate.
CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
KW Transferase; Methyltransferase; Transmembrane protein.
FT NON_TER 12
FT SEQUENCE 12 AA; 1321 MW; 6DB4A5766232D76B CRC64;
Query Match 26.7%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLP 8
Db 6 PVLP 9
|||||

RESULT 2
LMT3 LOCMI
ID LMT3 LOCMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamycotropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE AND SYNTHESIS.
RX TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamycotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamycotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
CC PIR; A61620; A61620.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYOKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.

FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;
Query Match 20.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 13e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15
Db 4 PFV 6
|||||

RESULT 3
ULAH HUMAN
ID ULAH HUMAN STANDARD; PRT; 9 AA.
AC P31934;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 94) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 12 kDa.
CC SWISS-2DPAGE; P31934; HUMAN.
DR NON_TER 1
DR VARIANT 3 3 A -> L.
FT NON_TER 1
FT SEQUENCE 9 AA; 990 MW; FICCTB172AB6DDCA CRC64;
Query Match 20.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLE 3
Db 5 DLE 7
|||||

RESULT 4
FAR6 PANRE
ID FAR6 PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRP-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoidea; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of FMRFamide-related
RT peptides (FARPs) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.

FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;
Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15
DB 6 PFV 8

RESULT 5
CH33 HUMAN
ID_UH33 HUMAN STANDARD; PRT; 10 AA.
AC P40930; 1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7995732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
1994.";
RL Electrophoresis 15:1459-1465(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.8, ITS MW IS: 47.3 Kda.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1049 MW; 6BBCDE41A041B76B CRC64;
Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11
DB 2 VEP 4

RESULT 6
R22 CONAM
ID_R22 CONAM STANDARD; PRT; 11 AA.
AC P42341;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S2 (Fragment).
GN RPS2.
OS Conopholis americana (Squawroot).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Orobanchaceae; Orobanchaceae; Conopholis.
OX NCBI_TaxID=4179;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92145776; PubMed=1723664;
RA Taylor G., Wolfe K.H., Morden K.W., Depamphilis C.W., Palmer J.D.;
RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss
of photosynthesis in a lineage of parasitic plants.";
RL Curr. Genet. 20:515-518(1991).
CC -!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
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DR EMBL; X64567; CAA45868.1; -.
DR PIR; S32575; S32575.
DR HAMAP; MF_00291; -; 1.
DR InterPro; IPR001865; Ribosomal S2.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.
KW Ribosomal protein; Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;
Query Match 20.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLE 3
DB 9 DLE 11

RESULT 7
FIBB RABIT
ID_FIBB RABIT STANDARD; PRT; 13 AA.
AC P14478;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 13 FIBRINOPEPTIDE B.
FT MOD_RES 4 4 SULFATION.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1493 MW; 9417F3B76337CB1A CRC64;
Query Match 20.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
DB 8 VLP 10

RESULT 8
PEDI HYDAT
ID_PEDI HYDAT STANDARD; PRT; 13 AA.
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)

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DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Unknown protein from 2D-page of heart tissue (Spot 7520) (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]_SEQUENCE.
RP TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Biocytos 18:2795-2802(1997).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.9, ITS MW IS: 55.4 kDa.
DR HSC-2DPAGE; P56535; DOG.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1457 MW; 9F5BD94B9306D76A CRC64;

Query Match 20.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db |||
7 VLP 9

RESULT 9
TEMP_RANTE STANDARD; PRT; 13 AA.
AC P56920;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tempurin B.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranchoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]_SEQUENCE.
RP TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevian family.
CC Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db |||
1 VLP 3

RESULT 10
UHA3 CANFA STANDARD; PRT; 13 AA.
ID UHA3 CANFA
AC P56535;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

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DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot 7520) (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]_SEQUENCE.
RP TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Biocytos 18:2795-2802(1997).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.9, ITS MW IS: 55.4 kDa.
DR HSC-2DPAGE; P56535; DOG.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1457 MW; 9F5BD94B9306D76A CRC64;

Query Match 20.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10
Db |||
7 PVE 9

RESULT 11
YPE2_LACLC STANDARD; PRT; 13 AA.
AC P42021;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PEPT 5'region (ORF2) (Fragment).
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=94245610; PubMed=8188586;
RX Mierau I., Haandrikman A.J., Velterop O., Tan P.S.T., Leenhouts K.L.,
RA Konings W.N., Venema G., Kok J.;
RT "Tripeptidase gene (pept) of Lactococcus lactis: molecular cloning
RT and nucleotide sequencing of pept and construction of a chromosomal
RL deletion mutant.";
RL J. Bacteriol. 176:2854-2861(1994).
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CC EMBL; L27596; AAA20625.1; --
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1392 MW; 3671D53271B459D7 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPF 12
Db |||
5 EPF 7

RESULT 12

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UC15_MAIZE
ID UC15_MAIZE STANDARD; PRT; 14 AA.
AC P80621;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 245)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.8, ITS MW IS: 35.7 KDa.
DR Maize-2DPAGE; P80621; COLEOPTILE.
DR MaizeDB; 123947; -.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1396 MW; C68949275F404CD2 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
DB 5 LPV 7
DB 5 LPV 7

RESULT 13
UC16_MAIZE
ID UC16_MAIZE STANDARD; PRT; 15 AA.
AC P80622;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 308)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.9, ITS MW IS: 18.6 KDa.
DR Maize-2DPAGE; P80622; COLEOPTILE.
DR MaizeDB; 123948; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1796 MW; D331A518F7440BE7 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11

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DB 12 VEP 14

RESULT 14
UC25_MAIZE
ID UC25_MAIZE STANDARD; PRT; 15 AA.
AC P80631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 77)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 31.6 KDa.
DR Maize-2DPAGE; P80631; COLEOPTILE.
DR MaizeDB; 123957; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1580 MW; 83C54CFC0CE1614D0 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10
DB 10 PVE 12

RESULT 15
LPK1_LOOMI
ID LPK1_LOOMI STANDARD; PRT; 16 AA.
AC P20404;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 1 (LOM-PK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=91224474; PubMed=2026322;
RA Schoofs L., Holman G.N., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
RT myotropic peptide of Locusta migratoria.";
RL Gen. Comp. Endocrinol. 81:97-104(1991).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A49761; A49761.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 16 16 AMIDATION.

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SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;
 Query Match 20.0%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15
 |||
 Db 11 PFV 13

RESULT 16
 PSBL_SYNNU
 ID PSBL_SYNNU STANDARD; PRT; 17 AA.
 AC P12241;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Photosystem II reaction center L protein (PSII 5 kDa protein)
 DE (fragment).
 GN PSBL.
 OS Synesochoccus vulcanus (Thermosynechococcus vulcanus).
 OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
 CX NCBI_TaxID=32053;
 RN [1]
 RP SEQUENCE.
 RA Ikeuchi M., Koike H., Inoue Y.;
 RT "Identification of psbI and psbL gene products in cyanobacterial
 photosystem II reaction center preparation.";
 RL FEBS Lett 251:155-160(1989).
 CC -!- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME
 CC -!- B559
 CC -!- SIMILARITY: BELONGS TO THE PSBL FAMILY.
 CC -!- SIMILARITY: BELONGS TO THE PSBL FAMILY.
 DR InterPro; IPR003372; PSII_PsBL.
 DR Pfam; PF02419; PSBL; 1.
 KW Photosynthesis; Photosystem II.
 FT NON TER 17
 SQ SEQUENCE 17 AA; 2018 MW; A86FD372B70B9847 CRC64;
 Query Match 20.0%; Score 3; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10
 |||
 Db 9 PVE 11

RESULT 17
 ALL2_CYDPO
 ID ALL2_CYDPO STANDARD; PRT; 18 AA.
 AC P82153;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 2.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 CX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=96034539; PubMed=9392829;
 RA Duve H., Janssen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RA "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 18 18
 AMIDATION.

SQ SEQUENCE 18 AA; 2169 MW; 8B66679C0CDF175C CRC64;
 Query Match 20.0%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
 |||
 Db 11 LPV 13

RESULT 18
 HEMH_THETS
 ID HEMH_THETS STANDARD; PRT; 18 AA.
 AC P80155;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ovohemerythrin (Yp14) (fragment).
 OS Theromyzon tessulatum (Leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
 CX NCBI_TaxID=13286;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Oocyte;
 RX MEDLINE=93049299; PubMed=1435663;
 RA Baert J.-L., Britel M., Sauviere P., Malecha J.;
 RT "Ovohemerythrin, a major 14-kDa yolk protein distinct from
 vitellogenin in leech.";
 RL Eur. J. Biochem. 209:563-569(1992).
 CC -!- FUNCTION: MAJOR YOLK PROTEIN. THIS IRON PROTEIN MAY PLAY A ROLE
 CC -!- IN THE DETOXIFICATION OF FREE IRON AFTER A BLOOD MEAL.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the hemerythrin family.
 DR PIR; S29264; S29264.
 DR HSP; P02247; 2MHR.
 DR InterPro; IPR002063; Hemerythrin.
 DR Pfam; PF01814; Hemerythrin; 1.
 DR PROSITE; PS00550; HEMERYTHRIN; PARTIAL.
 KW Oxygen transport; Metal-binding; Iron; Yolk.
 FT NON TER 18
 SQ SEQUENCE 18 AA; 2368 MW; 33397BEE587C81F1 CRC64;
 Query Match 20.0%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPF 12
 |||
 Db 5 EPF 7

RESULT 19
 COOT_SARBU
 ID COOT_SARBU STANDARD; PRT; 19 AA.
 AC Q09148;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE NEB-collostatin (Folliculostatin).
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 CX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95188911; PubMed=7883009;
 RA Byllemans D., Proost P., Samijn B., Borovsky D., Grauwels L.,
 RA Huybrechts R., van Damme J., van Beeumen J., de Loof A.;
 RT "Neb-collostatin, a second folliculostatin of the grey fleshfly,
 Neobellieria bullata.";

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RL Eur. J. Biochem. 228:45-49(1995).
CC -!- FUNCTION: HAS AN OSTIATIC ACTIVITY. IT INHIBITS YOLK SYNTHESIS SO
CC INHIBITING THE SUBSEQUENT YOLK DEPOSITION IN PREVITELLOGENIC
CC FOLLICLES.
CC -!- SIMILARITY: TO THE NONHELICAL REGIONS OF THE COLLAGEN FAMILY.
CC -!- CAUTION: NEB-COLLOSTATIN MAY BE PROTEOLYTICALLY CLEAVED FROM
CC COLLAGEN IV.
DR PIR, S69153; S69153.
SQ SEQUENCE 19 AA; 1880 MW; 41B6AF5F0CEB8251 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
Db 7 LPV 9

RESULT 20
CORN_THUOB STANDARD; PRT; 20 AA.
AC P80980;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIb-heart (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCB1_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
DR PIR: S77989; S77989.
KW Oxidoreductase; Mitochondrion.
FT NON PER 20
SQ SEQUENCE 20 AA; 2303 MW; 0A33BD34006E5AA6 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPV 6
Db 17 MPV 19

RESULT 21
MAX7_BOMMX STANDARD; PRT; 20 AA.
AC P83086;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 41, Last annotation update)
DE Maximin 7.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCB1_TaxID=161274;

RL Eur. J. Biochem. 228:45-49(1995).
CC -!- FUNCTION: HAS AN OSTIATIC ACTIVITY. IT INHIBITS YOLK SYNTHESIS SO
CC INHIBITING THE SUBSEQUENT YOLK DEPOSITION IN PREVITELLOGENIC
CC FOLLICLES.
CC -!- SIMILARITY: TO THE NONHELICAL REGIONS OF THE COLLAGEN FAMILY.
CC -!- CAUTION: NEB-COLLOSTATIN MAY BE PROTEOLYTICALLY CLEAVED FROM
CC COLLAGEN IV.
DR PIR, S69153; S69153.
SQ SEQUENCE 19 AA; 1880 MW; 41B6AF5F0CEB8251 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
Db 7 LPV 9

RESULT 20
CORN_THUOB STANDARD; PRT; 20 AA.
AC P80980;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIb-heart (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCB1_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
DR PIR: S77989; S77989.
KW Oxidoreductase; Mitochondrion.
FT NON PER 20
SQ SEQUENCE 20 AA; 2303 MW; 0A33BD34006E5AA6 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPV 6
Db 17 MPV 19

RESULT 21
MAX7_BOMMX STANDARD; PRT; 20 AA.
AC P83086;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 41, Last annotation update)
DE Maximin 7.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCB1_TaxID=161274;

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RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., McClean S., Orr D.F., Bjorson A.J., Rao P.F., Shaw C.;
RT "Isolation and structural characterisation of antimicrobial peptides
RT from the venom of the Chinese large-webbed bell toad (Bombina
RT maxima).";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: Has antimicrobial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
KW Amphibian defense peptide; Antibiotic.
SQ SEQUENCE 20 AA; 1947 MW; EC7541AALBF3BD49 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
Db 4 PVL 6

RESULT 22
MAX8_BOMMX STANDARD; PRT; 20 AA.
AC P83087;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Maximin 8.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCB1_TaxID=161274;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., McClean S., Orr D.F., Bjorson A.J., Rao P.F., Shaw C.;
RT "Isolation and structural characterisation of antimicrobial peptides
RT from the venom of the Chinese large-webbed bell toad (Bombina
RT maxima).";
RL Submitted (JUN-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: Has antimicrobial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
KW Amphibian defense peptide; Antibiotic.
SQ SEQUENCE 20 AA; 1977 MW; EC7541AD6E2F949 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
Db 4 PVL 6

RESULT 23
PSAL_SYNVU STANDARD; PRT; 20 AA.
AC P25937;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Photosystem I reaction center subunit XI (PSI-L) (PSI subunit V)
DE (Fragment).
KW PSAL.
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX NCB1_TaxID=32053;

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RN SEQUENCE
RX MEDLINE=89338747; PubMed=2503399;
RA koike H., Ikeuchi M., Hiyama T., Inoue Y.;
RT Identification of photosystem I components from the cyanobacterium,
RL Synechococcus vulcanus by N-terminal sequencing.";
FEBS Lett. 253:257-263(1989).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CELLULAR
CC -1- THYLAKOID MEMBRANE (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE PSAL FAMILY.
DR HAMAP; MF 00447; -; 1.
DR InterPro; IPR003757; PSI_Psal.
DR Pfam; PF02605; Psal; 1.
DR Photosystem I; Photosynthesis, Thylakoid, Transmembrane.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2170 MW; 730FECDD2EA02A2C CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFV 15
Db 12 PFV 14

RESULT 24
SB60_MAIZE
ID_SB60_MAIZE STANDARD; PRT; 20 AA.
AC P82668;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative 60 kDa spermidine-binding protein (Fragment).
DE Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RF SEQUENCE, AND SUBCELLULAR LOCATION.
RC STRAIN=cv. Cecilia; TISSU=coleoptile;
RX MEDLINE=21948208; PubMed=11950979;
RA Tassoni A., Napier R.M., Franceschetti M., Venis M.A., Ragni N.;
RT "Spermidine-binding proteins. Purification and expression analysis in
RT maize.";
RL Plant Physiol. 128:1303-1312(2002).
CC -1- FUNCTION: May have spermidine-binding activity.
CC -1- SUBUNIT: Dimer of 18 kDa and 60 kDa subunit (Probable).
CC -1- SUBCELLULAR LOCATION: Microsomal membrane.
CC -1- MISCELLANEOUS: On the 2D-gel its MW is: 60 kDa.
DR GO; GO:0005792; C:cytosol; NAS.
KW Membrane; Microsome.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2093 MW; 7FD730C00391579A CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEP 11
Db 6 VEP 8

RESULT 25
TRYL STREX
ID TRYL STREX STANDARD; PRT; 20 AA.
AC P80420;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin-like protease (EC 3.4.21.-) (Fragment).

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OS Streptomyces exfoliatus (Streptomyces hydrogenans).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1905;
RN [1]
RP SEQUENCE.
RC STRAIN=SMF13;
RX MEDLINE=95291424; PubMed=7773379;
RA Kim I.S., Lee K.J.;
RT "Physiological roles of leupeptin and extracellular proteases in
RT mycelium development of Streptomyces exfoliatus SMF13.";
EL Microbiology 141:1017-1025(1995).
CC -1- FUNCTION: INVOLVED IN MYCELIUM DIFFERENTIATION.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2A.
DR MEROPS; S01.101; -.
DR InterPro; IPR001254; Ser_protease_Try.
DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2129 MW; 4568F56D0E7393AF CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 FPF 14
Db 12 FPF 14

RESULT 26
EI03_LITRU
ID EI03_LITRU STANDARD; PRT; 5 AA.
AC P82099;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104899;
RN [1]
RP SEQUENCE.
RC TISSU=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FV 15
Db 1 FV 2

RESULT 27
PAP2_PARMA
ID PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moles sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleurocteniformes;
OC Soleiidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=67057369; PubMed=3782138;
RA Lazarovici P, Primor N, Loew L M;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moles sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713 (1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON TER
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 FP 13
DB 4 FP 5
RESULT 28
PRCT PERAM STANDARD; PRT; 5 AA.
ID P01373;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1993 (Rel. 31, Last annotation update)
DE Proctolin
OS Pariplaneta americana (American cockroach).
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Skarratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256 (1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=8123865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RN [3]
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;

RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211 (1990).
RN [4]
RP SEQUENCE.
RC SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72 (1986).
CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY;
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HOSHOA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71E7673B46000000 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 LP 8
DB 3 LP 4
RESULT 29
SUGA_ACHDO STANDARD; PRT; 5 AA.
ID P19991;
AC 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Suboesophageal ganglion pentapeptide.
OS Acheta domestica (House cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Acheta.
OX NCBI_TaxID=6997;
RN [1]
RP SEQUENCE.
RC "Isolation and structure of a peptide isolated from the
RT suboesophageal ganglion of Acheta domestica (orthoptera).";
RL Comp. Biochem. Physiol. 88C:185-187 (1987).
CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL
CC GANGLIA.
DR PIR; JS0319; JS0319.
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDD8000000 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 PF 12
DB 4 PF 5
RESULT 30
TPIS_CANFA STANDARD; PRT; 5 AA.
ID P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
GN TP11.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycero-
 phosphate
 CC -!- PATHWAY: Plays an important role in several metabolic pathways.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
 DR HSC-2DPAGE; P54714; DOG.
 DR InterPro; IPR000652; Triophos_ismrse.
 DR PROSITE; PS00171; TIM; PARTIAL.
 KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
 KW Pentose shunt.
 FT NON TER 1 1
 FT MOD RES 5 5
 SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FV 15
 DB 1 FV 2

RESULT 31
 ACPH RABBIT
 ID ACPH_RABBIT STANDARD; PRT; 6 AA.
 AC P25154;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
 DE (APH) (Acylaminoacyl-peptidase) (Fragment).
 GN APH.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Muscle;
 RX MEDLINE=92222120; PubMed=1807161;
 RA Krishna R.G., Chin C.C.Q., Wolf F.;
 RT "N-terminal sequence analysis of N alpha-acetylated proteins after
 unblocking with N-acylaminoacyl-peptide hydrolase.";
 RL Anal. Biochem. 199;45-50(1991).
 CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
 TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
 AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
 CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
 CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
 + peptide
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
 DR MEROPS; S09.004; -.
 DR InterPro; IPR002471; Prol_endopep_ser.
 DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
 KW Hydrolase; Acetylation.
 FT MOD RES 1 1
 FT NON TER 6 6
 SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 VL 7
 DB 5 VL 6

RESULT 32
 CIP1 MYTED
 ID CIP1_MYTED STANDARD; PRT; 6 AA.
 AC F13736;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Contraction-inhibiting peptide I (MIP I).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of Mytilus inhibitory peptides.";
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
 CC MUSCLES.
 CC -!- SIMILARITY: TO MIP II.
 DR PIR; A27696; A27696.
 KW Hormone; Amidation.
 FT MOD RES 6 6
 SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FV 15
 DB 5 FV 6

RESULT 33
 CIP2 MYTED
 ID CIP2_MYTED STANDARD; PRT; 6 AA.
 AC F13737;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Contraction-inhibiting peptide II (MIP II).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of Mytilus inhibitory peptides.";
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
 CC MUSCLES.
 CC -!- SIMILARITY: TO MIP I.
 DR PIR; B27696; B27696.
 KW Hormone; Amidation.
 FT MOD RES 6 6
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FV 15
||
Db 5 FV 6

RESULT 34
ID E101 LITRU STANDARD; PRT; 6 AA.
AC P82036;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 18-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella".
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 6
FT AMIDATION.
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FV 15
||
Db 1 FV 2

RESULT 35
ID TRP1_PSEPU STANDARD; PRT; 6 AA.
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TrpBA operon transcriptional activator (Fragment).
GN TRP1.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PPG1 C1S;
RX MEDLINE=89335826; PubMed=2503057;
RA Beery L., Crawford I.P.;
RT "DNA sequence of the cryptophan synthase genes of Pseudomonas
RT putida".
RL Biochimie 71:521-531(1989).
CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRP1 BINDS UPSTREAM OF THE
CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
RN [1]
RP SEQUENCE.

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DR EMBL; X13299; CAA31660.1; -;
DR InterPro; IPR000847; HTH_LYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; PARTIAL.
KW Tryptophan biosynthesis; Transcription regulation; Activator;
KW DNA-binding.
FT NON_TER 6
FT SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DL 2
||
Db 4 DL 5

RESULT 36
ID ALL3 CARMA STANDARD; PRT; 7 AA.
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 3.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidea; Fortuinidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas".
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 7 AA; 796 MW; 672879CDB476B70 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EP 11
||
Db 1 EP 2

RESULT 37
ID CARP_MYTED STANDARD; PRT; 7 AA.
AC P10470;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6650;
RN [1]
RP SEQUENCE.

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RX MEDLINE=89052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)
CC -!- INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
CC RETRACTOR MUSCLE.
DR PIR; A29342; ECMUCR.
KW Hormone; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5
DB 2 MP 3

RESULT 38
CCFL_ENTFA STANDARD; PRT; 7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adst J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces
RT conjugative transfer of the Streptococcus faecalis tetracycline
RT resistance plasmid, pCF10."
RL J. Biol. Chem. 263:14574-14578(1988).
CC -!- FUNCTION: cCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PCF10.
DR PIR; A30812; A30812.
KW Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FV 15
DB 6 FV 7

RESULT 39
EI05_LITRU STANDARD; PRT; 7 AA.
AC P82101;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 5.
OS Litoria rubella (Desert tree frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Anphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Reddyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RX TISSUE=Skin secretion;

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RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EP 11
DB 3 EP 4

RESULT 40
FARL_HELTI STANDARD; PRT; 7 AA.
AC P41871;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide GDPFLRF-amide.
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Helisoma.
OX NCBI_TaxID=27815;
RN [1]
RP SEQUENCE.
RX TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis.";
RL Peptides 15:31-36(1994).
CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
CC THE KIDNEY, MANTLE AND SKIN.
CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 851 MW; 69D40729D76A810 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PF 12
DB 3 PF 4

RESULT 41
PPH2_LYCPS STANDARD; PRT; 7 AA.
AC P83379;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Purple acid phosphatase isozyme IESAP2 (EC 3.1.3.2) (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND

```

RP GLYCOSYLATION.
 RC STRAIN=CV. MoneyMaker; TISSUE=Seed;
 RX MEDLINE=22361242; PubMed=12473124;
 RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
 RT "Purification and characterization of two secreted purple acid
 phosphatase isozymes from phosphate-starved tomato (Lycopersicon
 esculentum) cell cultures.";
 RL Bur. J. Biochem. 269:6278-6286 (2002).
 CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 alcohol + phosphate.
 CC -1- SUBUNIT: Monomer.
 CC -1- SURCELLULAR LOCATION: Secreted.
 CC -1- PTM: GLYCOSYLATION.
 CC -1- MISCELLANEOUS: In L. esculentum there are at least two isozymes of
 purple acid phosphatase.
 KW Hydrolase; Glycoprotein.
 FT NON_TER 1 1
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DL 2
 Db 6 DL 7

RESULT 42
 UN06 PINPS STANDARD; PRT; 7 AA.
 AC P81675;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of needles (N141) (Fragment).
 OS Pinus pinaster (Maritime pine).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OK NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 proteins.";
 RL Electrophoresis 20:1098-1108 (1999).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
 FT NON_TER 1 1
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 LP 8
 Db 5 LP 6

RESULT 43
 WWA1 ACHFU STANDARD; PRT; 7 AA.
 AC P35919;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Wamide-1.

OS Achatina fulica (Giant African snail).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 CC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OK NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 RX MEDLINE=93265912; PubMed=8495720;
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
 RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
 ganglia of the African giant snail, Achatina fulica.";
 RL FEBS Lett. 323:104-108 (1993).
 CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
 CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
 DR PIR; S33245; S33245.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7 7
 SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 EM 4
 Db 3 EM 4

RESULT 44
 WWA3 ACHFU STANDARD; PRT; 7 AA.
 AC P35921;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Wamide-3.
 OS Achatina fulica (Giant African snail).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 CC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OK NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 RX MEDLINE=93265912; PubMed=8495720;
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
 RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
 ganglia of the African giant snail, Achatina fulica.";
 RL FEBS Lett. 323:104-108 (1993).
 DR PIR; S33244; S33244.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7 7
 SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 EM 4
 Db 3 EM 4

RESULT 45
 ALL6 CYDPO STANDARD; PRT; 8 AA.
 AC P82157;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiaastatin 6.
 OS Cydia pomonella (Codling moth).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA "Lepidopteran peptides of the allatostatin superfamily.";
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997)
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Antidation.
 KM NCBI_TaxID=82600;
 FT MOD_RFS 8
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 LP 8
 Db 1 LP 2
 RESULT 46
 ANG2 BOTJA STANDARD; PRT; 8 AA.
 ID ANG2 BOTJA
 AC Q10582;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide II (fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake Bothrops jararaca.";
 RL Comp Biochem Physiol 113B:467-473(1996)
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR InterPro: IPR002125; Serpinin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 PF 12
 Db 7 PF 8
 RESULT 47
 CADI ENTFA STANDARD; PRT; 8 AA.
 ID CADI ENTFA
 AC P13268;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CADI.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=85051889; PubMed=6437872;
 RA Mori M., Segakami Y., Narita M., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B., Suzuki A.;
 RT "Isolation and structure of the bacterial sex pheromone, CADI, that
 RT induces plasmid transfer in Streptococcus faecalis.";
 RL FEBS Lett. 178:97-100(1984).
 CC -1- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC HEMOLYSIN PLASMID PADI.
 KW Pheromone.
 KM NCBI_TaxID=1351;
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 VL 7
 Db 5 VL 6
 RESULT 48
 CLP THICU STANDARD; PRT; 8 AA.
 ID CLP THICU
 AC P80488;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Chemolithotroph-specific protein (fragment).
 OS Thiobacillus cuprinus.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Comamonadaceae; Thiomonas.
 OX NCBI_TaxID=36860;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=DSM 5494;
 RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
 CC CHEMOLITHOTROPHICALLY.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PV 6
 Db 2 PV 3
 RESULT 49
 COM2 CONFU STANDARD; PRT; 8 AA.
 ID COM2 CONFU
 AC P58785;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leu-contryphan-P.
 OS Conus purpurascens (Purple cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=41690;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC STRAIN=Clipperton Island; TISSUE=Venom;
 RX MEDLINE=99388839; PubMed=10461743;
 RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
 RA Oliveira B.M.;
 RT "A novel D-leucine-containing Conus peptide: diverse conformational
 RT dynamics in the contryphan family.";

RL J. Pept. Res. 54:93-99(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
 CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
 KW Toxin; Hydroxylation; D-amino acid.
 FT DISULFID 2 4
 FT MOD RES 4 8 D-LEUCINE.
 SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VL 7
 ||
 DB 3 VL 4

RESULT 50

PK2_PERAM STANDARD; PRT; 8 AA.

AC P82692;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 CC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of the American cockroach."
 RT J. Comp. Neurol. 419:352-363(2000).
 RL Peptides 18:473-478(1997).
 RN [2]

RP TISSUE SPECIFICITY.
 RP MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of the American cockroach."
 RT J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro: IPR001484; Pyrokinin.
 DR PROSITE: P800539; PYROKININ; FALSE_NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 8
 FT SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PF 12
 ||
 DB 3 PF 4

RESULT 51

PK3_PERAM STANDARD; PRT; 8 AA.

ID PK3_PERAM
 AC P82618;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 CC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and abdominal neurohemal organs of the American cockroach."
 RT Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RP MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of the American cockroach."
 RT J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 8
 FT SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PF 12
 ||
 DB 3 PF 4

RESULT 52

UC26_MAIZE STANDARD; PRT; 8 AA.

AC P80632;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907) (Fragment).
 DE Zea mays (Maize).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD Clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Tournet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernellet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated genome analysis program."
 RT Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 7.0. ITS MW IS: 57.2 kDa.
 CC Maize-2PAGE; P80632; COLEOPTILE.
 FT NON_TER 1
 FT MOD_RES 8
 FT SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EP 11
Db 2 EP 3

RESULT 53
UF06 MOUSE
ID _UF06 MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RC MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
FT NON_TER 8
SQ SEQUENCE 8 AA; 817 MW; A35D0878676B05B1 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

Qy 10 EP 11
Db 3 EP 4

RESULT 54
BS43 SERPL
ID _BS43 SERPL STANDARD; PRT; 9 AA.
AC P83375;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serratia plumbitica.
OS Serratia plumbitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCB_TaxID=82996;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC STRAIN=J7;
RC MEDLINE=22293561; PubMed=12406768;
RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,
RA Van Beeumen J., Thonart P.;
RT "Characterization of serracin P, a phage-tail-like bacteriocin, and
its activity against *Erwinia amylovora*, the fire blight pathogen.";
RL Appl. Environ. Microbiol. 68:5704-5710(2002).
CC -1- FUNCTION: Major component of a prophage tail sheath (Probable).
CC -1- FUNCTION: Antibacterial activity against Gram-negative bacterium
CC *E. amylovora*.
DR InterPro: IPR006498; Tail tube.
DR Pfam: PF04985; Phage tube; 1.
KW Antibiotic; Bacteriocin.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1095 MW; 1B66D412C871E1FB CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VL 7
Db 8 VL 9

RESULT 55
CCAP CARMA
ID _CCAP CARMA STANDARD; PRT; 9 AA.
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Rukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCB_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RC SPECIES=C.maenas; TISSUE=pericardial organs;
RC Stangier J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
shore crab *Carcinus maenas*.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M.sexta;
RC MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi F.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
hawkmoth, *Manduca sexta*.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RC MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from *Tenebrio
molitor* and *Spodoptera eridania*.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
CC INTO THE HEMOLYMPH.
DR FIR; A26363; A26363.
DR FIR; S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 959 MW; CSA861A9CDD44EB9 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PF 12
Db 1 PF 2

RESULT 56
CXEL THUOB
ID _CXEL THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS *Thunnus obesus* (Bigeye tuna).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OX NCBI_TaxID=8241;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=97454291; PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver.";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
 DR PIR; S77984; S77984.
 DR InterPro; IPR001349; COX6A.
 DR PROSITE; PS01329; COX6A; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON TER 1
 FT NON TER 9
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FV 15
 DB 6 FV 7
 RESULT 57
 FAR5 PENMO
 ID FAR5 PENMO STANDARD; PRT; 9 AA.
 AC P83320;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuroptide FLPS (SMESLELRF-amide).
 OS Penaeus monodon (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupem J., Krungkarn C., Longyant S.,
 RA Chaivuthangkura P., Sithigorngul W., Petson A.;
 RT "Seven novel FMRamide-like neuroptide sequences from the eyestalk
 RT of the giant tiger prawn Penaeus monodon.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FAP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY
 KW Neuropeptide; Amidation.
 FT MOD_RES 9
 FT SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MP 5

Db 2 MP 3
 RESULT 58
 FIBB ERYPA
 ID FIBB ERYPA STANDARD; PRT; 9 AA.
 AC P19346;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
 DE FGB.
 GS Erythrocybus patas (Red guenon) (Husar).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Erythrocybus.
 OX NCBI_TaxID=9538;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85289140; PubMed=3928610;
 RA Nakamura S., Takenaka O., Takahashi K.;
 RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
 RT patas monkey (Erythrocybus patas): their amino acid sequences,
 RT restricted mutations, and a molecular phylogeny for macaques,
 RT guenons, and baboons.";
 RL J. Biochem. 97:1487-1492(1985).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA) LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR PIR; D24180; D24180.
 DR InterPro; IPR002181; Fibrinogen C.
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1
 FT NON TER 9
 FT NON TER 9
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 VL 7
 DB 4 VL 5
 RESULT 59
 KNL3 BOMVA
 ID KNL3 BOMVA STANDARD; PRT; 9 AA.
 AC P83058;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE [Thr6]bradykinin.
 OS Bombina variegata (Yellow-bellied toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
 OX NCBI_TaxID=8348;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Skin secretion;
 RA Chen T.B., Orr D.F., Bjournson A.J., McLean S., Rao P.F., Shaw C.;
 RT "Cloning and post-translational processing of frog skin kininogens.";
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.
 CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
 CC arterial smooth muscle and constriction of intestinal smooth

CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 PF 12
DB 7 PF 8
RESULT 60
LMIP LOCFI STANDARD; PRT; 9 AA.
AC P1759;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Locustamyo-inhibiting peptide (LOM-MIP).
OS Locusta migratoria (migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX MEDLINE=92179466; PubMed=1796179;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamyo-inhibiting
RT peptide (LOM-MIP), a novel biologically active neuro-peptide from
RT Locusta migratoria.";
RL Regul. Pept. 36:111-119(1991).
CC -!- FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HINDGUT AND
CC -!- OVIDUCT.
CC -!- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS
CC -!- IN THE SUBESOPHAGEAL GANGLION.
DR PIR; A6065; AKLQIM.
KW Amidation; Neuropeptide.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1060 MW; 387D7DD472AB6C3 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DL 2
DB 4 DL 5
RESULT 61
OXYA SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Asvatocin.
OS Scyllorhinus canicula (spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;

RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyllorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB44404B CRC64;
Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 PV 6
DB 7 PV 8
RESULT 62
OXYF SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Phasvatocin.
OS Scyllorhinus canicula (spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;

RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyllorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB4449DB CRC64;
Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 PV 6
DB 7 PV 8
RESULT 63
OXYT EISFO STANDARD; PRT; 9 AA.
AC P42998;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Annotocin.
OS Eisenia foetida (Common brandling worm) (Common dung-worm).

OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
 OC Lumbricina; Lumbricidae; Eisenia.
 OX NCBI_taxid=6396;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Pituitary; PubMed=8292046;
 RX MEDLINE=94121660; PubMed=8292046;
 RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
 RA Nomoto K.;
 RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
 Eisenia foetida.";
 RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
 CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
 CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
 CC NEPHRIDIAL FUNCTION.
 CC NEPHRIDIAL FUNCTION.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR: PC2021; PC2021.
 DR InterPro: IPR000981; Neurhyp_horm.
 DR Pfam: PF00220; hormone4; A_
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 996 MW; D4EB76EB45412C9 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FV 15
 DB 2 FV 3
 RESULT 64
 OXVY_SQUAC
 ID OXVY_SQUAC STANDARD; PRT; 9 AA.
 AC P43000;
 DT 01-NOV-1995 (Rel. 32; Created)
 DT 01-NOV-1995 (Rel. 32; Last sequence update)
 DT 01-NOV-1995 (Rel. 32; Last annotation update)
 DE Valitocin.
 OS Squalus acanthias (Spiny dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalae; Squaloidei; Squalidae; Squalus.
 OX NCBI_taxid=7797;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=73031727; PubMed=5083097;
 RA Acher R., Chauvet J., Chauvet M.-T.;
 RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
 RT isolated from a cartilaginous fish, Squalus acanthias.";
 RL Eur. J. Biochem. 29:12-19(1972).
 RN (2)
 RP SEQUENCE.
 RX MEDLINE=72128038; PubMed=4622083;
 RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
 RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
 RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
 RT spiny dog-fish (Squalus acanthias).";
 RL C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro: IPR000981; Neurhyp_horm.
 DR Pfam: PF00220; hormone4; I_
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FV 15
 DB 2 FV 3
 RESULT 65
 PTSP_BOMMO
 ID PTSP_BOMMO STANDARD; PRT; 9 AA.
 AC P82003;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Prothoracicostatic Peptide (Bom-PTSP).
 DE Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_taxid=7091;
 RN (1)
 RP SEQUENCE.
 RC STRAIN=C145 X N140; TISSUE=Brain;
 RX MEDLINE=20002634; PubMed=10531308;
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
 RA Katsuka H.;
 RT "Identification of a prothoracicostatic peptide in the larval brain of
 RT the silkworm, Bombyx mori.";
 RL J. Biol. Chem. 274:31169-31173(1999).
 RN (2)
 RP ERRATUM.
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
 RA Katsuka H.;
 RL J. Biol. Chem. 275:9892-9892(2000).
 CC -!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
 CC gland.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR.
 KW Hormone; Amidation.
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1090 MW; 3878C5B4472AB6C3 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DL 2
 DB 4 DL 5
 RESULT 66
 SAMP_MUSCA
 ID SAMP_MUSCA STANDARD; PRT; 9 AA.
 AC P19095;
 DT 01-NOV-1990 (Rel. 16; Created)
 DT 01-NOV-1990 (Rel. 16; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Serum amyloid P-component (SAP) (Fragment).
 DE Mustelus canis (Smooth dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes; Triakidae;
 OC Mustelus
 OX NCBI_taxid=7812;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=83160932; PubMed=6403520;
 RA Robey F.A., Tanaka T., Liu T.-Y.;
 RT "Isolation and characterization of two major serum proteins from the
 RT dogfish, Mustelus canis, C-reactive protein and amyloid P
 RT component.";
 RL J. Biol. Chem. 258:3889-3894(1983).
 CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCORD

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FV 6
 DB 7 FV 8
 RESULT 65
 PTSP_BOMMO
 ID PTSP_BOMMO STANDARD; PRT; 9 AA.
 AC P82003;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Prothoracicostatic Peptide (Bom-PTSP).
 DE Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_taxid=7091;
 RN (1)
 RP SEQUENCE.
 RC STRAIN=C145 X N140; TISSUE=Brain;
 RX MEDLINE=20002634; PubMed=10531308;
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
 RA Katsuka H.;
 RT "Identification of a prothoracicostatic peptide in the larval brain of
 RT the silkworm, Bombyx mori.";
 RL J. Biol. Chem. 274:31169-31173(1999).
 RN (2)
 RP ERRATUM.
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
 RA Katsuka H.;
 RL J. Biol. Chem. 275:9892-9892(2000).
 CC -!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
 CC gland.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR.
 KW Hormone; Amidation.
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1090 MW; 3878C5B4472AB6C3 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DL 2
 DB 4 DL 5
 RESULT 66
 SAMP_MUSCA
 ID SAMP_MUSCA STANDARD; PRT; 9 AA.
 AC P19095;
 DT 01-NOV-1990 (Rel. 16; Created)
 DT 01-NOV-1990 (Rel. 16; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Serum amyloid P-component (SAP) (Fragment).
 DE Mustelus canis (Smooth dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes; Triakidae;
 OC Mustelus
 OX NCBI_taxid=7812;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=83160932; PubMed=6403520;
 RA Robey F.A., Tanaka T., Liu T.-Y.;
 RT "Isolation and characterization of two major serum proteins from the
 RT dogfish, Mustelus canis, C-reactive protein and amyloid P
 RT component.";
 RL J. Biol. Chem. 258:3889-3894(1983).
 CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCORD

CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC PIR; B20569; B20569.
DR InterPro; IPR001759; Pentaxin.
DR PROSITE; PS00289; PENTAXIN; PARTIAL.
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT DOMAIN 1
FT NON TER 9
SQ SEQUENCE 9 AA; 965 MW; D05B5735B386769 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;
Qy 12 FP 13
Db 2 FP 3
RESULT 67
ULAE HUMAN STANDARD; PRT; 9 AA.
ID ULAE HUMAN
AC P31931;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Unknown protein from 2D-page of liver tissue (Spot 115) (Fragment).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8113870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222 (1993).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 11 kDa.
DR SWISS-2DPAGE; P31931; HUMAN.
FT NON TER 9
SQ SEQUENCE 9 AA; 1096 MW; 477B3B173AE729C7 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;
Qy 2 LE 3
Db 6 LE 7
RESULT 68
UN19 CLOPA STANDARD; PRT; 9 AA.
ID UN19 CLOPA
AC P81355;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Unknown protein CP 19 from 2D-page (Fragment).
OS Clostridium pasteurianum.
CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
CC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=53291870; PubMed=9629918;

RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806 (1998).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.5, ITS MW IS: 38.0 kDa.
DR VARIANT 8
FT NON TER 9
SQ SEQUENCE 9 AA; 1128 MW; E33B9B0AF5BB19DA CRC64;
Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;
Qy 3 EM 4
Db 7 EM 8
RESULT 69
UPA3 HUMAN STANDARD; PRT; 9 AA.
ID UPA3 HUMAN
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714 (1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
DR SWISS-2DPAGE; P30089; HUMAN.
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAP769C737 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;
Qy 12 FP 13
Db 4 FP 5
RESULT 70
ANG1 BOTJA STANDARD; PRT; 10 AA.
ID ANG1 BOTJA
AC Q10581;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide I (Fragment).
OS Angiotrop jararaca (Jararaca).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Leptodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;
CC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;

```

RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PF 12
DB 7 PF 8

RESULT 71
ANGT_BOVIN
ID _ANGT_BOVIN STANDARD; PRT; 10 AA.
AC P01017;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin III)]
DE (Fragment).
GN AGT OR SERPIN48.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Elliot D.F., Peart W.S.;
RT "The amino acid sequence in a hypertensin.";
RL Biochem. J. 63:246-254(1957).
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
CC plasma.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR PIR; A90345; A90345.
DR PDB; 3ER5; 15-JUL-92.
DR InterPro: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1282 MW; CEFEDD761F2DB42 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PF 12
DB 7 PF 8

RESULT 72
ANGT_CHICK
ID _ANGT_CHICK STANDARD; PRT; 10 AA.
AC P01018;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
DE (Fragment).
GN AGT OR SERPIN48.
OS Gallus gallus (Chicken), and
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031, 93934;
RN [1]
RP SEQUENCE.
RA MEDLINE=74127845; PubMed=4361802;
RX Nakayama T., Nakajima T., Sokabe H.;
RT "Comparative studies on angiotensins. 3. Structure of fowl
RT angiotensin and its identification by DNS-method.";
RL Chem. Pharm. Bull. 21:2085-2087(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C.g.japonica;
RX MEDLINE=9084684; PubMed=2191893;
RA Takei Y., Hasegawa Y.;
RT "Vasopressor and depressor effects of native angiotensins and
RT inhibition of these effects in the Japanese quail.";
RL Gen. Comp. Endocrinol. 79:12-22(1990).
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR PIR; A60824; A60824.
DR PIR; A90917; A90917.
DR InterPro: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1232 MW; CEFEDD761F2DB42 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PF 12
DB 7 PF 8

RESULT 73
CATB_SHEEP
ID CATB_SHEEP STANDARD; PRT; 10 AA.
AC P83205;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).
DE CTSE.
GN Ovis aries (Sheep).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.

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OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Placenta;
RA MEDLINE=22394055; PubMed=12506352;
RA El Amir B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,
RA Mboko H.B., Beckers J.-F.M.P.;
RT "Isolation and partial characterization of three pregnancy-associated
RT glycoproteins from the ewe placenta.";
RL Mol. Reprod. Dev. 64:199-206(2003).
CC -!- FUNCTION: Thiol protease which is believed to participate in
CC intracellular degradation and turnover of proteins. Has also been
CC implicated in tumor invasion and metastasis.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity
CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in
CC small molecule substrates (thus differing from cathepsin L). In
CC addition to being an endopeptidase, shows peptidyl-dipeptidase
CC activity, liberating C-terminal dipeptides.
CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked
CC by a disulfide bond (By similarity).
CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR InterPro: IPR000169; SHPOT acsite.
DR PROSITE: PS00640; THIOL PROTEASE ASN; PARTIAL.
DR PROSITE: PS00139; THIOL PROTEASE CYS; PARTIAL.
DR PROSITE: PS00639; THIOL PROTEASE HIS; PARTIAL.
KW Hydrolase; Thiol protease; Lysosome.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LP 8
DB 1 LP 2

RESULT 74
COXA_ONCMY STANDARD; PRT; 10 AA.
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RA MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR PIR: S43625; S43625.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; C53C5B1AB02C33D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VE 10
DB 5 VE 6

RESULT 75
ESL_LACCA STANDARD; PRT; 10 AA.
ID ESL_LACCA
AC P81758;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Putative esterase/lipase (EC 3.1.-.-) (Fragment).
OS Lactobacillus casei.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1582;
RN [1]
RP SEQUENCE.
RC STRAIN=IFPL731;
RA Lopez de Felipe F.;
RL Submitted (MAR-1999) to the SWISS-PROT data bank.
KW Hydrolase; Serine esterase.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1070 MW; 1C6132D732CAB1A0 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VL 7
DB 6 VL 7

Search completed: November 25, 2003, 18:17:25
Job time : 7.26064 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 36.1436 Seconds
(without alignments)
107.095 Million cell updates/sec

Title: US-09-641-801-5
Perfect score: 15
Sequence: 1 DLEMPVLPEPPFV 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL 23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	33.3	20	Q8KUI9	Q8kui9 neisseria m
2	4	26.7	8	P82598	P82598 rattus norv
3	4	26.7	16	Q9WMG6	Q9wmg6 sigma virus
4	4	26.7	17	Q65373	Q65373 argyria pseu
5	4	26.7	18	Q8CJD4	Q8cjd4 rattus norv
6	4	26.7	19	Q11338	Q11338 molluscum c
7	4	26.7	20	Q9R3R7	Q9r3r7 mycobacteri
8	3	20.0	7	Q50556	Q50556 actinobacil
9	3	20.0	8	Q9TRX8	Q9trx8 bos taurus
10	3	20.0	8	Q89498	Q89498 murine hepa
11	3	20.0	9	P82568	P82568 streptococ
12	3	20.0	9	Q9P8E5	Q9p8e5 kluyveromyc
13	3	20.0	9	Q9UCN5	Q9ucn5 homo sapien
14	3	20.0	9	Q9FXL0	Q9fxl0 lilium long
15	3	20.0	9	Q64972	Q64972 avian rous-
16	3	20.0	10	Q9R5N2	Q9r5n2 clostridium

17	3	20.0	10	2	Q9R5N1	Q9r5n1 clostridium
18	3	20.0	10	2	Q9R5N3	Q9r5n3 clostridium
19	3	20.0	10	6	Q9N1X1	Q9n1x1 equus cabal
20	3	20.0	10	8	Q8WBR7	Q8wbr7 chaitophoru
21	3	20.0	10	11	Q9QVJ5	Q9qvj5 rattus sp.
22	3	20.0	10	11	Q63389	Q63389 rattus norv
23	3	20.0	10	11	Q9QVJ6	Q9qvj6 rattus sp.
24	3	20.0	10	11	Q9ESU5	Q9esu5 mus musculu
25	3	20.0	10	13	Q8JFE7	Q8jfe7 ficedula al
26	3	20.0	10	13	Q8JFJ3	Q8jff3 ficedula hy
27	3	20.0	11	5	P82700	P82700 leucophaea
28	3	20.0	11	10	Q9S8Z9	Q9s8z9 psophocarpa
29	3	20.0	12	4	Q9HBU4	Q9hbu4 homo sapien
30	3	20.0	12	4	Q9UGS1	Q9ugs1 homo sapien
31	3	20.0	12	8	Q9G196	Q9g196 sargassum p
32	3	20.0	12	10	Q9S8F0	Q9s8f0 sea mayas (m
33	3	20.0	12	10	P82441	P82441 nicotiana t
34	3	20.0	13	4	Q96Q86	Q96q66 homo sapien
35	3	20.0	13	5	Q9TRW4	Q9trw4 tityus serr
36	3	20.0	13	8	Q33417	Q33417 digitalis p
37	3	20.0	13	11	Q88176	Q88176 mus musculu
38	3	20.0	13	11	Q9QVK6	Q9qv66 rattus sp.
39	3	20.0	13	12	Q9PXB5	Q9pqb5 duck hepati
40	3	20.0	13	12	Q9WMG5	Q9wmg5 sigma virus
41	3	20.0	13	13	P82830	P82830 rana luteiv
42	3	20.0	14	2	P83159	P83159 anabaena sp
43	3	20.0	14	5	Q9TWN0	Q9twn0 trypanosom
44	3	20.0	14	11	Q70599	Q70599 rattus norv
45	3	20.0	14	12	Q9EON0	Q9eon0 human herpe
46	3	20.0	14	12	Q9EON1	Q9eon1 human herpe
47	3	20.0	14	12	Q99BW2	Q99bw2 human herpe
48	3	20.0	15	2	Q9R5Z5	Q9r5z5 streptococc
49	3	20.0	15	2	Q9CP39	Q9cp39 pseudomonas
50	3	20.0	15	2	Q8RKN0	Q8rkn0 escherichia
51	3	20.0	15	4	Q9BXX4	Q9bxx4 homo sapien
52	3	20.0	15	4	Q9HCX8	Q9hcx8 homo sapien
53	3	20.0	15	4	Q9BXQ0	Q9bxq0 homo sapien
54	3	20.0	15	6	Q28822	Q28822 cryptotolagu
55	3	20.0	15	6	Q8H279	Q8hz79 bos taurus
56	3	20.0	15	7	Q9TNO5	Q9tnq5 mus sp. maj
57	3	20.0	15	7	Q9TNO1	Q9tnq1 mus sp. ber
58	3	20.0	15	8	Q9T2G9	Q9t2g9 solanum tub
59	3	20.0	15	8	Q37016	Q37016 nicotiana a
60	3	20.0	15	8	Q78794	Q78794 platellia l
61	3	20.0	15	10	Q9S8F1	Q9s8f1 sea mayas (m
62	3	20.0	15	11	Q9QV34	Q9qv34 rattus sp.
63	3	20.0	16	2	Q8KMS4	Q8kms4 escherichia
64	3	20.0	16	2	P82597	P82597 bacillus sp
65	3	20.0	16	4	Q9UCD4	Q9ucd4 homo sapien
66	3	20.0	16	6	Q9TRK9	Q9trk9 canis famil
67	3	20.0	16	7	Q9TNN9	Q9tnn9 homo sapien
68	3	20.0	16	8	Q36789	Q36789 solanum nig
69	3	20.0	16	11	Q9QUW8	Q9quw8 cavia (guin
70	3	20.0	16	13	Q9PT90	Q9pt90 gallus gall
71	3	20.0	17	4	Q95794	Q95794 homo sapien
72	3	20.0	17	4	Q95795	Q95795 homo sapien
73	3	20.0	17	4	Q9Y3P6	Q9y3f6 homo sapien
74	3	20.0	17	4	Q9UC43	Q9uc43 homo sapien
75	3	20.0	17	6	Q9TRH5	Q9trh5 bos taurus
76	3	20.0	17	10	Q9S8K1	Q9s8k1 solanum tub
77	3	20.0	17	12	Q8V9K6	Q8v9k6 human papil
78	3	20.0	17	16	Q8X4A4	Q8x4a4 escherichia
79	3	20.0	18	2	Q9RGK1	Q9rgk1 bordetella
80	3	20.0	18	4	Q9UC87	Q9uc87 homo sapien
81	3	20.0	18	4	Q9UCF4	Q9ucf4 homo sapien
82	3	20.0	18	4	Q9BQT0	Q9bqt0 homo sapien
83	3	20.0	18	4	Q9HBD9	Q9hbd9 homo sapien
84	3	20.0	18	4	Q9UC58	Q9uc58 homo sapien
85	3	20.0	18	5	Q9TWM9	Q9twm9 tetrahymena
86	3	20.0	18	8	Q98365	Q98365 myosurus mi
87	3	20.0	18	10	Q9T2G8	Q9t2g8 solanum tub
88	3	20.0	18	10	Q9S8F9	Q9s8f9 populus tre
89	3	20.0	18	11	Q61840	Q61840 mus musculu

90 Q9f4q2 pseudomonas
 91 Q44608 buchnera ap
 92 P74875 salmonella
 93 O87732 streptomyces
 94 Q9uc82 homo sapien
 95 Q9twg5 latrodectus
 96 Q9trp6 bos taurus
 97 Q9tu42 mammutus p
 98 Q9tu41 loxodonta v
 99 Q36925 nicotiana v
 100 Q9s8m8 triticum ae

ALIGNMENTS

RESULT 1
 Q8KUI9 PRELIMINARY; PRT; 20 AA.
 AC Q8KUI9
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Nitrogen regulatory protein P-II (Fragment).
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]_TaxID=487;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CL1.
 RX MEDLINE=22040572; PubMed=12045242;
 RA Comanducci M., Bandini S., Brunelli B., Adu-Bobie J., Arico B.,
 RA Capeccchi B., Giuliani M.M., Maignani V., Santini L., Savino S.,
 RA Granoff D.M., Gaugant D.A., Eliza M., Rappuoli R., Mora M.;
 RT "Nada, a novel vaccine candidate of Neisseria meningitidis."
 RL J. Exp. Med. 195;1445-1454(2002).
 DR EMBL; AF452480; AAMS3107.1; -.
 DR InterPro; IPR002187; PII_glnB.
 DR Pfam; PF00543; P-II; 1.
 FT NON TER 1
 SQ SEQUENCE 20 AA; 2165 MW; 5CE529B59D995B5C CRC64;

Query Match 33.3%; Score 5; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPVE 10
 Db 1 VLPVE 5

RESULT 2
 P82598 PRELIMINARY; PRT; 8 AA.
 AC P82598
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE 38kDa non-arginase growth inhibitory factor (NAGIF) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]_TaxID=10116;
 RP SEQUENCE.
 RC Strain=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=20198203; PubMed=10731662;
 RA Kim K.-Y., Choi I., Kim S.-S.;
 RT "Purification and characterization of a novel inhibitor of the
 RT proliferation of hepatic stellate cells."
 RL J. Biochem. 127;23-27(2000).
 SQ SEQUENCE 17 AA; 1882 MW; BFECC2A95495FE6A CRC64;

Query Match 26.7%; Score 4; DB 12; Length 17;

CC HEPATIC STELLATE CELLS (HSC). ALSO INHIBITS THE GROWTH OF BOVINE
 CC ENDOTHELIAL CELLS AND 3T6 FIBROBLASTS.
 CC -!- SIMILARITY: IDENTICAL TO THE 63-70 AA REGION OF THE RAT ZAG
 CC PROTEIN.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 914 MW; 80A3676B02D76B1D CRC64;

Query Match 26.7%; Score 4; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 83e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEP 11
 Db 3 PVEP 6

RESULT 3
 Q9WMG6 PRELIMINARY; PRT; 16 AA.
 AC Q9WMG6
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE 2 protein (fragment).
 GN 2.
 OS Sigma virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; unclassified Rhabdoviridae.
 OX NCBI_TaxID=11301;
 RN [1]_TaxID=11301;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212481; PubMed=8384742;
 RA Teninges D., Bras F., Dezelee S.;
 RT "Genome organization of the sigma rhabdovirus: six genes and a gene
 RT overlap."
 RL Virology 193;1018-1023(1993).
 DR EMBL; S57847; AAD40699.1; -.
 FT NON TER 1
 SQ SEQUENCE 16 AA; 1904 MW; F96DBC468601967E CRC64;

Query Match 26.7%; Score 4; DB 12; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVEP 8
 Db 11 PVEP 14

RESULT 4
 Q65373 PRELIMINARY; PRT; 17 AA.
 AC Q65373
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE ORF 2 minigene.
 OS Orgyia pseudotsugata single capsid nuclear polyhedrosis virus
 OS (OPSNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=10450;
 RN [1]_TaxID=10450;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93286576; PubMed=8389803;
 RA Russell R.L., Rohmann G.F.;
 RT "Nucleotide sequence of the ubiquitin-39k gene region from the Orgyia
 RT pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."
 RL J. Gen. Virol. 74;1191-1195(1993).
 DR EMBL; D13375; BAA02640.1; -.
 SQ SEQUENCE 17 AA; 1882 MW; BFECC2A95495FE6A CRC64;

Query Match 26.7%; Score 4; DB 12; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy 6 VLPV 9
Db 2 VLPV 5

RESULT 5
Q8CJDA PRELIMINARY; PRT; 18 AA.
ID Q8CJDA
AC Q8CJDA
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Podocin (Fragment).
GN NPHS2
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Morita H., Yoshimura A., Makino R., Inui K., Nakao N., Usami T.,
RA Roselli S., Antignac C., Matsuyama M., Ideura T.;
RT "Rat genome fragment containing a part of exons and all of the 3'UTR
of Nph2 as well as microsatellite sites."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB094124; BAC23094.1; -.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2033 MW; D47829DCFF0EF4B CRC64;

Query Match 26.7%; Score 4; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEP 11
Db 4 PVEP 7

RESULT 6
O11338 PRELIMINARY; PRT; 19 AA.
ID O11338
AC O11338
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE H1-7-1 protein (Fragment).
GN H1-7-1
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
RA Lopez-Esteban J.L., Esteban M., Martin-Gallardo A.;
RT "A Random DNA Sequencing, Computer-Based Approach for the Generation
of a Gene Map of Molluscum Contagiosum Virus."
RL Virus Genes 0:0-0(1997).
DR EMBL; U86916; AAB57971.1; -.
DR InterPro; IPR004900; Pox_P35.
DR Pfam; PF03213; Pox_P35; 1.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2018 MW; 1ECAF8E98F95ED65 CRC64;

Query Match 26.7%; Score 4; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9
Db 1

Db 12 VLPV 15

RESULT 7
Q9RSR7 PRELIMINARY; PRT; 20 AA.
ID Q9RSR7
AC Q9RSR7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DB 30,000 DALTON NATIVE antigen (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RX MEDLINE=92078747; PubMed=1720803;
RA Salata R.A., Sanson A.J., Malhotra I.J., Wiker H.G., Harboe M.,
RA Phillips N.B., Daniel T.M.;
RT "Purification and characterization of the 30,000 dalton native antigen
of Mycobacterium tuberculosis and characterization of six monoclonal
antibodies reactive with a major epitope of this antigen."
RL J. Lab. Clin. Med. 118:589-598(1991).
DR HSSP; P31953; 1DQV.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2218 MW; 7950F039639EE959 CRC64;

Query Match 26.7%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVE 10
Db 6 LPVE 9

RESULT 8
O50556 PRELIMINARY; PRT; 7 AA.
ID O50556
AC O50556
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GlyA (Fragment).
GN GLYA
OS Actinobacillus actinomycetemcomitans (Haemophilus
actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33384;
RX MEDLINE=96355846; PubMed=8751884;
RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
RA Kraig B.;
RT "cis Elements and trans factors are both important in strain-specific
regulation of the leukotoxin gene in Actinobacillus
actinomycetemcomitans."
RL Infect. Immun. 64:3451-3460(1996).
DR EMBL; U51862; AAB88721.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPV 9
Db 3 LPV 5

RESULT 9

Q9TRX8 PRELIMINARY; PRT; 8 AA.
 AC Q9TRX8
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Osteopontin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestomii;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91282766; PubMed=1676261;
 RA Prince C.W., Dickie D., Krumdieck C.L.;
 RT "Osteopontin, a substrate for transglutaminase and factor XIII
 activity.";
 RL Biochem. Biophys. Res. Commun. 177:1205-1210(1991).
 FT NON TER 1 1
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 920 MW; 05DAFAF76322D767 CRC64;

Query Match 20.0%; Score 3; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
 Db 1 LPV 3

RESULT 10

Q89498 PRELIMINARY; PRT; 8 AA.
 AC Q89498
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE CORONAVIRUS proviral defective INTERFERING particle (DISSE) OBTAINED
 DE AFTER SERIAL PASSAGE 17, with 2 recombination sites and ORFs (DISSE).
 OS Murine hepatitis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 OX NCBI_TaxID=11138;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89020822; PubMed=2845661;
 RA Makino S., Shieh C.K., Soe L.H., Baker S.C., Lai M.M.;
 RT "Primary structure and translation of a defective interfering RNA of
 murine coronavirus.";
 RL Virology 166:550-560(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88062951; PubMed=2824826;
 RA Soe L.H., Shieh C.K., Baker S.C., Chang M.F., Lai M.M.C.;
 RT "Sequence and translation of the murine coronavirus 5' end genomic RNA
 reveals the N-terminal structure of the putative RNA polymerase.";
 RL J. Virol. 61:3968-3976(1987).
 DR EMBL; M23258; AAA91862.1; -.
 DR EMBL; M18040; AAA46465.1; -.
 SQ SEQUENCE 8 AA; 815 MW; ECB732C72862D766 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPV 6
 Db 1 MPV 3

RESULT 11

P82568 PRELIMINARY; PRT; 9 AA.
 AC P82568
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE Unknown protein from 2D-page (fragment).
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=13114;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC STRAIN=JRS4;
 RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
 RA VanBogelen R.A.;
 RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
 proteins.";
 RL Submitted (MAY-2000) to the SWISS-PROT data bank.
 CC -1- MASS SPECTROMETRY: MW=22592.04; METHOD=ELECTROSPRAY.
 FT NON TER 1 1
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
 Db 1 LPV 3

RESULT 12

Q9P8E5 PRELIMINARY; PRT; 9 AA.
 AC Q9P8E5
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE HIS4 protein (Fragment).
 GN HIS4.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL-Y1140;
 RX MEDLINE=9448382; PubMed=10518937;
 RA Lamas-Macielas M., Esperanza Cerdan E., Freire-Picos M.A.;
 RT "Kluyveromyces lactis HIS4 transcriptional regulation: similarities
 RT and differences to Saccharomyces cerevisiae HIS4 gene.";
 RL FEBS Lett. 458:72-76(1999).
 DR EMBL; AJ238494; CAB87125.1; -.
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1015 MW; 5770D2D72D2D767 CRC64;

Query Match 20.0%; Score 3; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
 Db 2 LPV 4

RESULT 13

Q9UCN5 PRELIMINARY; PRT; 9 AA.
 ID Q9UCN5

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AC Q9UCN5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE "Cell-surface heparin/HEPARANSULFATE-binding protein peptide 2
DE (fragment)".
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92291065; PubMed=1601862;
RA Raboudi N., Julian J., Rohde L.H., Carson D.D.;
RT "Identification of cell-surface heparin/heparan sulfate-binding
RT proteins of a human uterine epithelial cell line (RL95)".;
RL J. Biol. Chem. 267:11930-11939(1992)
SQ SEQUENCE 9 AA; 1008 MW; CB56D0544732C732 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
Db 1 PVL 3

RESULT 14
Q9FXL0 PRELIMINARY; PRT; 9 AA.
AC Q9FXL0;
DT 01-MAR-2001 (TrEMBLrel. 15, Created)
DT 01-MAR-2001 (TrEMBLrel. 15, Last sequence update)
DE LIMA protein (fragment).
GN LIMA
OS Lilium longiflorum (Trumpet lily).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
OX NCBI_TaxID=4690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Hinomoto;
RA Uefuji H., Takase H., Hitatsuka K.;
RT "Lilium longiflorum LIMA gene, promoter region and partial sequence.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB050987; BAB17856.1;
FT NON_TER 9
SQ SEQUENCE 9 AA; 1021 MW; 6F8BD76685A6C2CB CRC64;

Query Match 20.0%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPV 6
Db 6 MPV 8

RESULT 15
Q64972 PRELIMINARY; PRT; 9 AA.
AC Q64972;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rous associated virus type 1 (RAV-1) ml protein, 3' end, and env
DE Protein (fragment).
OS Avian rous-associated virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11950;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=99037349; PubMed=2846875;
RA Marx M., Crisanti P., Eychene A., Bechade C., Laugier D.,
RA Ghysdael J., Pessac B., Calothy G.;
RT "Activation and transduction of c-mil sequences in chicken neuroretina
RT cells induced to proliferate by infection with avian lymphomatosis
RT virus.";
RL J. Virol. 62:4627-4633(1988).
DR EMBL; M25399; AAA42548.1;
FT NON_TER 1
SQ SEQUENCE 9 AA; 1033 MW; 83AED7673411B5A1 CRC64;

Query Match 20.0%; Score 3; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
Db 6 LPV 8

RESULT 16
Q9RSN2 PRELIMINARY; PRT; 10 AA.
AC Q9RSN2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Neurotoxin type A HN+ 57 kDa SUBUNIT=SAMPLE 2 (fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
RT without hemagglutinating activity: do they share common amino acid
RT sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1225 MW; EC3DE932D366C1BA CRC64;

Query Match 20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db 7 VLP 9

RESULT 17
Q9RSN1 PRELIMINARY; PRT; 10 AA.
AC Q9RSN1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Neurotoxin type A HN+ 57 kDa subunit (fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
RT without hemagglutinating activity: do they share common amino acid
RT sequences and genes?";

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RL J. Protein Chem. 10:415-425(1991).

FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1172 MW; ESDAE932D416C1BA CRC64;

Query Match 20.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
 DB 7 VLP 9

RESULT 18

Q9R5N3 PRELIMINARY; PRT; 10 AA.

ID Q9R5N3
 AC Q9R5N3
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Neurotoxin type B Hx+ 57 Ada subunit (Fragment).
 OS Clostridium botulinum.
 OC Clostridia; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 CX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE.

RA MEDLINE=92143938; PubMed=1781887;
 RA Somers E.; Dasgupta B.R.;
 RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
 RT without hemagglutinating activity: do they share common amino acid
 RT sequences and genes?";
 RL J. Protein Chem. 10:415-425(1991).
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1221 MW; C3DBE932D416C1B2 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
 DB 7 VLP 9

RESULT 19

Q9N1X1 PRELIMINARY; PRT; 10 AA.

ID Q9N1X1
 AC Q9N1X1
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
 DE Alcohol dehydrogenase 3 (Fragment).
 GN ADH3.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 CX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE=20082971; PubMed=10613847;
 RA Caetano A.R.; Shue Y.L.; Lyons L.A.; O'Brien S.J.; Laughlin T.F.,
 RA Bowling A.T.; Murray J.D.;
 RT "A comparative gene map of the horse (Equus caballus).";
 RL Genome Res. 9:1239-1249(1999).
 DR EMBL; AFI34056; AAF31299.1; .
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1144 MW; C4EA25676502D6DD CRC64;

Query Match

20.0%; Score 3; DB 6; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11
 DB 5 VEP 7

RESULT 20

Q8WER7 PRELIMINARY; PRT; 10 AA.

ID Q8WER7
 AC Q8WER7
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
 DE Cytochrome oxidase subunit I (Fragment).
 GN COI.
 OS Chaitophorus leucomelas.
 OC Mitochondrion.
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 CC Aphidoidea; Drepanosiphidae; Chaitophorus.
 CX NCBI_TaxID=136351;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Shingleton A.W.; Stern D.L.;
 RT "Molecular phylogenetic evidence for multiple origins of ant mutualism
 RT within the aphid genus Chaitophorus";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF444288; AAL38565.1; .
 KW Mitochondrion.
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 1194 MW; 6E553D5042D7672B CRC64;

Query Match 20.0%; Score 3; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
 DB 4 LPV 6

RESULT 21

Q9QVJ5 PRELIMINARY; PRT; 10 AA.

ID Q9QVJ5
 AC Q9QVJ5
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Myo-inositol hexakisphosphate phosphohydrolase (Fragment).
 OS Rattus sp.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 CX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.

RA MEDLINE=91370007; PubMed=1654110;
 RA Yang W.J.; Matsuda Y.; Sano S.; Masutani H.; Nakagawa H.;
 RT "Purification and characterization of phytase from rat intestinal
 RT mucosa";
 RL Biochim. Biophys. Acta 1075:75-82(1991).
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1086 MW; 37A8EA4B1B02D7 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10
 DB 3 PVE 5

RESULT 22
Q63389 PRELIMINARY; PRT; 10 AA.
AC Q63389;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Ornithine decarboxylase (ODC).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRague-Dawley; Tissue=Testis;
RX MEDLINE=8925378; PubMed=2722815;
RA Wen L., Huang J.K., Blackshear P.J.;
RT "Rat ornithine decarboxylase gene. Nucleotide sequence, potential regulatory elements, and comparison to the mouse gene.";
RL J. Biol. Chem. 264:9016-9021(1989).
DR EMBL; J04791; AAA66163.1; -.
SQ SEQUENCE 10 AA; 1074 MW; 30F6BE69D415BDC7 CRC64;
Query Match 20.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 PVL 7
Db 8 PVL 10
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RESULT 23
Q9QVJ6 PRELIMINARY; PRT; 10 AA.
AC Q9QVJ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE MYO-inositol hexakisphosphate phosphohydrolase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE
RX MEDLINE=91370007; PubMed=1654110;
RA Yang W.J., Matsuda Y., Sano S., Masutani H., Nakagawa H.;
RT "Purification and characterization of phytase from rat intestinal mucosa";
RL Biochim. Biophys. Acta 1075:75-82(1991).
DR EMBL; AF454217; AAM22903.1; -.
SQ SEQUENCE 10 AA; 1124 MW; 28B8EA4B1B1B02D7 CRC64;
Query Match 20.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 PVE 10
Db 3 PVE 5
|||
RESULT 24
Q9ESU5 PRELIMINARY; PRT; 10 AA.
AC Q9ESU5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Fas death receptor (Fragment).
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He;
RX MEDLINE=20127858; PubMed=10660538;
RA Munsch D., Watanabe-Fukunaga R., Bourdon J.C., Nagata S., May E.,
Yonish-Rouach E., Reisdorf P.;
RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a p53-responsive element that is activated by p53 mutants unable to induce apoptosis.";
RL J. Biol. Chem. 275:3867-3872(2000).
DR EMBL; AF282865; AAG02410.1; -.
KW Receptor.
FT NON TER 10
SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;
Query Match 20.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 VLP 8
Db 7 VLP 9
|||
RESULT 25
Q8JFE7 PRELIMINARY; PRT; 10 AA.
AC Q8JFE7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula albicollis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=59894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bc5; and Bc8;
RX MEDLINE=21918460; PubMed=11918793;
RA Primmer C., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with limited available sequence information: high nucleotide diversity revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454217; AAM22903.1; -.
DR EMBL; AF454218; AAM22904.1; -.
FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 1206 MW; 1FAAC9676732C86B CRC64;
Query Match 20.0%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 VLP 8
Db 5 VLP 7
|||
RESULT 26
Q8JFJ3 PRELIMINARY; PRT; 10 AA.
AC Q8JFJ3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula hypoleuca.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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SQ SEQUENCE 11 AA; 1120 MW; 8391BACBD77772D1 CRC64;
Query Match 20.0%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 01-MAY-2000 (TREMBlRel. 13, Last sequence update)

RP SEQUENCE FROM N.A.
RA Barlow K.;

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RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035398; CAB63074.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1430 MW; AF7740ABECB69AA6 CRC64;
Query Match 20.0%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 LEM 4
Db 3 LEM 5

RESULT 31
O9GI96 PRELIMINARY; PRT; 12 AA.
ID O9GI96;
AC O9GI96;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
DE (Fragment).
DE RBGS.
GN Sargassum polycystum.
OC Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
OC Sargassum.
OC NCBI_TaxID=127578;
OX NCBI_TaxID=127578;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=nepl27;
RC Phillips N.E.;
RA "Testing the systematics of the genus Sargassum (Fucales,
RT Phaeophyceae) with the Rubisco operon.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244344; AAF98114.1; -.
KW Chloroplast.
KW NON_TER 12
SQ SEQUENCE 12 AA; 1379 MW; 373D121250CEB867 CRC64;
Query Match 20.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 PFF 14
Db 8 PFF 10

RESULT 32
O9S8F0 PRELIMINARY; PRT; 12 AA.
ID O9S8F0;
AC O9S8F0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Glutathione S-transferase isoform II (EC 2.5.1.18) (Fragment).
DE Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OC NCBI_TaxID=4577;
OX NCBI_TaxID=4577;
RN [1] SEQUENCE.
RP MEDLINE=95322859; PubMed=7599527;

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RA Holt D.C., Lay V.J., Clarke E.D., Dinmore A., Jepson I., Bright S.W.,
RA Greenland A.J.;
RT "Characterization of the safener-induced glutathione S-transferase
RT isoform II from maize.";
RL Planta 196:295-302(1995).
SQ SEQUENCE 12 AA; 1382 MW; C28977F65975B05D CRC64;
Query Match 20.0%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 PFF 15
Db 8 PFF 10

RESULT 33
P82441 PRELIMINARY; PRT; 12 AA.
ID P82441;
AC P82441;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 26 kDa cell wall protein (Fragment).
DE Nicotiana tabacum (Common tobacco).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
OC NCBI_TaxID=4097;
OX NCBI_TaxID=4097;
RN [1] SEQUENCE.
RP STRAIN=cv. PETIT HAVANA;
RC Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
KW NON_TER 12
SQ SEQUENCE 12 AA; 1234 MW; 340012240872C9D7 CRC64;
Query Match 20.0%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 PFF 15
Db 5 PFF 7

RESULT 34
Q96Q66 PRELIMINARY; PRT; 13 AA.
ID Q96Q66;
AC Q96Q66;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mitochondrial ribosomal protein L38 (Fragment).
GN MRP238.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1] SEQUENCE FROM N.A.
RP MEDLINE=21429115; PubMed=11543634;
RX Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.,
RA Watanabe K., Tanaka T.;
RT "The human mitochondrial ribosomal protein genes: Mapping of 54 genes
RT to the chromosomes and implications for human disorders.";
RL Genomics 77:65-70(2001).

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DR EMBL; AB051345; BAB54935.1; -.
 KW Ribosomal protein. 13
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1440 MW; 22C088BAFD21448 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred.No. 9.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPV 6
 DB 1 MPV 3
 |||

RESULT 35

Q9TWR4 PRELIMINARY; PRT; 13 AA.

AC Q9TWR4; 2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
 DE Peptide T-BRAYKININ potentiator.
 OS Tityus serrulatus (Brazilian scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthoidea; Buthidae; Tityus.
 OX NCBI_TaxID=6887;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=94024945; PubMed=8212046;
 RA Ferreira L.A., Alves E.W., Henriques O.B.;
 RT "Peptide T, a novel bradykinin potentiator isolated from Tityus
 serrulatus scorpion venom.";
 RL Toxicon 31:941-947(1993).
 SQ SEQUENCE 13 AA; 1604 MW; 35770B0644FC02D7 CRC64;

Query Match 20.0%; Score 3; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred.No. 9.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10
 DB 6 PVE 8
 |||

RESULT 36

Q33417 PRELIMINARY; PRT; 13 AA.

AC Q33417; 1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
 DE Rps19, protein (Fragment).
 GN Rps19.
 OS Digitalis purpurea (Common foxglove).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Lamiales; Antirrhinaceae; Digitalis.
 OX NCBI_TaxID=4164;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96397499; PubMed=8804393;
 RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
 RT "Ebb and Flow of the Chloroplast Inverted Repeat.";
 RL Mol. Gen. Genet. 252:195-206(1996).
 DR EMBL; Z71251; CA94968.1; -.
 KW Chloroplast.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1518 MW; 4D775A09A55D4333 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred.No. 9.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15
 DB 9 PFV 11
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RESULT 37

O88176 PRELIMINARY; PRT; 13 AA.

AC O88176; 1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Neural cell adhesion molecule (Fragment).
 GN NCAM1 OR NCAM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=balb-c; TISSUE=Liver;
 RX MEDLINE=98250618; PubMed=9582442;
 RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
 RT "A cis-acting regulatory element that affects the alternative splicing
 of a muscle-specific exon in the mouse NCAM gene.";
 RL Biochim. Biophys. Acta 1397:305-315(1998).
 DR EMBL; AB001873; BA31275.1; -.
 DR MGD; MGI:97281; Ncam1
 FT NON_TER 13
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 13;
 Best Local Similarity 100.0%; Pred.No. 9.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
 DB 4 LPV 6
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RESULT 38

O9QVK6 PRELIMINARY; PRT; 13 AA.

AC O9QVK6; 2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
 DE Phosphoglycerate mutase P29 (EC 2.7.5.3) (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91373341; PubMed=1832670;
 RA Hoppner W., Beckert L., Buck F., Seitz H.J.;
 RT "Is the p29 protein involved in the rapid regulation of
 phosphoenolpyruvate carboxykinase (GTP)?";
 RL J. Biol. Chem. 266:17257-17260(1991).
 SQ SEQUENCE 13 AA; 1456 MW; 39099D8CBA6D2D7 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 13;
 Best Local Similarity 100.0%; Pred.No. 9.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
 DB 5 LPV 7
 |||

RESULT 39

Q9PXB5 .
 ID Q9PXB5 PRELIMINARY; PRT; 13 AA.
 AC Q9PXB5;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
 DE 170 kDa DHRV pre-S region binding protein (Fragment).
 OS Duck hepatitis B virus (DHBV).
 OC Viruses; Retrovirus; Hepadnaviridae; Avihepadnavirus.
 OX NCBI_TaxID=12639;
 RL [1]
 RP SEQUENCE
 RX MEDLINE=96013813; PubMed=7474130;
 RA Tong S., Li J., Hands J.R.;
 RT "Interaction between duck hepatitis B virus and a 170-kilodalton cellular protein is mediated through a neutralizing epitope of the pre-S region and occurs during viral infection.";
 RL J. Virol. 69:7106-7112(1995).
 SQ SEQUENCE 13 AA; 1397 MW; DC47BFE014BCD772 CRC64;
 Query Match 20.0%; Score 3; DB 12; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PVL 7
 Db 7 PVL 9
 RESULT 40
 Q9WMS5
 ID Q9WMS5 PRELIMINARY; PRT; 13 AA.
 AC Q9WMS5;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE 3 protein (fragment).
 GN GENE 3.
 OS Sigma virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; unclassified Rhabdoviridae.
 OX NCBI_TaxID=11301;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212481; PubMed=8384742;
 RA Teninges D., Bress F., Dezelee S.;
 RT "Genome organization of the sigma rhabdovirus: six genes and a gene overlap.";
 RL Virology 193:1018-1023(1993).
 DR EMBL; S57850; AAD40700.1; -.
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1456 MW; 9AF4F3FDE75E32D5 CRC64;
 Query Match 20.0%; Score 3; DB 12; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 VLP 8
 Db 7 VLP 9
 RESULT 41
 P82830
 ID P82830 PRELIMINARY; PRT; 13 AA.
 AC P82830;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE Temporin-11A.
 OS Rana luteiventris.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.

OX NCBI_TaxID=58176;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=SKIN;
 RX MEDLINE=20117700; PubMed=10651828;
 RA Gozaya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E., Conlon J.M.;
 RT "Peptides with antimicrobial activity from four different families isolated from the skins of the North American frogs Rana luteiventris, Rana berlandieri and Rana pipiens.";
 RL Eur. J. Biochem. 267:894-900(2000).
 CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
 CC -!- S.AUREUS.
 CC -!- MASS SPECTROMETRY: MM=1366.8; METHOD=ELECTROSPRAY.
 CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN FAMILY.
 KW Antibiotic; Amidation.
 FT MOD RES 13 13
 SQ SEQUENCE 13 AA; 1368 MW; 92541A7649A3D685 CRC64;
 Query Match 20.0%; Score 3; DB 13; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 VLP 8
 Db 1 VLP 3
 RESULT 42
 P83159
 ID P83159 PRELIMINARY; PRT; 14 AA.
 AC P83159;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Phycobilisome 32.1 kDa linker polypeptide, phycocyanin-associated, rod (fragment).
 OS Anabaena sp. (strain L311).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TaxID=29412;
 RN [1]
 RP SEQUENCE.
 RA Apke S.K., Uhlemann E., Schmid R., Altendorf K.;
 RL Submitted (Oct-2001) to the SWISS-PROT data bank.
 CC -!- FUNCTION: ROD LINKER PROTEIN, ASSOCIATED WITH PHYCOCYANIN. LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION AND THE LOCATION OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN ORDER TO MEDIATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
 CC -!- SUBCELLULAR LOCATION: THIS PROTEIN OCCURS IN THE ROD, IT IS ASSOCIATED WITH PHYCOCYANIN (BY SIMILARITY).
 CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
 KW Phycobilisome; Photosynthesis.
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1405 MW; 96823E44F60A3115 CRC64;
 Query Match 20.0%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 ERF 12
 Db 12 ERF 14
 RESULT 43
 Q9TWW0
 ID Q9TWW0 PRELIMINARY; PRT; 14 AA.
 AC Q9TWW0;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)

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DE Histone C (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE
RX MEDLINE=93064852; PubMed=1437281;
RA Bender K., Betschart B., Schaller J., Kampfer U., Hecker H.;
RT "Sequence differences between histones of procyclic Trypanosoma brucei
RT brucei and higher eukaryotes.";
RL Parasitology 105:97-104(1992).
SQ SEQUENCE 14 AA; 1480 MW; 460FF4E8876C4EC7 CRC64;

Query Match 20.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred.No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
DB 8 VLP 10

RESULT 44
ID O70599 PRELIMINARY; PRT; 14 AA.
AC O70599;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Thymidine kinase (EC 2.7.1.21) (Fragment).
OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Sauer M.;
RL Thesis (1999), University of Vienna. Inst. of Molecular Biology.
DR EMBL; AU006455; CAA07030.1; -.
KW Kinase; Transferase.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1579 MW; 294979C45CB2E8B7 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 14;
Best Local Similarity 100.0%; Pred.No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
DB 9 VLP 11

RESULT 45
Q9EON0 PRELIMINARY; PRT; 14 AA.
ID Q9EON0
AC Q9EON0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Immediate early protein ICP47 (Fragment).
GN US12.
OS Human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10296;
RN [1]
RP SEQUENCE FROM N.A.
RA Maertzdorf J., Van der lელიj A., Baarma G.S., Osterhaus A.D.M.E.,
RA Verjans G.M.G.M.;
RT "Herpes Simplex Virus type 1 (HSV-1) Induced Retinitis Following
RT Herpes Simplex Encephalitis: Indications for Brain-to-Eye Transmission
RT of HSV-1.";

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RL Ann. Neurol. 48:0-0(2000).
DR EMBL; AF290018; AAG3134.1; -.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1631 MW; BDE58B6F5C2A94D6 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred.No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
DB 5 LEM 7

RESULT 46
Q9BON1 PRELIMINARY; PRT; 14 AA.
ID Q9BON1
AC Q9BON1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Immediate early protein ICP47 (Fragment).
GN US12.
OS Human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10296;
RN [1]
RP SEQUENCE FROM N.A.
RA Maertzdorf J., Van der lელიj A., Baarma G.S., Osterhaus A.D.M.E.,
RA Verjans G.M.G.M.;
RT "Herpes Simplex Virus type 1 (HSV-1) Induced Retinitis Following
RT Herpes Simplex Encephalitis: Indications for Brain-to-Eye Transmission
RT of HSV-1.";
RL Ann. Neurol. 48:0-0(2000).
DR EMBL; AF290017; AAG3133.1; -.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1631 MW; BDE58B6F5C2A94D6 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred.No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
DB 5 LEM 7

RESULT 47
Q9BOW2 PRELIMINARY; PRT; 14 AA.
ID Q9BOW2
AC Q9BOW2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Immediate early protein ICP47 (Fragment).
GN US12.
OS Human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21119878; PubMed=11273067;
RA Remeliger L., Maertzdorf J., Doornbal P., Verjans G.M.G.M.,
RA Osterhaus A.D.M.E.;
RT "Herpes simplex virus type 1 transmission through corneal
RT transplantation.";
RL Lancet 357:442-442(2001).
DR EMBL; AF324428; AAK12110.1; -.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1631 MW; BDE58B6F5C2A94D6 CRC64;

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Query Match      20.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
   |||
   5 LEM 7
Db

RESULT 48
ID Q9R5Z5 PRELIMINARY; PRT; 15 AA.
AC Q9R5Z5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Streptolysin O (Fragment).
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
CC Streptococcus.
CX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93273535; PubMed=8500915;
RA Gerlach D., Kohler W., Gunther E., Mann K.;
RT "Purification and characterization of streptolysin O secreted by
RT Streptococcus equisimilis (group C).";
RL Infect. Immun. 61:2727-2731(1993).
SQ SEQUENCE 15 AA; 1716 MW; 7C02547F72FF85BE CRC64;

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMP 5
   |||
   4 EMP 6
Db

RESULT 49
ID Q9JF39 PRELIMINARY; PRT; 15 AA.
AC Q9JF39;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HrpK (Fragment).
GN HRPK.
OS Pseudomonas syringae (pv. syringae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CC Pseudomonadaceae; Pseudomonas.
CX NCBI_TaxID=321;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=61;
RA MEDLINE=97348579; PubMed=9204563;
RX Alfano J.R., Kim H.S., Delaney T.P., Collmer A.;
RT "Evidence that the Pseudomonas syringae pv. syringae hrp-linked hrpA
RT gene encodes an Avr-like protein that acts in an hrp-dependent manner
RT within tobacco cells.";
RL Mol. Plant Microbe Interact. 10:580-588(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=61;
RA MEDLINE=20243785; PubMed=10781092;
RX Alfano J.R., Charkowski A.O., Deng W.L., Badel J.L.,
RX Petnicki-Ocwieja T., van Dijk K., Collmer A.;
RT "The Pseudomonas syringae Hrp pathogenicity island has a tripartite
RT mosaic structure composed of a cluster of type III secretion genes
RT bounded by exchangeable effector and conserved effector loci that
RT contribute to parasitic fitness and pathogenicity in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4856-4861(2000).
RL EMBL; AF232003; AAF71482.1; -.

FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1696 MW; C0E7FAC1E44EAB20 CRC64;

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
   |||
   4 PVL 6
Db

RESULT 50
ID Q8RKN0 PRELIMINARY; PRT; 15 AA.
AC Q8RKN0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative transposase ORF1005 (Fragment).
GN ORF1005.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=743-D;
RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,
RA Prats G.;
RT "A novel complex sula-type integrin in Escherichia coli carrying the
RT bla(CRX-M-9) gene.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092058; AAM15719.1; -.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1751 MW; 2D706E3A12001249 CRC64;

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
   |||
   10 LPV 12
Db

RESULT 51
ID Q9BXX4 PRELIMINARY; PRT; 15 AA.
AC Q9BXX4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Transcription factor PAX 5 (PAX5) (Fragment).
GN PAX5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirabayashi Y., Rahman M., Sasaki T.;
RT "Identification of a novel repressor element in the 5'UTR of human
RT BSAP/FoxA3.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354098; PubMed=11460166;
RX Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
RX Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
RT "Hypermethylation of multiple proto-oncogenes in B-cell diffuse large-
RT cell lymphomas.";
RL Nature 412:341-346(2001).

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DR EMBL; AF268279; AAK25737.1; -.
 DR EMBL; AF386790; AAK70869.1; -.
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1809 MW; 3F95BB53FB3F7A8E CRC64;

Query Match 20.0%; Score 3; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLE 3
 DB 2 DLE 4

RESULT 52
 Q9HCX8 PRELIMINARY; PRT; 15 AA.
 AC Q9HCX8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE CAMP-specific phosphodiesterase 4D.
 GN PDE4DN1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20374482; PubMed=10913353;
 RA Miro X., Casacuberta J.M., Gutierrez-Lopez M.D., Landazuri M.O.,
 RA Puigdomenech P.;
 RT "Phosphodiesterases 4D and 7A splice variants in the response of HUVEC
 RT cells to TNF-alpha";
 RL Biochem. Biophys. Res. Commun. 274:415-421(2000).
 DR EMBL; AJ250852; CAC03756.1; -.
 SQ SEQUENCE 15 AA; 1972 MW; 36C1CF0521236FEE CRC64;

Query Match 20.0%; Score 3; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PFF 14
 DB 7 PFF 9

RESULT 53
 Q9EXQ0 PRELIMINARY; PRT; 15 AA.
 AC Q9EXQ0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Tissue transglutaminase (EC 2.3.2.13) (Fragment).
 GN TGM2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tissue=Brain;
 RA Citron B.A., Santa Cruz K.S., Davies P.J.A., Festoff B.W.;
 RT "Intron-exon swapping of transglutaminase mRNA and neuronal tau
 RT aggregation in Alzheimer's disease";
 RL J. Biol. Chem. 0:0-0(2001).
 DR EMBL; AF311286; AAK15272.1; -.
 KW Acyltransferase; Transferase.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1641 MW; C340982AFBFBF851 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PFF 12
 DB 2 PFF 4

RESULT 54
 Q28822 PRELIMINARY; PRT; 15 AA.
 AC Q28822;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Voltage-dependent dihydropyridine-sensitive calcium channel alpha 1
 DE subunit 155 kDa isoform (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92265303; PubMed=1316766;
 RA Malouf N.N., McMahon D.K., Hainsworth C.N., Kay B.K.;
 RT "A two-motif isoform of the major calcium channel subunit in skeletal
 RT muscle";
 RL Neuron 8:899-906(1992).
 DR EMBL; S36895; AAB22180.1; -.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1796 MW; 841B2D08BFE99DB CRC64;

Query Match 20.0%; Score 3; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
 DB 13 LEM 15

RESULT 55
 Q8HZ79 PRELIMINARY; PRT; 15 AA.
 AC Q8HZ79;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Alpha-synuclein (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tompkins M.M., Gai W.P., Douglas S., Bunn S.J.;
 RT "Alpha-synuclein expression localizes to the Golgi apparatus in bovine
 RT adrenal medullary chromaffin cells";
 RL submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AY124580; AAW94359.1; -.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1774 MW; 1715433C9115DADA CRC64;

Query Match 20.0%; Score 3; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMP 5
 DB 1 EMP 3

RESULT 56

Q9TN05 PRELIMINARY; PRT; 15 AA.
 AC Q9TN05;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Major histocompatibility complex class II bound peptide (Fragment).
 DE Mus sp.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=94082939; PubMed=8260091;
 RA Freed J.H., Marrack P.,
 FT "tissue-specific expression of self peptides bound by major
 RT histocompatibility complex class II molecules.";
 RL Chem. Immunol. 57:88-112(1993).
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1607 MW; CBE93F7E8C5E7425 CRC64;

Query Match 20.0%; Score 3; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9

Db 10 LPV 12

RESULT 57

Q9TN01 PRELIMINARY; PRT; 15 AA.
 AC Q9TN01;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Beta 2M- class I-binding PEPTIDE-MAJOR histocompatibility complex
 DE H-2KB-specific molecule POORLY associated with beta 2-microglobulin (Fragment).
 DE Mus sp.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=94240094; PubMed=8183884;
 RA Joyce S., Kuzushima K., Kepecs G., Angeletti R.H., Nathenson S.G.;
 FT "Characterization of an incompletely assembled major
 RT histocompatibility class I molecule (H-2Kb) associated with unusually
 RT long peptides: implications for antigen processing and presentation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149(1994).
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1754 MW; 2CEACDA0F1180DC7 CRC64;

Query Match 20.0%; Score 3; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9

Db 7 LPV 9

RESULT 58

Q9T2G9 PRELIMINARY; PRT; 15 AA.
 ID Q9T2G9

Q9T2G9;
 AC 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Carbonic anhydrase (EC 4.2.1.1) (Fragment).
 OS Solanum tuberosum (Potato).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=96327808; PubMed=8680307;
 RA Rumeau D., Cuine S., Fina L., Gault N., Nicole M., Peltier G.;
 FT "Subcellular distribution of carbonic anhydrase in Solanum tuberosum
 RT L. leaves: characterization of two compartment-specific isoforms.";
 RL Planta 199:79-88(1996).
 SQ SEQUENCE 15 AA; 1647 MW; CA5B7063CDD32976 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10

Db 10 PVE 12

RESULT 59

Q37016 PRELIMINARY; PRT; 15 AA.
 ID Q37016;
 AC Q37016;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE RPS19, protein (Fragment).
 GN RPS19.
 OS Nicotiana glauca (Winged tobacco) (Persian tobacco),
 OS Nicotiana glauca (Common tobacco), and
 OS Nicotiana glauca (Tobacco).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Aceridae; lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4087, 4097, 35889;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
 RL Mol. Gen. Genet. 0:0-0(1996).
 DR EMBL; 271239; CAA94944.1; -;
 DR EMBL; 271236; CAA94937.1; -;
 DR EMBL; 271238; CAA94942.1; -;
 DR InterPro; IPR002222; Ribosomal_S19.
 DR Pfam; PF00203; Ribosomal_S19; I.
 KW Chloroplast.
 FT NON_TER 15 15
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1756 MW; 09DE1D775A138C5D CRC64;

Query Match 20.0%; Score 3; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15

Db 9 PFV 11

RESULT 60

Q78794 PRELIMINARY; PRT; 15 AA.
 ID Q78794
 AC Q78794;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE Mitochondrial ribosomal protein S14 (Fragment).
 GN RPS14.
 OS Pyraliella littoralis.
 OG Mitochondrion.
 OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;
 OC Acinetosporaceae; Pyraliella.
 OX NCBI_TaxID=2885;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ROSCOFF;
 RX MEDLINE=98239704; PubMed=9571021;
 RA Rouvolet S., Oudot M.-P., Fontaine J.-M., Kloareg B.,
 RA Loiseux-De Goer S.L.,
 RT "Witnessing the evolution of transcription in mitochondria: the
 mitochondrial genome of the primitive brown alga *Pyraliella littoralis*
 (L.) Kjellm. encodes a 77-like RNA polymerase.";
 RL J. Mol. Biol. 277:1047-1057(1998).
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -!- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.
 DR EMBL; AF034976; AAC23952.1; -.
 DR InterPro; IPR001209; Ribosomal S14.
 DR PROSITE; PS00527; RIBOSOMAL S14; PARTIAL.
 KW Ribosomal protein; Mitochondrion; Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1599 MW; 2D406410C588731B CRC64;

Query Match 20.0%; Score 3; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1e+04; 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;

QY 6 VLP 8
 DB 6 VLP 8

RESULT 61
 Q9S8F1 PRELIMINARY; PRT; 15 AA.
 AC Q9S8F1;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
 DE Glutathione S-transferase isoform II (SC 2.5.1.18) (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95322859; PubMed=7599527;
 RA Holt D.C., Lay V.J., Clarke E.D., Dinsmore A., Jepson I., Bright S.W.,
 RA Greenland A.J.;
 RT "Characterization of the safener-induced glutathione S-transferase
 isoform II from maize.";
 RL Planta 196:295-302(1995).
 SQ SEQUENCE 15 AA; 1530 MW; 2F105C48F7DD3A56 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1e+04; 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;

QY 4 MPV 6
 DB 5 MPV 7

RESULT 62
 Q9QV34 PRELIMINARY; PRT; 15 AA.
 ID Q9QV34
 AC Q9QV34;

DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DE CHOLIC acid transport protein P50 (Fragment).
 DE CHOLIC acid transport protein P50 (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94183413; PubMed=8136027;
 RA Hoffmann A., Mullner S., Ziegler K., Rasold H.;
 RT "Purification and partial sequence of proteins involved in the cholic
 acid transport into rat liver hepatocytes.";
 RL J. Protein Chem. 12:765-769(1993).
 SQ SEQUENCE 15 AA; 1597 MW; D719DFB7C75AC0B CRC64;

Query Match 20.0%; Score 3; DB 11; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
 DB 3 PVL 5

RESULT 63
 Q8KM54 PRELIMINARY; PRT; 16 AA.
 ID Q8KM54;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Transposase (Fragment).
 GN TNPA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82137098; PubMed=6277510;
 RA Casadaban M.J., Chou J., Cohen S.N.;
 RT "Overproduction of the Tn3 transposition protein and its role in DNA
 transposition.";
 RL Cell 28:345-354(1982).
 DR EMBL; J01833; AAM54741.1; -.
 FT NON TER 16
 SQ SEQUENCE 16 AA; 1921 MW; 4E376F4D2E554F8 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPV 6
 DB 12 MPV 14

RESULT 64
 P82597 PRELIMINARY; PRT; 16 AA.
 ID P82597;
 AC P82597;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE Thermolabile monoacylglycerol lipase (MGUP) (24 kDa) (SC 3.1.1.23)
 DE (Fragment).
 OS Bacillus sp.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1409;
 RN [1]
 RP SEQUENCE.

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RC STRAIN=H-257;
RX MEDLINE=20196254; PubMed=10731713;
RA Inamura S.; Kitaura S.;
RT "Purification and characterization of a monoacylglycerol lipase from
RL the moderately thermophilic Bacillus sp. H-257.";
RJ J. Biochem. 127:419-425(2000).
CC -1- FUNCTION: HYDROLYZES MONOACYLGLYCEROLS, WITH THE HIGHEST ACTIVITY
CC OCCURRING WITH 1-MONOLAUROYLGLYCEROL.
CC -1- ENZYME REGULATION: NOT INHIBITED BY CHOLATE, BUT SLIGHTLY
CC INHIBITED BY TRITON X-100 AND DEOXYCHOLATE.
CC -1- SUBUNIT: MONOMER.
CC -1- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 4.66. OPTIMUM
CC TEMPERATURE IS 75 DEGREES CELSIUS AND MAXIMUM ACTIVITY AT PH 6-8.
CC -1- MISCELLANEOUS: THIS LIPASE IS NOT SECRETED EXTRACELLULARLY AS
CC OTHER BACTERIAL LIPASES.
KW Hydrolase.
FT NON TER. 16 16
SQ SEQUENCE 16 AA; 1787 MW; 900CF59289521D8F CRC64;

Query Match 20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
DB 5 PVL 7
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|||

RESULT 65
Q9UCD4 PRELIMINARY; PRT; 16 AA.
AC Q9UCD4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Cytochrome P450 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=94028977; PubMed=9215410;
RX Wrighton S.A., Stevens J.C., Becker G.W., VandenBranden M.;
RT "Isolation and characterization of human liver cytochrome P450 2C19:
RT correlation between 2C19 and S-mephenytoin 4'-hydroxylation.";
RL Arch. Biochem. Biophys. 306:240-245(1993).
SQ SEQUENCE 16 AA; 1792 MW; 68C719F62D2C7BEC CRC64;

Query Match 20.0%; Score 3; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15
DB 3 PFV 5
|||
|||

RESULT 66
Q9TRK9 PRELIMINARY; PRT; 16 AA.
AC Q9TRK9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 21, Last annotation update)
DE Casein kinase II=24 kDa polypeptide (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RA MEDLINE=93054738; PubMed=1331100;

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RA Ou W.J., Thomas D.Y., Bell A.W., Bergeron J.J.;
RT "Casein kinase II phosphorylation of signal sequence receptor alpha
RT and the associated membrane chaperone calnexin.";
RL J. Biol. Chem. 267:23789-23796(1992).
FT NON TER. 16 16
SQ SEQUENCE 16 AA; 2053 MW; F31011034124F59B CRC64;

Query Match 20.0%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPF 12
DB 6 EPF 8
|||
|||

RESULT 67
Q9TNN9 PRELIMINARY; PRT; 16 AA.
AC Q9TNN9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 20S proteasome subunit X (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=94215713; PubMed=8163024;
RX Akiyama K., Kagawa S., Tamura T., Shimbara N., Takashina M.,
RX Kristensen P., Hendil K.B., Tanaka K., Ichihara A.;
RT "Replacement of proteasome subunits X and Y by LMP7 and LMP2 induced
RT by interferon-gamma for acquirement of the functional diversity
RT responsible for antigen processing.";
RL FEBS Lett. 343:85-88(1994).
KW MHC.
SQ SEQUENCE 16 AA; 1892 MW; BB869802A16657F1 CRC64;

Query Match 20.0%; Score 3; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLB 3
DB 5 DLB 7
|||
|||

RESULT 68
Q36789 PRELIMINARY; PRT; 16 AA.
AC Q36789;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Rps19, protein (Fragment).
GN RPS19.
OS Solanum nigrum (Black nightshade).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4112;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96397499; PubMed=8804393;
RX Goulding S.E., Omsstead R.G., Morden C.W., Wolfe K.H.;
RT "Ebb and Flow of the Chloroplast Inverted Repeat.";
RL Mol. Gen. Genet. 252:195-206(1996).
DR EMBL; Z71249; CAA94964.1; -.
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; 1.

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Q9Y3F6

ID Q9Y3F6 PRELIMINARY; PRT; 17 AA.
 AC Q9Y3F6;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE EST00098 protein (Fragment).
 GN EST00098.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99299247; PubMed=10369878;
 RA Gilley J., Fried M.;
 RT "Extensive gene order differences within regions of conserved synteny
 between the Fugu and human genomes: implications for chromosomal
 RT volution and the cloning of disease genes";
 RL Hum. Mol. Genet. 8:1313-1320(1999).
 DR EMBL Y17449; CAB4366.1; -.
 FT NON-TER 17
 SQ SEQUENCE 17 AA; 1695 MW; 1EA4692B032AF8D0 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred.No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPV 6
 Db 1 MPV 3

RESULT 74

OSUC43
 ID Q9UC43 PRELIMINARY; PRT; 17 AA.
 AC Q9UC43;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Interferon-alpha-induced protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96132854; PubMed=8557639;
 RA Rich S.A., Bose M., Tempst P., Rudofsky U.H.;
 RT "Purification, microsequencing, and immunolocalization of p36, a new
 RT interferon-alpha-induced protein that is associated with human lupus
 RT inclusions";
 RL J. Biol. Chem. 271:1118-1126(1996).
 SQ SEQUENCE 17 AA; 2027 MW; 762BE7300049ACEC CRC64;

Query Match 20.0%; Score 3; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred.No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVL 7
 Db 8 PVL 10

RESULT 75

Q9TRH5
 ID Q9TRH5 PRELIMINARY; PRT; 17 AA.
 AC Q9TRH5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Alpha-S1-casein homolog (Fragment).
 OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93231344; PubMed=1299613;
 RA Neuteboom B., Giuffrida M.G., Conti A.;
 RT "Isolation of a new ligand-carrying casein fragment from bovine
 RT mammary gland microsomes";
 RL FEBS Lett. 305:189-191(1992).
 SQ SEQUENCE 17 AA; 1950 MW; 8890EF0685A0537F CRC64;

Query Match 20.0%; Score 3; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred.No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PPF 13
 Db 4 PPF 6

Search completed: November 25, 2003, 18:25:19
 Job time : 38.1936 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 48.5904 Seconds
(without alignments)
48.999 Million cell updates/sec

Title: US-09-641-801-5
Perfect score: 15
Sequence: 1 DLEMPVLPVEPPFV 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries:

Database : A Geneseq 19Jun03:*

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- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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- 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	22	AAE07250
2	15	100.0	15	22	AAE07250
3	15	100.0	15	22	AAE07250
4	15	100.0	15	22	AAE07250
5	15	100.0	15	22	AAE07250
6	15	100.0	15	23	AAE07252
7	15	100.0	15	23	AAE07252
8	15	100.0	15	23	AAE07252
9	10	66.7	10	22	AAE07187

10	10	60.0	9	22	AAE07197	Modified colostrin
11	10	40.0	6	22	AAE075678	HLA class I bindin
12	5	33.3	5	17	AAW03289	CNS-inhibiting pep
13	5	33.3	6	23	ABG32212	Sheep colostrinin
14	5	33.3	8	13	ABR21263	N-terminal of gene
15	5	33.3	10	24	AAE47208	Staphylococcus aur
16	5	33.3	10	24	AAE47319	Staphylococcus aur
17	5	33.3	11	24	AAW03290	CNS-inhibiting pep
18	5	33.3	13	17	AAW03291	CNS-inhibiting pep
19	5	33.3	15	16	AAE07630	Endocarditis speci
20	5	33.3	18	22	AAE72267	Colostrinin deriv
21	5	33.3	18	22	AAE72520	Colostrinin deriv
22	5	33.3	18	22	AAE72520	Colostrinin deriv
23	5	33.3	18	22	AAE72522	Colostrinin deriv
24	5	33.3	18	23	AAE20249	Ewe colostrinin pe
25	5	33.3	18	23	AAE20249	Colostrinin consti
26	5	33.3	18	23	AAE51056	Colostrinin consti
27	5	33.3	18	23	AAE014598	Neural cell regula
28	4	26.7	4	20	AAW04512	Transposon phoA pr
29	4	26.7	4	20	AAW78500	Dioxin-binding pep
30	4	26.7	5	19	AAE65791	Polyprolyl inhibi
31	4	26.7	5	22	AAE73397	Human gene 9-encod
32	4	26.7	5	23	ABG64291	Human albumin fusi
33	4	26.7	5	24	ABU12267	Chymotrypsin inhib
34	4	26.7	6	17	AAE95892	Chymotrypsin inhib
35	4	26.7	7	17	AAW04273	Angiotensin conver
36	4	26.7	7	17	AAE95891	Milk derived anti-
37	4	26.7	7	19	AAW59314	Angiotensin conver
38	4	26.7	7	20	AAV50072	Non-polio enterovi
39	4	26.7	7	20	AAV16900	Coxsackievirus A V
40	4	26.7	7	21	AAE96209	Heat shock protein
41	4	26.7	7	21	AAE72042	Arabidopsis AHAS s
42	4	26.7	7	22	AAE97087	Melanoma antigen,
43	4	26.7	7	23	AAE97087	Human leukocyte an
44	4	26.7	8	15	AAE58331	Javelin peptide #2
45	4	26.7	8	17	AAW05539	Hypotensive polype
46	4	26.7	8	18	AAW36802	Peptide fragment #
47	4	26.7	8	19	AAW59334	Synthetic peptide
48	4	26.7	8	22	AAW98148	Non-polio enterovi
49	4	26.7	8	22	AAW98148	Human peptide #142
50	4	26.7	8	22	AAE47584	Human peptide #142
51	4	26.7	8	22	AAU06199	Ag85 complex deriv
52	4	26.7	8	24	ABG73074	Peptide released f
53	4	26.7	9	17	AAW07056	Ag85 complex deriv
54	4	26.7	9	18	AAW34903	MHC class I peptid
55	4	26.7	9	18	AAW34903	Synthetic peptide
56	4	26.7	9	22	AAE47585	Synthetic peptide
57	4	26.7	9	22	AAE93364	Ag85 complex deriv
58	4	26.7	9	22	AAE82787	Vaccine related MH
59	4	26.7	9	22	AAE07191	Epitope of mycobac
60	4	26.7	9	22	AAE75912	Colostrinin peptid
61	4	26.7	9	22	AAE75912	Hepatitis B virus
62	4	26.7	9	23	AAU99719	Hepatitis B virus
63	4	26.7	9	23	ABP61737	Mouse MHC Ld/beta2
64	4	26.7	9	23	AAU98288	Human KRPI tryptic
65	4	26.7	9	23	AAU94070	M. tuberculosis Ag
66	4	26.7	9	23	AAU94117	Human novel protei
67	4	26.7	9	23	AAU94489	Human novel protei
68	4	26.7	9	23	AAU94707	Human novel protei
69	4	26.7	9	24	AAU95042	Human novel protei
70	4	26.7	9	24	ABR10368	Human cancer-relat
71	4	26.7	9	24	ABR10399	Human cancer-relat
72	4	26.7	9	24	ABR10408	Human cancer-relat
73	4	26.7	9	24	ABR10438	Human cancer-relat
74	4	26.7	9	24	ABR10455	Human cancer-relat
75	4	26.7	9	24	ABR10580	Human cancer-relat
76	4	26.7	9	24	ABR10595	Human cancer-relat
77	4	26.7	9	24	ABR10599	Human cancer-relat
78	4	26.7	9	24	ABR10794	Human cancer-relat
79	4	26.7	9	24	ABR10794	Human cancer-relat
80	4	26.7	9	24	ABR10800	Human cancer-relat
81	4	26.7	9	24	ABR10809	Human cancer-relat
82	4	26.7	9	24	ABR10853	Human cancer-relat
						Human cancer-relat

83 4 26.7 9 24 ABR11038 Human cancer-relat
 84 4 26.7 9 24 ABR11059 Human cancer-relat
 85 4 26.7 9 24 ABR11193 Human cancer-relat
 86 4 26.7 9 24 ABR11193 Human cancer-relat
 87 4 26.7 9 24 ABR11222 Human cancer-relat
 88 4 26.7 9 24 ABR11235 Human cancer-relat
 89 4 26.7 9 24 ABR11376 Human cancer-relat
 90 4 26.7 9 24 ABR11404 Human cancer-relat
 91 4 26.7 9 24 ABR11431 Human cancer-relat
 92 4 26.7 9 24 ABR11444 Human cancer-relat
 93 4 26.7 9 24 ABR11592 Human cancer-relat
 94 4 26.7 9 24 ABR11632 Human cancer-relat
 95 4 26.7 9 24 ABR11664 Human cancer-relat
 96 4 26.7 9 24 ABR20170 Human cancer-relat
 97 4 26.7 9 24 ABR20224 Human cancer-relat
 98 4 26.7 9 24 ABR21366 Human cancer-relat
 99 4 26.7 9 24 ABR21569 Human cancer-relat
 100 4 26.7 9 24 ABR21616 Human cancer-relat

ALIGNMENTS

RESULT 1

AA72250
 ID AAB72250 standard; peptide; 15 AA.

AC AAB72250;

DT 14-MAY-2001 (first entry)

DE Colostrinin derived cytokine inducing peptide SEQ ID 5.

KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.

OS Synthetic.

FN WO200111937-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US22818.

PR 17-AUG-1999; 99US-0149311.

PA (TEXA) UNIV TEXAS SYSTEM.

PE (REG-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2001-202804/20.

PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -

PS Claim 1; Page 34; 50pp; English.

CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrinum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.

XX SQ Sequence 15 AA;
 Query Match 100.0%; Score 15; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLEMPVLVEPPFPV 15
 DB 1 DLEMPVLVEPPFPV 15
 RESULT 2
 AAB72504
 ID AAB72504 standard; Peptide; 15 AA.
 XX AC AAB72504;
 XX DT 09-MAY-2001 (first entry)
 XX DE Colostrinin peptide #5.
 XX KW Dermatological; oxidative stress regulator; colostrinin.
 XX OS Unidentified.
 XX FN WO200112650-A2.
 XX PD 22-FEB-2001.
 XX PF 17-AUG-2000; 2000WO-US22665.
 XX PR 17-AUG-1999; 99US-0149310.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Stanton GJ, Hughes TK, Boldogh I;
 XX DR WPI; 2001-218342/22.
 XX PT Modulating oxidative stress level in a cell, involves contacting the
 XX cell with an oxidative stress regulator selected from colostrinin, its
 XX constituent peptide, analog or their combinations -
 XX PS Claim 6; Page 25; 48pp; English.
 XX CC The present invention relates to a method for modulating the oxidative
 XX stress level in a cell or a patient, comprising contacting the cell with,
 XX or administering to the patient, an oxidative stress regulator selected
 XX from colostrinin, or its constituent peptide (e.g. the present peptide),
 XX to change the level of an oxidizing species in the cell. The method can
 XX be used to treat oxidative damage to skin, by decreasing or preventing an
 XX increase in the level of damage to a biomolecule of the patient.
 XX SQ Sequence 15 AA;
 Query Match 100.0%; Score 15; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLEMPVLVEPPFPV 15
 DB 1 DLEMPVLVEPPFPV 15
 RESULT 3
 AAB72536
 ID AAB72536 standard; Peptide; 15 AA.
 XX AC AAB72536;
 XX DT 09-MAY-2001 (first entry)
 XX

DE Colostrinin peptide #5.
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX Unidentified.
 OS WO200112651-A2.
 XX 22-FEB-2001.
 XX 17-AUG-2000; 2000WO-US22774.
 XX 17-AUG-1999; 99US-0149633.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Boldogh I;
 XX WPI; 2001-228545/23.
 XX Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 XX Claim 6; Page 21; 35pp; English.
 XX The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 XX Sequence 15 AA;
 SQ Query Match 100.0%; Score 15; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. NO. 1.8e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DLEMPVLVPVPPFFV 15
 Db 1 DLEMPVLVPVPPFFV 15
 RESULT 4
 AAB59322 standard; Peptide; 15 AA.
 ID AAB59322;
 AC AAB59322;
 XX 21-MAR-2001 (first entry)
 XX Ewe colostrinin peptide fragment B-7.
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX Ovis sp.
 OS WO200075173-A2.
 XX 14-DEC-2000.
 XX 02-JUN-2000; 2000WO-GB02128.
 XX 02-JUN-1999; 99GB-0012852.
 XX (REGG-) REGEN THERAPEUTICS PLC.
 XX Georgiades JA;
 XX WPI; 2001-071058/08.
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 XX characterized by amyloid plaques -
 XX Claim 7; Page 27; 63pp; English.
 XX The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX Sequence 15 AA;
 SQ Query Match 100.0%; Score 15; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. NO. 1.8e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DLEMPVLVPVPPFFV 15
 Db 1 DLEMPVLVPVPPFFV 15
 RESULT 5
 AAE20232 standard; peptide; 15 AA.
 ID AAE20232;
 AC AAE20232;
 XX 18-JUN-2002 (first entry)
 XX Colostrinin constituent peptide #5.
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnery.
 XX Unidentified.
 XX Key Location/Qualifiers
 FT Modified-site 15 /note= "Optionally C-terminal amide"
 FT WO200213850-A1.
 XX 21-FEB-2002.
 XX 17-AUG-2000; 2000WO-US22776.
 XX 17-AUG-2000; 2000WO-US22776.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Stanton GJ, Hughes TK, Boldogh I;
 XX WPI; 2002-269151/31.
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 XX Claim 6; Page 25; 51pp; English.
 XX The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

SQ Sequence 15 AA;
 Query Match 100.0%; Score 15; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-09; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

QY 1 DLEMPVLVEPPFV 15
 |||||
 Db 1 DLEMPVLVEPPFV 15

RESULT 6
 AAM51040
 ID AAM51040 standard; Peptide; 15 AA.

XX AAM51040;

AC 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide.

XX Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Modified-site 15
 FT /note= "Optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.
 XX (REG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is preferred for use as an immunological regulator and as a
 CC blood cell regulator in claimed methods of the invention. It is
 CC classified as having a beta-casein homologue precursor. Methods
 CC are claimed for: inducing a cytokine in a cell by contact with an
 CC immunological regulator, where the cell is present in a cell
 CC culture, a tissue, an organ or an organism, and the cell is
 CC mammalian, including human; modulating an immune response in a cell
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a
 CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator
 CC is administered topically or as part of a dietary supplement, and
 CC where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation
 CC by contacting blood cells with a blood cell regulator, where the
 CC blood cells are present in a cell culture or an organism, are
 CC mammalian or human, and where the blood cells are increased in
 CC number or differentiated; and a method for modulating blood cell
 CC proliferation in a patent. A claimed cytokine-inducing composition
 CC comprises a pharmaceutical carrier and an active agent such as the
 CC present peptide. Cytokines induced by this peptide in human
 CC leucocyte cultures include interferon-gamma, tumour necrosis
 CC factor-alpha, interleukin-6 and interleukin-10.

SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLVEPPFV 15
 |||||
 Db 1 DLEMPVLVEPPFV 15

RESULT 7

AA014581

ID AA014581 standard; peptide; 15 AA.

XX AA014581;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 5.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 15
 FT /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton GJ, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 15; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLEMPVLVPVPPFFV 15
 |||||
 Db 1 DLEMPVLVPVPPFFV 15
 |||||
 RESULT 8
 AAB59352
 ID AAB59352 standard; Peptide; 16 AA.
 XX
 AC AAB59352;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Ewe colostrinin peptide fragment derived sequence #12.
 XX
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 OS Ovis sp.
 XX
 PN WO200075173-A2.
 XX
 PD 14-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-GB02128.
 XX
 PR 02-JUN-1999; 99GB-0012852.
 XX
 PA (REG-) REGEN THERAPEUTICS PLC.
 XX
 FI Georgiades JA;
 XX
 DR WPI; 2001-071058/08.
 XX
 PT Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 PS Claim 8; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis, and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 15; DB 22; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.9e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLEMPVLVPVPPFFV 15
 |||||
 Db 2 DLEMPVLVPVPPFFV 16
 |||||
 RESULT 9
 AAE07187
 ID AAE07187 standard; peptide; 10 AA.
 XX
 AC AAE07187;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Colostrinin peptide 3.
 XX
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral.
 XX
 OS Unidentified.
 XX
 FN WO200155199-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-GB00329.
 XX
 PR 26-JAN-2000; 2000GB-0001825.
 XX
 PA (REG-) REGEN THERAPEUTICS PLC.
 XX
 FI Georgiades JA;
 XX
 DR WPI; 2001-488775/53.
 XX
 PT Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -
 XX
 PS Claim 1; Page 15; 40pp; English.
 XX
 CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is colostrinin peptide 3 related to the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 66.7%; Score 10; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FVLVPVPPFF 14
 |||||
 Db 1 FVLVPVPPFF 10
 |||||
 RESULT 10
 AAE07197
 ID AAE07197 standard; peptide; 10 AA.
 XX

AC AAE07197;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Modified colostrinin cyclic peptide #3.
 XX
 XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral; cyclic.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "N-terminal acetyl; this residue forms a cyclic
 FT linkage with Pro found at the C-terminal end"
 FT
 XX
 PN WO200155199-A1.
 XX
 XX 02-AUG-2001.
 PD
 XX 26-JAN-2001; 2001WO-GB00329.
 XX
 XX 26-JAN-2000; 2000GB-0001825.
 PR
 XX (REGG-) REGEN THERAPEUTICS PLC.
 PA
 XX Georgiades JA;
 XX
 PI WPI; 2001-488775/53.
 DR
 XX Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -
 XX
 PS Example 2; Page 8; 40pp; English.
 XX
 CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improve the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is modified colostrinin cyclic peptide #3 related to
 CC the invention.
 XX
 SQ Sequence 10 AA;
 XX
 Query Match 60.0%; Score 9; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PVLVPEPFP 13
 DB 2 PVLVPEPFP 10

RESULT 11
 AAB75678
 ID AAB75678 standard; Peptide; 10 AA.
 XX
 AC AAB75678;
 XX
 DT 10-APR-2001 (first entry)
 XX
 DE HLA class I binding motif in HOM-TES-84 SEQ ID NO:81.
 DE
 XX Human; cancer associated antigen precursor; cancer associated antigen;
 KW seminoma; HLA; human leukocyte antigen; cytostatic; gene therapy;
 KW vaccine; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200100874-A2.
 XX
 PD 04-JAN-2001.
 XX
 XX 23-JUN-2000; 2000WO-US17207.
 XX
 XX 30-JUN-1999; 99US-0346498.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Sahin U, Tureci O, Pfreundschuh M;
 XX WPI; 2001-112465/12.
 DR
 XX Diagnosing a disorder characterized by expression of a human cancer
 PT associated antigen precursor, comprises detecting interaction of an
 PT agent with a nucleic acid molecule encoding the antigen precursor -
 XX
 PS Example 10; Page 63; 126pp; English.
 XX
 CC The present invention describes a method for diagnosing a disorder
 CC characterised by expression of a human cancer associated antigen (CAA)
 CC precursor (I) coded by a NA Group 1 nucleic acid molecule (N1)
 CC comprising contacting the biological sample with an agent (A) that
 CC specifically binds to N1, (I) or its fragment, complexed with an human
 CC leukocyte antigen (HLA) molecule and determining the interaction between
 CC the agent and N1 or (I). (I) has cytostatic activity and can be used in
 CC gene therapy and vaccine production. The method can be used for treating
 CC a subject with a condition characterised by expression of (I) in cells
 CC of a subject. AAB75607 and AAB75608 represent proteins from human cancer
 CC associated antigen precursors, and AAB75609 to AAB75602 represent HLA
 CC class I binding motifs in human cancer associated antigen precursors
 CC given in the exemplification of the present invention.
 XX
 SQ Sequence 10 AA;
 XX
 Query Match 40.0%; Score 6; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 VLPVEP 11
 DB 3 VLPVEP 8

RESULT 12
 AAW03289
 ID AAW03289 standard; peptide; 6 AA.
 XX
 AC AAW03289;
 XX
 DT 23-MAR-1997 (first entry)
 XX
 DE CNS-inhibiting peptide from casein.
 XX
 XX CNS-inhibiting peptide from casein.
 KW casein; central nervous system; CNS inhibiting; antitussive;
 KW analgesic; sedative.

[illegible]

PR 06-MAR-1991; 91GB-0004744.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.

PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonnett TP;

DR WPI; 1992-056862/07.
DR N-PSDB; AAQ21099.

PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.

PS Example 11; Fig 15; 209pp; English.

The sequence is the N-terminal of alkaline phosphatase encoded by a PCR amplified DNA fragment comprising the *phoA* gene (Chang et al. Gene 44, 121-125, 1986). The template used for the PCR was pK86 which contains a *phoA* gene encoding an alkaline phosphatase which differs from that of Chang et al by a mutation which converts arginine to alanine at position 166. The PCR prod. was ligated into the *fd* gene III contg. vector, *fdCAT2* derived from *fdPrp/Xh* which was in turn derived from *fd-tet* (Zachet, AN et al., 1980, Gene 9, 127-140), a tetracycline resistant version of the *fd* bacteriophage (ATCC No.37000). (Prep. of *fdPrp/Xh* is described in AAQ21095.) The clone having the *PhoA* gene fused in frame to gene III was designated *fd-phoA166*. The first five amino acids of the mature fusion came from gene III. The phage expressed active alkaline phosphatase enzyme from the *phoA*-gene III fusion, on the phage surface.

N.B. *fdCAT2* is also referred to as *fd-tet-DOG1* and *fdDOG1*. See also AAR21260-307, 309-311; AAR22450, 565-581.

Query Match 33.3%; Score 5; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels

RESULT 15
ABR47208
ID ABR47208 standard; Peptide; 10 AA.

10-JUN-2003 (first entry)

Staphylococcus aureus CHIPS-related peptide #2397.

CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; chemotactic peptide receptor; CCR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiant; cerebroprotective; neuroprotective; nootropic; dermatological; gynecological; immunosuppressive; anti-HIV.

OS	Staphylococcus aureus.
OS	Synthetic.

WO2003006048-A1.

23-JAN-2003.

11-JUL-2001; 2001WO-EP08004.

XX
PR 11-JUL-2001; 2001WO-EP08004.
XX
PA (JARI-) JARI PHARM BV.

PI Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;

DR WPI; 2003-247783/25.

Combination of peptides derived from chemotaxis inhibiting protein from *Staphylococcus aureus* (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases -

AA
PS
Example 1; Page 55; 89pp; English.

The present invention relates to peptides (ABR44931-ABR47162 and ABR47163-ABR47385) derived from the chemotaxis inhibitory protein (CHIPS) from *Staphylococcus aureus*. These peptide fragments are useful in the prophylaxis or treatment of diseases involving the type 1 (TLR1) and/or type 2 (TLR2) cell surface receptors (CD14, CD28, CD30, CD36, CD44, CD54, CD58, CD59, CD68, CD71, CD74, CD80, CD86, CD95, CD101, CD102, CD103, CD104, CD105, CD106, CD107, CD108, CD109, CD110, CD112, CD113, CD114, CD115, CD116, CD117, CD118, CD119, CD120, CD121, CD122, CD123, CD124, CD125, CD126, CD127, CD128, CD129, CD130, CD131, CD132, CD133, CD134, CD135, CD136, CD137, CD138, CD139, CD140, CD141, CD142, CD143, CD144, CD145, CD146, CD147, CD148, CD149, CD150, CD151, CD152, CD153, CD154, CD155, CD156, CD157, CD158, CD159, CD160, CD161, CD162, CD163, CD164, CD165, CD166, CD167, CD168, CD169, CD170, CD171, CD172, CD173, CD174, CD175, CD176, CD177, CD178, CD179, CD180, CD181, CD182, CD183, CD184, CD185, CD186, CD187, CD188, CD189, CD190, CD191, CD192, CD193, CD194, CD195, CD196, CD197, CD198, CD199, CD200, CD201, CD202, CD203, CD204, CD205, CD206, CD207, CD208, CD209, CD210, CD211, CD212, CD213, CD214, CD215, CD216, CD217, CD218, CD219, CD220, CD221, CD222, CD223, CD224, CD225, CD226, CD227, CD228, CD229, CD230, CD231, CD232, CD233, CD234, CD235, CD236, CD237, CD238, CD239, CD240, CD241, CD242, CD243, CD244, CD245, CD246, CD247, CD248, CD249, CD250, CD251, CD252, CD253, CD254, CD255, CD256, CD257, CD258, CD259, CD260, CD261, CD262, CD263, CD264, CD265, CD266, CD267, CD268, CD269, CD270, CD271, CD272, CD273, CD274, CD275, CD276, CD277, CD278, CD279, CD280, CD281, CD282, CD283, CD284, CD285, CD286, CD287, CD288, CD289, CD290, CD291, CD292, CD293, CD294, CD295, CD296, CD297, CD298, CD299, CD300, CD301, CD302, CD303, CD304, CD305, CD306, CD307, CD308, CD309, CD310, CD311, CD312, CD313, CD314, CD315, CD316, CD317, CD318, CD319, CD320, CD321, CD322, CD323, CD324, CD325, CD326, CD327, CD328, CD329, CD330, CD331, CD332, CD333, CD334, CD335, CD336, CD337, CD338, CD339, CD340, CD341, CD342, CD343, CD344, CD345, CD346, CD347, CD348, CD349, CD350, CD351, CD352, CD353, CD354, CD355, CD356, CD357, CD358, CD359, CD360, CD361, CD362, CD363, CD364, CD365, CD366, CD367, CD368, CD369, CD370, CD371, CD372, CD373, CD374, CD375, CD376, CD377, CD378, CD379, CD380, CD381, CD382, CD383, CD384, CD385, CD386, CD387, CD388, CD389, CD390, CD391, CD392, CD393, CD394, CD395, CD396, CD397, CD398, CD399, CD400, CD401, CD402, CD403, CD404, CD405, CD406, CD407, CD408, CD409, CD410, CD411, CD412, CD413, CD414, CD415, CD416, CD417, CD418, CD419, CD420, CD421, CD422, CD423, CD424, CD425, CD426, CD427, CD428, CD429, CD430, CD431, CD432, CD433, CD434, CD435, CD436, CD437, CD438, CD439, CD440, CD441, CD442, CD443, CD444, CD445, CD446, CD447, CD448, CD449, CD450, CD451, CD452, CD453, CD454, CD455, CD456, CD457, CD458, CD459, CD460, CD461, CD462, CD463, CD464, CD465, CD466, CD467, CD468, CD469, CD470, CD471, CD472, CD473, CD474, CD475, CD476, CD477, CD478, CD479, CD480, CD481, CD482, CD483, CD484, CD485, CD486, CD487, CD488, CD489, CD490, CD491, CD492, CD493, CD494, CD495, CD496, CD497, CD498, CD499, CD500, CD501, CD502, CD503, CD504, CD505, CD506, CD507, CD508, CD509, CD510, CD511, CD512, CD513, CD514, CD515, CD516, CD517, CD518, CD519, CD520, CD521, CD522, CD523, CD524, CD525, CD526, CD527, CD528, CD529, CD530, CD531, CD532, CD533, CD534, CD535, CD536, CD537, CD538, CD539, CD540, CD541, CD542, CD543, CD544, CD545, CD546, CD547, CD548, CD549, CD550, CD551, CD552, CD553, CD554, CD555, CD556, CD557, CD558, CD559, CD560, CD561, CD562, CD563, CD564, CD565, CD566, CD567, CD568, CD569, CD570, CD571, CD572, CD573, CD574, CD575, CD576, CD577, CD578, CD579, CD580, CD581, CD582, CD583, CD584, CD585, CD586, CD587, CD588, CD589, CD590, CD591, CD592, CD593, CD594, CD595, CD596, CD597, CD598, CD599, CD600, CD601, CD602, CD603, CD604, CD605, CD606, CD607, CD608, CD609, CD610, CD611, CD612, CD613, CD614, CD615, CD616, CD617, CD618, CD619, CD620, CD621, CD622, CD623, CD624, CD625, CD626, CD627, CD628, CD629, CD630, CD631, CD632, CD633, CD634, CD635, CD636, CD637, CD638, CD639, CD640, CD641, CD642, CD643, CD644, CD645, CD646, CD647, CD648, CD649, CD650, CD651, CD652, CD653, CD654, CD655, CD656, CD657, CD658, CD659, CD660, CD661, CD662, CD663, CD664, CD665, CD666, CD667, CD668, CD669, CD670, CD671, CD672, CD673, CD674, CD675, CD676, CD677, CD678, CD679, CD680, CD681, CD682, CD683, CD684, CD685, CD686, CD687, CD688, CD689, CD690, CD691, CD692, CD693, CD694, CD695, CD696, CD697, CD698, CD699, CD700, CD701, CD702, CD703, CD704, CD705, CD706, CD707, CD708, CD709, CD710, CD711, CD712, CD713, CD714, CD715, CD716, CD717, CD718, CD719, CD720, CD721, CD722, CD723, CD724, CD725, CD726, CD727, CD728, CD729, CD730, CD731, CD732, CD733, CD734, CD735, CD736, CD737, CD738, CD739, CD740, CD741, CD742, CD743, CD744, CD745, CD746, CD747, CD748, CD749, CD750, CD751, CD752, CD753, CD754, CD755, CD756, CD757, CD758, CD759, CD760, CD761, CD762, CD763, CD764, CD765, CD766, CD767, CD768, CD769, CD770, CD771, CD772, CD773, CD774, CD775, CD776, CD777, CD778, CD779, CD780, CD781, CD782, CD783, CD784, CD785, CD786, CD787, CD788, CD789, CD790, CD791, CD792, CD793, CD794, CD795, CD796, CD797, CD798, CD799, CD800, CD801, CD802, CD803, CD804, CD805, CD806, CD807, CD808, CD809, CD810, CD811, CD812, CD813, CD814, CD815, CD816, CD817, CD818, CD819, CD820, CD821, CD822, CD823, CD824, CD825, CD826, CD827, CD828, CD829, CD830, CD831, CD832, CD833, CD834, CD835, CD836, CD837, CD838, CD839, CD840, CD841, CD842, CD843, CD844, CD845, CD846, CD847, CD848, CD849, CD850, CD851, CD852, CD853, CD854, CD855, CD856, CD857, CD858, CD859, CD860, CD861, CD862, CD863, CD864, CD865, CD866, CD867, CD868, CD869, CD870, CD871, CD872, CD873, CD874, CD875, CD876, CD877, CD878, CD879, CD880, CD881, CD882, CD883, CD884, CD885, CD886, CD887, CD888,

Sequence	10 AA;
SQ	

Query Match 33.3%; Score 5; DB 24; Length 10;
Best Local Similarity 100.0%; Pred.No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels

RESULT 16
ABR47319
ID ABR47319 standard; Peptide; 10 AA.

AA	DT	10-JUN-2003	(first entry)

XX DE Staphylococcus aureus CHIPS-related peptide #2508.

CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiac; cerebroprotective; neuroprotective; nootropic; dermatological; gynecological; immunosuppressive; anti-HIV.

OS	Staphylococcus aureus.
OS	Synthetic.

XX
PN
WO2003006048-A1.

23-JAN-2003.

11-JUL-2001; 2001WO-EP08004.

PR 11-JUL-2001; 2001WO-EP08004.

PA (JARI-) JARI PHARM BV.

PI Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;

DR WPI; 2003-247783/25.

XX Combination of peptides derived from chemotaxis inhibiting protein from

PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in

PT prophylaxis and treatment of inflammation, cardiovascular, skin and

PT kidney diseases

XX

PS Example 1; Page 56; 89pp; English.

XX

CC The present invention relates to peptides (ABR44811-ABR47162 and

CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)

CC from Staphylococcus aureus. The peptide fragments are useful in the

CC prophylaxis or treatment of diseases or disorders involving the

CC CSA-receptor (CSAR) and/or formylated peptide receptor (FPR) or

CC neutrophils, monocytes and endothelial cells or involving acute or

CC chronic inflammation reactions. The diseases or disorders include

CC cardiovascular diseases, disease of the central nervous system,

CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint

CC diseases, respiratory diseases and HIV infection.

XX

SQ Sequence 10 AA;

Query Match 33.3%; Score 5; DB 24; Length 10;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VERPP 13

DB 3 VERPP 7

RESULT 17

AAW03290

ID AAW03290 standard; peptide; 11 AA.

AC AAW03290;

XX

XX 23-MAR-1997 (first entry)

XX

XX CNS-inhibiting peptide from casein.

DE

DE casein; central nervous system; CNS inhibiting; antitussive;

XX

XX analgesic; sedative.

KW

KW Synthetic.

OS

OS JP08269090-A.

PN

PN 15-OCT-1996.

PD

PD 28-MAR-1995; 95JP-0094516.

PP

PP 28-MAR-1995; 95JP-0094516.

PF

PF (SNOW) SNOW BRAND MILK PROD CO LTD.

PR

PR WPI; 1996-515013/51.

PA

PA New peptide(s) obtd. by digestion of casein - useful as drugs

XX

XX displaying e.g. CNS inhibiting, antitussive, analgesic and sedative

XX

XX activities

PS

PS Claim 1; Page 2; 11pp; Japanese.

XX

XX Acid casein was prepared from raw milk by acid precipitation, and

CC

CC beta casein was formed by the product by the method of Hipp et al.

CC

CC This material was digested with porcine pepsin. The digested protein

CC

CC was neutralised with NaOH, then heated to inactivate the enzyme. The

CC

CC product was further digested with bovine pancreatin, trypsin and porcine

CC

CC kidney-derived IAP and then subjected to reverse phase chromatography

CC

CC to provide the present peptide.

CC

CC The peptide is useful as a drug having CNS inhibiting, antitussive,

CC

CC analgesic and sedative activities

XX SQ Sequence 11 AA;

Query Match 33.3%; Score 5; DB 17; Length 11;

Best Local Similarity 100.0%; Pred. No. 56;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEPP 12

DB 2 PVEPP 6

RESULT 18

AAW03291

ID AAW03291 standard; peptide; 13 AA.

XX

XX AAW03291;

AC

XX 23-MAR-1997 (first entry)

DT

XX CNS-inhibiting peptide from casein.

DE

DE casein; central nervous system; CNS inhibiting; antitussive;

XX

XX analgesic; sedative.

KW

KW Synthetic.

OS

OS JP08269090-A.

PN

PN 15-OCT-1996.

PD

PD 28-MAR-1995; 95JP-0094516.

PP

PP 28-MAR-1995; 95JP-0094516.

PF

PF (SNOW) SNOW BRAND MILK PROD CO LTD.

PA

XX

XX WPI; 1996-515013/51.

DR

XX

XX New peptide(s) obtd. by digestion of casein - useful as drugs

PT

PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative

PT

PT activities

PS

PS Claim 1; Page 2; 11pp; Japanese.

XX

XX Acid casein was prepared from raw milk by acid precipitation, and

CC

CC beta casein was formed by the product by the method of Hipp et al.

CC

CC This material was digested with porcine pepsin. The digested protein

CC

CC was neutralised with NaOH, then heated to inactivate the enzyme. The

CC

CC product was further digested with bovine pancreatin, trypsin and porcine

CC

CC kidney-derived IAP and then subjected to reverse phase chromatography

CC

CC to provide the present peptide.

CC

CC The peptide is useful as a drug having CNS inhibiting, antitussive,

CC

CC analgesic and sedative activities

XX

SQ Sequence 13 AA;

Query Match 33.3%; Score 5; DB 17; Length 13;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEPP 12

DB 2 PVEPP 6

RESULT 19

AAW03290

ID AAW03290 standard; peptide; 15 AA.

XX

XX AAW03290;

AC

XX 18-APR-1996 (first entry)

DT

XX DE Endocarditis specific antigen fragment.
 XX KW Streptococci; enterococci; sera; antibodies; diagnosis;
 KW prophylaxis; treatment; therapy; infection; endocarditis;
 KW septicemia.
 XX OS Streptococcus oralis.
 XX PN WO9520658-A2.
 XX PD 03-AUG-1995.
 XX PF 30-JAN-1995; 95WO-0800186.
 XX PR 28-JAN-1994; 94GB-0001689.
 XX PA (UYMA-) UNIV VICTORIA MANCHESTER.
 XX PI Burnie JP, Matthews RC;
 XX WI; 1995-275443/36.
 XX PT New purified bacterial protein - used to develop prods. for the
 PT diagnosis and treatment of infections due to streptococci and
 PT enterococci
 XX PS Claim 7; Page 75; 92pp; English.
 XX CC Purified bacterial proteins expressed during infection by
 CC Streptococci or enterococci and isolated from human sera may be used
 CC to develop products e.g. antibodies, for use in the diagnosis,
 CC prophylaxis and treatment of infections caused by these organisms,
 CC especially endocarditis and septicemia. Fragments of the proteins
 CC may also be used. This is an endocarditis specific antigen fragment
 CC and was isolated from Streptococcus oralis (See AAR79626-633).
 XX SQ Sequence 15 AA;
 Query Match 33.3%; Score 5; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 LPVEP 11
 Db 10 LPVEP 14
 RESULT 20
 AAB72267
 ID AAB72267 standard; peptide; 18 AA.
 XX AC AAB72267;
 XX DT 14-MAY-2001 (first entry)
 XX DE Colostrinin derived cytokine inducing peptide SEQ ID 22.
 XX KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.
 XX OS Synthetic.
 XX PN WO200111937-A2.
 XX PD 22-FEB-2001.
 XX PF 17-AUG-2000; 2000WO-US22818.
 XX PR 17-AUG-1999; 99US-0149311.
 XX

PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX WI; 2001-202804/20.
 XX DR
 XX PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -
 XX PS Claim 1; Page 34; 50pp; English.
 XX CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.
 XX SQ Sequence 18 AA;
 Query Match 33.3%; Score 5; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 PVEPF 12
 Db 10 PVEPF 14
 RESULT 21
 AAB72520
 ID AAB72520 standard; Peptide; 18 AA.
 XX AC AAB72520;
 XX DT 09-MAY-2001 (first entry)
 XX DE Colostrinin peptide #21.
 XX KW Dermatological; oxidative stress regulator; colostrinin.
 XX OS Unidentified.
 XX PN WO200112650-A2.
 XX PD 22-FEB-2001.
 XX PF 17-AUG-2000; 2000WO-US22665.
 XX PR 17-AUG-1999; 99US-0149310.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Stanton GJ, Hughes TK, Boldogh I;
 XX WI; 2001-218342/22.
 XX DR
 XX PT Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -
 XX PS Claim 6; Page 26; 48pp; English.
 XX CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,

CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidizing species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.

XX Sequence 18 AA;

Query Match 33.3%; Score 5; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEPF 12
 |||||
 Db 10 PVEPF 14

RESULT 22

AAB72552
 ID AAB72552 standard; Peptide; 18 AA.

XX AC AAB72552;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #21.

XX KW Neuroprotective; neural cell differentiation regulator; colostrinin;
 XX colostrinum.

XX OS Unidentified.

XX PN WO200112651-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22774.

XX PR 17-AUG-1999; 99US-0149633.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Boldogh I;

XX DR WPI; 2001-226545/23.

XX FT Use of colostrinin, its constituent peptide or analog as a neural cell
 XX regulator, for promoting neural cell differentiation and treating
 XX damaged neural cells in a patient -

XX PS Claim 6; Page 21; 35pp; English.

XX CC The present invention relates to a method for promoting neural cell
 XX differentiation and treating damaged neural cells, using colostrinin and
 XX colostrinin constituent peptides (e.g. the present peptide) as a neural
 XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.

XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEPF 12
 |||||
 Db 10 PVEPF 14

RESULT 23

AAB59330
 ID AAB59330 standard; Peptide; 18 AA.

XX AC AAB59330;

XX DT 21-MAR-2001 (first entry)
 XX DE Ewe colostrinin peptide fragment C-5.
 XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX PN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

XX PA (SEGE-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-071058/08.

XX PT Peptides having an N-terminal amino acid sequence isolated from
 XX colostrinin for treating e.g. disorders of the central nervous system
 XX and immune system, viral and bacterial infections, and diseases
 XX characterized by amyloid plaques -

XX PS Claim 7; Page 27; 63pp; English.

XX CC The present invention provides the sequences of a number of peptides
 XX found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 XX fragment of colostrum. These peptides can be used in the treatment of
 XX central nervous system disorders such as senile dementia, Parkinson's
 XX disease, Alzheimer's disease, psychosis and neurosis, immune system
 XX disorders such as bacterial and viral infections, to improve the
 XX development of a child's immune system, as a dietary supplement, and to
 XX promote the dissolution of beta-amyloid plaques.

XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEPF 12
 |||||
 Db 10 PVEPF 14

RESULT 24

AAE20249
 ID AAE20249 standard; peptide; 18 AA.

XX AC AAE20249;

XX DT 18-JUN-2002 (first entry)

XX DE Colostrinin constituent peptide #21.

XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 XX therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 XX tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 XX transplantation; implantation; dermatological; vulnery.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Modified-site 18 /note= "Optionally C-terminal amide"

XX PN WO200213850-A1.

XX PD 21-FEB-2002.
 XX PF 17-AUG-2000; 2000WO-US22776.
 XX PR 17-AUG-2000; 2000WO-US22776.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Stanton GJ, Hughes TK, Boldogh I;
 XX DR WPI; 2002-269151/31.
 XX PT Composition useful for the modulation of blood cell proliferation in a
 XX PT patient comprises a blood cell regulator selected from colostrinin, its
 XX PT constituent peptide and/or analog -
 XX PS Claim 6; Page 26; 51pp; English.
 XX CC The invention relates to a composition which comprises a blood cell
 XX CC regulator selected from colostrinin, its constituent peptide and/or
 XX CC analogue. The invention is used for modulating the oxidative stress
 XX CC level in a cell e.g. mammalian or human cell present in a cell culture,
 XX CC tissue, organ, or organism; or for treating oxidative damage to the skin
 XX CC of a patient e.g. animal or human; to modulate oxidative stress during/
 XX CC after a premature birth or normal birth, preventing/delaying aging in a
 XX CC patient, enhancing wound healing, and the reduction of side effects of
 XX CC cosmetic procedures. The method changes the level of an oxidizing species
 XX CC in the cell, such as decreases or prevents increase in the level of
 XX CC damage to a biomolecule of the patient selected from DNA, protein and/or
 XX CC lipid, compared to the same conditions when the oxidative stress
 XX CC enhancer is not present. The modulation of oxidative stress results in
 XX CC enhanced repair, regeneration, and replacement of cells, tissues and
 XX CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 XX CC external organs), as well as enhanced preservation of such organs for
 XX CC transplantation, implantation, or scientific research. The present
 XX CC sequence is a colostrinin constituent peptide.
 XX SQ Sequence 18 AA;
 Query Match 33.3%; Score 5; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 PVEPFF 12
 Db 10 PVEPFF 14
 RESULT 25
 AAO14598
 ID AAO14598 standard; Peptide; 18 AA.
 XX AC AAO14598;
 XX AC AAO14598;
 XX DT 30-MAY-2002 (first entry)
 XX DE Colostrinin constituent peptide (casein amino acids 121-138).
 XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;
 XX KW blood cell regulator; cytokine inducer; beta-casein; human.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Modified-site 18
 XX FT /note= "optional C-terminal amidation"
 XX PN WO200213849-A1.
 XX XX 21-FEB-2002.
 XX PF 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PA (REGG-) REGEN THERAPEUTICS PLC.
 XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX XX WPI; 2002-269150/31.
 XX PT Modulation of blood cell proliferation in a patient involves use of
 XX PT blood cell regulator selected from colostrinin, its constituent peptide
 XX PT and/or analogue -
 XX PS Claim 1; Page 34; 54pp; English.
 XX CC The present sequence is that of a colostrinin constituent peptide
 XX CC that is preferred for use as an immunological regulator and as a
 XX CC blood cell regulator in claimed methods of the invention. It is
 XX CC classified as having a beta-casein homologue precursor, and
 XX CC corresponds to casein amino acids 121-138. Methods are claimed
 XX CC for: inducing a cytokine in a cell by contact with an immunological
 XX CC regulator, where the cell is present in a cell culture, a tissue,
 XX CC an organ or an organism, and the cell is mammalian, including human;
 XX CC modulating an immune response in a cell by contact with the
 XX CC immunological regulator under conditions effective to induce a
 XX CC cytokine; modulating an immune response in a patient by administering
 XX CC an immunological regulator under conditions effective to induce a
 XX CC cytokine, where the immunological regulator is administered topically
 XX CC or as part of a dietary supplement, and where the immune response is
 XX CC specific or non specific, an interferon response or an antibody
 XX CC response; modulating blood cell proliferation by contacting blood
 XX CC cells with a blood cell regulator, where the blood cells are present
 XX CC in a cell culture or an organism, are mammalian or human, and where
 XX CC the blood cells are increased in number or differentiated; and a
 XX CC method for modulating blood cell proliferation in a patient. A
 XX CC claimed cytokine-inducing composition comprises a pharmaceutical
 XX CC carrier and an active agent such as the present peptide. Cytokines
 XX CC induced by this peptide in human leucocyte cultures include
 XX CC interferon-gamma, tumour necrosis factor-alpha and interleukin-10.
 XX SQ Sequence 18 AA;
 Query Match 33.3%; Score 5; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 PVEPFF 12
 Db 10 PVEPFF 14
 RESULT 26
 AAO14598
 ID AAO14598 standard; peptide; 18 AA.
 XX AC AAO14598;
 XX AC AAO14598;
 XX DT 27-MAY-2002 (first entry)
 XX DE Neural cell regulatory colostrinin peptide 21.
 XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 XX KW neural cell treatment.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 XX FT Modified-site 18
 XX FT /note= "Optional C-terminal amide"
 XX PN WO200213851-A1.


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XX PD 21-FEB-2002.
XX PF 17-AUG-2000; 2000WO-US22777.
XX PR 17-AUG-2000; 2000WO-US22777.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Boldogh I, Stanton JG, Hughes TK;
XX DR WPI; 2002-269152/31.
XX PT Promoting cell differentiation in a patient involves use of blood cell
XX PT regulator selected from colostrinin, its constituent peptide and/or
XX PS analog -
XX PS Claim 7; Page 21; 37pp; English.
XX CC The invention comprises a method for promoting cell differentiation (e.g.
XX CC neural cell differentiation). The method involves contacting cells with a
XX CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
XX CC cells in morphology to form neural cells. Colostrinin is a proline-rich
XX CC polypeptide aggregate that is present in colostrum. The method of the
XX CC invention is useful for promoting the differentiation of cells and for
XX CC treating damaged neural cells in a patient. The present amino acid
XX CC sequence represents a specifically claimed colostrinin peptide used in
XX CC the method of the invention.
XX SQ Sequence 18 AA;
      Query Match      33.3%; Score 5; DB 23; Length 18;
      Best Local Similarity 100.0%; Pred. No. 88;
      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 8 PVEPFF 12
DB 10 PVEPFF 14
      |||||
      |||||

RESULT 27
AAR04512
ID AAR04512 standard; protein; 20 AA.
AC AAR04512;
DT 25-MAR-2003 (updated)
DE 20-SEP-1990 (first entry)
DE Transposon phoA product.
KW Transposon; Tn5; alkaline phosphatase; phoA; export DNA.
OS E.coli.
FH Key Location/Qualifiers
FT Region 1..17
FT /label=Tn product
FT Region 18..20
FT /label=first three aa of alkaline phosphatase
XX XX US4914025-A.
XX PD 03-APR-1990.
XX PF 05-DEC-1985; 85US-0805486.
XX PR 05-DEC-1985; 85US-0805486.
XX PA (MANO/) MANOIL C.
XX PI Manoil C, Beckwith J, Syvanen M, Isbert RR, Hoffman CS, Wright A;

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DR WPI; 1990-147416/19.
DR N-PSDB; AAR04280.
XX Identification of export DNA sequences in transformed bacteria -
XX PT using transposon contg.-structural gene for alkaline phosphatase
XX PT which requires export DNA for expression.
XX PS Disclosure; Page ?; ?pp; English.
XX CC XI-Ser, Pro, Thr or Ala.
XX CC Pref the transposon is Tn5 and the detectable gene product is
XX CC alkaline phosphatase. Transformants containing an export DNA
XX CC sequence and where transposition has occurred can be screened
XX CC for their ability to secrete alkaline phosphatase.
XX CC (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 20 AA;
      Query Match      33.3%; Score 5; DB 11; Length 20;
      Best Local Similarity 100.0%; Pred. No. 97;
      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 10 EPFFPF 14
DB 12 EPFFPF 16
      |||||
      |||||

RESULT 28
AAR78500
ID AAR78500 standard; peptide; 4 AA.
AC AAR78500;
DT 21-MAY-1999 (first entry)
DE Dioxin-binding peptide.
KW Dioxin; random peptide phage display library; identification; ligand;
KW affinity; molecular target; drug; toxin.
OS Synthetic.
XX WO9902733-A1.
XX PD 21-JAN-1999.
XX PF 07-JUL-1998; 98WO-US14082.
XX PR 07-JUL-1997; 97US-0051781.
XX PR 07-JUL-1997; 97US-0051780.
XX PA (UYFL ) UNIV FLORIDA STATE.
XX PI Makowski DR, Makowski L, Sanganeer HJ;
XX WPI; 1999-120933/10.
XX Identifying protein that binds to small ligands - by screening
XX against a peptide library in which each member is coupled to nucleic
XX acid encoding it, sequencing in selected library members, deducing
XX peptide sequence and searching proteins for the sequence
XX Example 3; Page 48; 52pp; English.
XX This sequence represents a dioxin-binding peptide generated by a random
XX peptide phage display library. The invention relates to a method of
XX identifying a protein (P) that binds to a ligand (L), of molecular weight
XX below 5 kD, other than a nucleic acid, peptide or protein, by:
XX (a) screening (L) against a peptide or protein library consisting of
XX genetic packages in which each peptide or protein member is coupled to
XX nucleic acid encoding it; (b) separating library members with greatest
XX affinity for (L); (c) determining the nucleic acid sequences encoding the
XX separated library members and translating these to peptide sequences,

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CC and (d) identifying proteins that contain a portion of the translated
 CC sequence or which correspond to consensus peptide sequences derived by
 CC statistical analysis of the translated sequences. The method is used
 CC to identify molecular targets for drugs and toxins, particularly for
 CC determining their mode of action and to identify secondary targets
 CC associated with side effects.

XX SQ Sequence 4 AA;
 Query Match 26.7%; Score 4; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPFF 13
 Db 1 EPFF 4
 |||||

RESULT 29
 ID AAW65791 standard; peptide; 5 AA.
 AC AAW65791;
 DT 19-OCT-1998 (first entry)
 DE Polypyrrol inhibitor of cyclophilin.
 KW polypyrrol; cyclophilin; inhibitor; neurotrophic compound; PPI;
 KW peptidyl-prolyl isomerase; rotamase; immunophilin protein; degeneration;
 KW neuronal damage.
 XX Synthetic.
 OS
 PN WO9825950-A1.
 PD 18-JUN-1998.
 PF 08-DEC-1997; 97WO-US23102.
 XX 09-DEC-1996; 96US-0761902.
 PR (GUIL-) GUILFORD PHARM INC.
 PA Hamilton GS, Steiner JP, Wei L;
 PI WPI; 1998-348444/30.
 DR Effecting neuronal activity in mammals - by administering tetra-
 PT and penta- peptide inhibitors of cyclophilin and rotamase enzyme,
 PT useful in treatment of neuronal damage or degeneration disorders
 XX
 PS Claim 11; Page 40; 70pp; English.
 CC The invention relates to a method of effecting a neuronal activity. It
 CC comprises administering a neurotrophic compound with an affinity for a
 CC cyclophilin type immunophilin. The immunophilin shows peptidyl-prolyl
 CC isomerase (rotamase) activity. The neurotrophic compound achieves the
 CC stimulation of damaged neurons, promotion of neuronal regeneration or
 CC prevention of neurodegeneration, and treatment of neurological disorder.
 CC The neurotrophic compounds are potent peptidyl-proline isomerase
 CC (rotamase) inhibitors. They are of use in disorders which include
 CC peripheral neuropathy caused by physical injury or disease state, i.e.
 CC physical injury to the brain or spinal cord, stroke, or neurological
 CC disorder leading to neurodegeneration, notably Alzheimer's and
 CC Parkinson's diseases, or amyotrophic lateral sclerosis. The neurotrophic
 CC compounds avoid the side effects of immunosuppressant drugs including
 CC nephrotoxicity, impaired glomerular filtration, interstitial fibrosis,
 CC involuntary tremor, headaches, and hypertension. They are also free from
 CC the difficulties in delivery and bioavailability of large molecular
 CC weight proteins. The present sequence represents a specifically claimed
 CC neurotrophic compound.

XX SQ Sequence 5 AA;
 Query Match 26.7%; Score 4; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPFF 14
 Db 2 PPFF 5
 |||||

RESULT 30
 ID AAG73397 standard; peptide; 5 AA.
 XX AAG73397;
 AC AAG73397;
 DT 10-AUG-2001 (first entry)
 DE Human gene 9-encoded secreted protein HETAM53, SEQ ID NO:168.
 XX
 KW Human; secreted protein; proliferative disorder; cancer; chromosome 4;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; attherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder; tumour;
 KW endocrine disorder; infection; wound healing; vulnery;
 KW cell culture; chemotaxis; food additive;
 KW binding partner identification.
 XX
 OS Homo sapiens.
 XX
 PN WO200134628-A1.
 PD 17-MAY-2001.
 PF 08-NOV-2000; 2000WO-US30653.
 XX 12-NOV-1999; 99US-0164735.
 PR 27-JUL-2000; 2000US-0221193.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Ruben SM, Komatoulis GA, Birse CE, Ni J, Moore PA;
 XX WPI; 2001-329066/34.
 DR N-PSDB; AAH32573.
 XX
 PT Nucleic acids encoding 35 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX
 PS Claim 11; Page 537; 604pp; English.
 CC AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted
 CC protein genes, and AAG73346-AAG73448 represent the proteins they encode.
 CC AAG73449-AAG73519 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 52 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders (e.g., schizophrenia, asthma,
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,

CC identifying a superstructure encompassing alternative beta-strand
 CC arrangements, representing the superstructure by an integer-linear
 CC programming mathematical model, with the model maximising the total
 CC hydrophobic contact energy, and then solving the model. The method can
 CC also apply energy modelling with a full atom force field potential to
 CC generate a constrained global optimisation problem, optionally applying a
 CC torsion angle dynamics algorithm and then solving the constrained global
 CC optimisation problem to determine the three-dimensional structure of the
 CC polypeptide. The method is useful for determining the tertiary structure
 CC of a polypeptide and is accurate and reliable. The sequences presented in
 CC ABU12237-ABU12295 are the pentapeptides of the chymotrypsin inhibitor,
 CC 3C12, which were used to predict the alpha-helical regions in an example
 CC of the method of the invention.

XX Sequence 5 AA;

Query Match 26.7%; Score 4; DB 24; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9
 Db 2 VLPV 5
 |||||

RESULT 33

ABU12267
 ID ABU12267 standard; Peptide; 5 AA.

XX AC ABU12267;

DT 18-FEB-2003 (first entry)

DE Chymotrypsin inhibitor 2, 3C12, alpha helix prediction pentapeptide #31.

KW ASTRO-FOLD; ab initio; alpha-helix; beta-sheet; disulphide bridge;
 KW atomistic modelling; low energy conformation; entropic energy;
 KW free energy; equilibrium probability; helical cluster; integer-linear;
 KW mathematical model; hydrophobic contact energy;
 KW atom force field potential; global optimisation; torsion angle;
 KW dynamic algorithm; three-dimensional structure; tertiary structure;
 KW chymotrypsin inhibitor; 3C12.

XX OS Hordeum vulgare.

XX FN WO200279872-A2.

XX PD 10-OCT-2002.

XX PF 19-FEB-2002; 2002WO-US04644.

XX PR 16-FEB-2001; 2001US-0788006.

XX PA (UYPR-) UNIV PRINCETON.

XX PI Floudas CA, Klepeis JL;

XX DR WPI; 2003-058449/05.

XX Determining helix regions, and beta sheets of polypeptide, involves
 PT partitioning peptide, atomistic modeling by selected force, generating
 PT ensemble low energy, and calculating free energies for each peptide -
 XX Example 1; Page 62; 147pp; English.

XX The invention discloses a ASTRO-FOLD approach for the ab initio
 CC prediction method for determining the existence and location of
 CC alpha-helix regions and arrangement of beta-sheets and disulphide bridges
 CC of a polypeptide. The method comprises defining the first segment of the
 CC amino acid sequence, performing atomistic modelling upon each segment,
 CC generating an ensemble of low energy conformations, determining the
 CC entropic and free energy for each segment and then ascertaining the
 CC equilibrium probabilities for helical clusters. The segments consist of

CC pentapeptides, with each further segment including a majority of the
 CC amino acid residues of the first segment, together with an additional
 CC amino acid residue(s), adjacent to the first amino acid sequence. The
 CC beta-sheets and disulphide bridges of a polypeptide are determined by
 CC identifying a superstructure encompassing alternative beta-strand
 CC arrangements, representing the superstructure by an integer-linear
 CC programming mathematical model, with the model maximising the total
 CC hydrophobic contact energy, and then solving the model. The method can
 CC also apply energy modelling with a full atom force field potential to
 CC generate a constrained global optimisation problem, optionally applying a
 CC torsion angle dynamics algorithm and then solving the constrained global
 CC optimisation problem to determine the three-dimensional structure of the
 CC polypeptide. The method is useful for determining the tertiary structure
 CC of a polypeptide and is accurate and reliable. The sequences presented in
 CC ABU12237-ABU12295 are the pentapeptides of the chymotrypsin inhibitor,
 CC 3C12, which were used to predict the alpha-helical regions in an example
 CC of the method of the invention.

XX Sequence 5 AA;

Query Match 26.7%; Score 4; DB 24; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9
 Db 1 VLPV 4
 |||||

RESULT 34

AAR95892
 ID AAR95892 standard; peptide; 6 AA.

XX AC AAR95892;

DT 18-NOV-1996 (first entry)

DE Angiotensin converting enzyme inhibitor #2.

KW Angiotensin converting enzyme; inhibitor; ACE; hypotensive; health food;
 KW animal milk; drug; proteinase; carboxypeptidase.

XX OS Synthetic.

XX PN JP08039994-A.

XX PD 16-APR-1996.

XX PF 28-APR-1995; 95JP-0105262.

XX PR 02-AUG-1994; 94JP-0181653.

XX PA (CALV) CALFIS SHOKUHIN KOGYO KK.

XX DR WPI; 1996-246958/25.

XX PT New ACE-inhibiting peptide derived from animal milk - useful as
 PT hypotensive drug or health food component

XX PS Claim 1; Page 6; 7pp; Japanese.

XX AAR95891 and AAR95892 represent angiotensin converting enzyme (ACE)
 CC inhibitors. These sequences have hypotensive activity, and can be used
 CC in drugs and health foods. These sequences are prepared by treating
 CC animal milk with a proteinase and then a carboxypeptidase. These
 CC peptides are highly safe, and can be easily prepared at low cost.

XX Sequence 6 AA;

Query Match 26.7%; Score 4; DB 17; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9
 Db 2 VLPV 5

RESULT 35

AAW04273
 ID AAW04273 standard; peptide; 7 AA.

XX AC AAW04273;
 XX DT 06-JUN-1997 (first entry)
 XX DE Milk derived anti-hypertensive peptide.
 XX KW Anti-hypertensive; fermentation; animal milk; Lactobacillus;
 XX KW microorganism; digestion; protease; reduction; blood pressure.
 XX OS Mammalian spp.
 XX PN EP737690-A2.
 XX PD 16-OCT-1996.
 XX PF 10-APR-1996; 96EP-0302522.
 XX PR 10-APR-1995; 95JP-0084247.
 XX PA (CALV) CALPIS FOOD IND CO LTD.
 XX PI Maeno M;
 XX DR WPI; 1996-457284/46.
 XX PT Antihypertensive compns. derived from milk - by fermentation or
 XX PT protease digestion
 XX PS Claim 1; Page 9; 10pp; English.

XX CC The present anti-hypertensive (AH) peptide was prepared by
 CC fermenting an animal milk starting material with a Lactobacillus
 CC microorganism, especially L. helveticus, L. delbrueckii subspecies
 CC bulgaricus or L. acidophilus, or digesting it with a protease at
 CC 20-50 degrees C for 3-30 hours, obtaining an eluent by
 CC ultrafiltration and then fractionating the eluent by reverse phase
 CC HPLC. An AH composition comprising the peptide is safe and reduces
 CC blood pressure at low oral doses, e.g. 0.2-10, preferably
 CC 1 mg/kg/day or 5-20 ml/kg/day when ingested as a yogurt. The change
 CC in the systolic blood pressure of spontaneously hypertensive rats
 CC treated intragastrically with 1 mg/kg of body weight of the present
 CC AH peptide was minus 24 +/- 7.8 mmHg.

XX SQ Sequence 7 AA;

Query Match 26.7%; Score 4; DB 17; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9
 Db 2 VLPV 5

RESULT 36

AAR95891
 ID AAR95891 standard; peptide; 7 AA.

XX AC AAR95891;
 XX DT 18-NOV-1996 (first entry)
 XX DE Angiotensin converting enzyme inhibitor #1.

XX KW Angiotensin converting enzyme; inhibitor; ACE; hypotensive; health food;
 XX KW animal milk; drug; proteinase; carboxypeptidase.

XX OS Synthetic.

XX PN JF08099994-A.
 XX PD 16-APR-1996.

XX PF 28-APR-1995; 95JP-0105262.
 XX PR 02-AUG-1994; 94JP-0181653.

XX PA (CALV) CALPIS SHOKUHIN KOGYO KK.
 XX DR WPI; 1996-245958/25.
 XX KW New ACE-inhibiting peptide derived from animal milk - useful as
 XX PT hypotensive drug or health food component

XX PS Claim 1; Page 6; 7pp; Japanese.
 XX CC AAR95891 and AAR95892 represent angiotensin converting enzyme (ACE)
 XX CC inhibitors. These sequences have hypotensive activity, and can be used
 XX CC in drugs and health foods. These sequences are prepared by treating
 XX CC animal milk with a proteinase and then a carboxypeptidase. These
 XX CC peptides are highly safe, and can be easily prepared at low cost.

XX SQ Sequence 7 AA;

Query Match 26.7%; Score 4; DB 17; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9
 Db 3 VLPV 6

RESULT 37

AAW59314
 ID AAW59314 standard; peptide; 7 AA.

XX AC AAW59314;
 XX DT 24-SEP-1998 (first entry)
 XX DE Non-polio enterovirus peptide fragment 38A.

XX KW Non-polio enterovirus; NPEV; enteroviral disease; aseptic meningitis;
 XX KW vaccination.
 XX OS Enterovirus sp.
 XX PN WO9814611-A2.
 XX PD 09-APR-1998.
 XX PF 01-OCT-1997; 97WO-US17734.
 XX PR 02-OCT-1996; 96US-0027353.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Kilpatrick D;
 XX DR WPI; 1998-240106/21.

XX PT Identifying non-polio enteroviruses - using primers which hybridise
 XX PT to sense and antisense strands that encode conserved non-polio
 XX PT enterovirus peptide sequences
 XX PS Claim 4; Page 23; 47pp; English.

XX The peptide sequences AAW59298-W59344 are amplified by primers to detect
 CC the presence of a non-polio enterovirus (NPEV) in a sample. The primers
 CC and assays are used to detect NPEVs in a sample, to serotype these
 CC viruses, to diagnose enteroviral diseases and medical conditions, and to
 CC correlate (or disprove a correlation between) specific symptoms or
 CC combinations of symptoms with the presence of a particular enterovirus.
 CC They can be used for diseases such as aseptic meningitis. The detection
 CC of NPEV infections and their correlation with medical conditions will
 CC make possible vaccines and methods of treatment.

XX SQ Sequence 7 AA;
 Query Match 26.7%; Score 4; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPVL 7
 DB 1 MPVL 4

RESULT 38
 AAY50072
 ID AAY50072 standard; peptide; 7 AA.
 XX AC AAY50072;
 XX DT 19-JAN-2000 (first entry)
 XX DE Cocksackievirus A VPI conserved epitope 38.
 XX KW Virus; epitope; target; degenerate; PCR; primer; amplification;
 KW VPI; nonstructural protein 2A; conserved; base analogue; inosine;
 KW predetermined nucleotide; diagnosis; enterovirus; poliovirus.
 XX OS Synthetic.
 OS Cocksackievirus.
 PN WO9953097-A2.
 PD 21-OCT-1999.
 XX PF 06-APR-1999; 99WO-US07513.
 XX PR 15-APR-1998; 98US-0081944.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Kilpatrick DR;
 XX WPI; 1999-620444/53.
 XX N-PSDB; AAZ30991.
 XX Designing degenerate polymerase chain reaction primers -
 XX Example 3; Page 18; 30pp; English.

XX This sequence represents a conserved Cocksackievirus A
 CC (serotype A9) VPI epitope. The invention relates to a novel
 CC method for designing degenerate PCR primers (AAZ30975-231000, AAZ32601-
 CC AAZ32611) for amplifying target polynucleotides. This method comprises
 CC identifying uniquely conserved amino acid sequences (e.g., this
 CC epitope) in target proteins; synthesizing degenerate polynucleotides
 CC encoding the conserved sequences; and substituting the synthesised
 CC polynucleotides with up to four predetermined nucleotides (e.g.,
 CC inosine) at degenerate nucleotide positions. The nucleic acids
 CC comprise no more than 7 degenerate positions, have no more
 CC than 2 adjacent predetermined nucleotides and the predetermined
 CC nucleotides are 3 bases away from the 3' end of the synthesised strand.
 CC The degenerate primers are useful for amplifying target polynucleotides
 CC by the polymerase chain reaction (PCR). The use of the method of
 CC designing degenerate primers useful for the detection of polioviruses

CC in clinical samples is described in US585477. The degenerate primers
 CC facilitate PCR amplification of unknown polynucleotides, where the amino
 CC acid sequence encoded is known. The primers also allow for the
 CC correlation of the subsequent molecular based diagnosis with a
 CC serologically derived diagnosis.

XX SQ Sequence 7 AA;
 Query Match 26.7%; Score 4; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPVL 7
 DB 1 MPVL 4

RESULT 39
 AAY16900
 ID AAY16900 standard; peptide; 7 AA.
 XX AC AAY16900;
 XX DT 20-JUL-1999 (first entry)
 XX DE Heat shock protein (hsp) binding peptide.
 XX KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;
 KW surface protein; tethering peptide; chaperone process; cytokine; cancer;
 KW neoplastic disease; infectious disease; bacterium; immune system; fungus;
 KW acquired immune deficiency; autoimmune disease.
 XX OS Synthetic.
 XX PN WO9922761-A1.
 XX PD 14-MAY-1999.
 XX PF 22-OCT-1998; 98WO-US22335.
 XX PR 31-OCT-1997; 97US-0961707.
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 XX Hartl U, Hoe MH, Houghton A, Mayhew M, Moroi Y;
 XX Overfelli O, Rothman JE;
 XX WPI; 1999-313177/26.
 XX Identifying peptides which bind heat shock proteins
 XX Examples; Page 20; 155pp; English.

XX The invention relates to conjugate peptides engineered to noncovalently
 CC bind to heat shock proteins (hsp). A method of identifying a hsp binding
 CC peptide comprises (a) contacting a phage display library having
 CC bacteriophage expressing, in a surface protein, inserted peptides with a
 CC hsp target and bound to a benzoinone ansamycin antibiotic (BAA), in a
 CC physiologic binding buffer; (b) isolating a phage binding to the hsp
 CC target; and (c) identifying the inserted peptide expressed. The peptides
 CC which bind to a hsp can be used as tethering peptides for a hsp which may
 CC serve as an accessory in a chaperone process and/or may comprise a
 CC cytokine. They can also be coupled to antigens to induce an immune
 CC response. Such compositions can be used for treating neoplastic disease,
 CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
 CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
 CC disease of the immune system, e.g. acquired immune deficiencies or
 CC autoimmune diseases.

XX SQ Sequence 7 AA;
 Query Match 26.7%; Score 4; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVL 7
| | | |
Db 4 MPVL 7

RESULT 40
AA936209
ID AAY96209 standard; Peptide; 7 AA.
AC AAY96209;
XX
DT 11-AUG-2000 (first entry)
XX
DE Arabidopsis AHAS small subunit F3 gene fragment N-terminal sequence.
XX
KW Herbicide-resistance; acetoxyhydroxy-acid synthase; AHAS;
KW acetolactate synthase; imidazolinone; sulfonyleurea;
KW triazopyrimidine sulfonamide; sulfamoylurea; enzyme;
KW pyrimidyl-oxy-benzoic acid; sulfonyleurea; transgenic plant;
KW branched-chain amino acid synthesis.
XX
OS Arabidopsis.
XX
PN WO200026330-A2.
XX
PD 11-MAY-2000.
XX
PF 28-OCT-1999; 99WO-US25452.
XX
PR 29-OCT-1998; 98US-0106239.
XX
PA (AMCY) AMERICAN CYANAMID CO.
XX
PI Kakefuda G, Costello C, Sun M, Fu W;
XX
DR WPI; 2000-365633/31.
XX
PT New polynucleotide encoding eukaryotic acetoxyhydroxy-acid synthase
PT small subunit protein for producing transgenic herbicide resistant
PT plants and identifying mutations affecting enzymatic activity of the
PT synthetase -
XX
PS Disclosure; Page 25; 57pp; English.
XX
CC Arabidopsis acetoxyhydroxy-acid synthase (AHAS) small subunit is needed
CC for branched-chain amino acid synthesis and so is essential for life.
CC AHAS is also known as acetolactate synthase. Inhibition of this enzyme
CC in plants would lead to plant death and therefore inhibitors would be
CC potential herbicides. Certain herbicides are known to inhibit AHASs:
CC imidazolinones, sulfonyleureas, triazopyrimidine sulfonamides,
CC pyrimidyl-oxy-benzoic acids, sulfamoylureas and sulfonyleureas.
CC Mutant AHAS may be resistant to these herbicides and may be used to
CC create herbicide resistant transgenic plants e.g. dicot and monocot crop
CC plants. A thrombin cleavage site was incorporated into an AHAS small
CC subunit gene. The AHAS small subunit gene fragments were cloned into
CC plasmid expression vectors, and were expressed as glutathione
CC transferase/ AHAS small subunit fusion proteins. The glutathione
CC transferase was then cleaved via the thrombin cleavage site. Cleavage
CC however modifies the N-terminal sequence of the AHAS small subunit gene
CC fragments, in that the glycine and serine residues of the cleavage site
CC are maintained on the AHAS protein. The present sequence details the
CC N-terminal sequence of one such AHAS small subunit gene fragment,
CC F3, which is a near full length AHAS small subunit gene, with the
CC modification due to cleavage.
XX
SQ Sequence 7 AA;

Query Match 26.7%; Score 4; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVL 7
| | | |
Db 4 MPVL 7

RESULT 42
ABG97087
ID ABG97087 standard; Peptide; 7 AA.
XX
AC ABG97087;

Qy 9 VEPF 12
| | | |
Db 3 VEPF 6

RESULT 41
AAU72042
ID AAU72042 standard; Peptide; 7 AA.
XX
AC AAU72042;
XX
DT 26-FEB-2002 (first entry)
XX
DE Melanoma antigen, javelin peptide #28.
XX
KW Melanoma antigen; MART-1; MAGE-1; gp100; cytostatic; immune response;
KW immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYE01; GM2;
KW tyrosinase related protein 1; tyrosinase related protein 2; vaccine;
KW javelin molecule; melanoma antigen recognised by T cells-1; human.
XX
OS Bacteriophage M13.
XX
PN WO200178655-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US12449.
XX
PR 17-APR-2000; 2000US-197462P.
XX
PA (HOUG/) HOUGHTON A.
PA (LIVL/) LIVINGSTON P.
PA (ALAW/) AL-AWQATI Q.
PA (MAYH/) MAYHEW M.
PA (HOEN/) HOE M.
XX
PI Houghton A, Livingston P, Al-awqati Q, Mayhew M, Hoe M;
XX
DR WPI; 2001-663092/76.
XX
PT Anti cancer vaccine for the treatment of melanoma comprises a heat
PT shock protein and a melanoma antigen i.e. tyrosinase -
XX
PS Disclosure; Page 16; 150pp; English.
XX
CC The invention relates to a method of induction of an immune response,
CC comprising administration of an immunotherapeutic composition, comprising
CC a heat shock protein, and a melanoma antigen, where the melanoma
CC antigen is selected from tyrosinase, tyrosinase related protein 1,
CC tyrosinase related protein 2, gp 100, MAGE antigens, BAGE antigens,
CC NYE01, MART antigens, GM2, antigenic portions and combinations of these.
CC The melanoma antigen is covalently bound to a javelin molecule, where the
CC melanoma antigen bound to the javelin molecule is non-covalently bound to
CC the heat shock protein. The composition is useful for inducing an immune
CC response for the treatment of melanoma. AAU71980-AAU72481 represent
CC melanoma antigen peptides of the invention.
XX
SQ Sequence 7 AA;

Query Match 26.7%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVL 7
| | | |
Db 4 MPVL 7

RESULT 42
ABG97087
ID ABG97087 standard; Peptide; 7 AA.
XX
AC ABG97087;

XX DT 16-DEC-2002 (first entry)
XX DE Human leukocyte antigen (HLA) B15 ligand #416.
XX KW Soluble human leukocyte antigen; HLA; sHLA; cell phar
XX KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
XX KW viral infection; cancer; autoimmune disease; vaccine development; MHC;
XX KW major histocompatibility complex; diagnostic development;
XX KW HLA class I polymorphism; HLA-B15 allotype; ligand.
XX OS Homo sapiens.
XX PN WO200262846-A2.
XX PD 15-AUG-2002.
XX PF 18-DEC-2001; 2001WO-US49744.
XX PR 18-DEC-2000; 2000US-256409P.
XX PR 18-DEC-2000; 2000US-256410P.
XX PR 10-OCT-2001; 2001US-0974366.
XX PA (HILD/) HILDEBRAND W H.
XX PA (PRIL/) PRILLIMAN K R.
XX PI Hildebrand WH, Prilliman KR;
XX DR WPI; 2002-698563/75.
XX PT Producing soluble human leukocyte antigen (HLA) in cell phar
XX PT for studies of peptide loading for characterizing human immune
XX PT responses involves using HLA allelic cDNA or genomic DNA as starting
XX PT material -
XX PS Disclosure; Page 184; 300pp; English.
XX CC The invention describes a method of producing soluble human leukocyte
XX CC antigen (HLA) molecules (sHLA) in cell phar involving amplifying HLA
XX CC allelic DNA by PCR using a locus specific primer to produce truncated a
XX CC PCR product (P), inserting P into mammalian expression vector;
XX CC electroporating the plasmid into a host cell; inoculating the cell phar
XX CC with the host cell such that cell phar produces sHLA. A multimeric HLA
XX CC complex (I) is useful for testing functionality of peptide ligands bound
XX CC by at least two soluble HLA molecules. (I) can be tested for its ability
XX CC to serve as ligands for cytotoxic T lymphocytes (CTL) and induce immune
XX CC responses in humans. (I) is useful for studying T cell responses to
XX CC pathological conditions such as viral infections and cancer, and for
XX CC modulating the human immune system to induce tolerance in autoimmune
XX CC diseases. The individual secreted major histocompatibility complex (MHC)
XX CC molecules produced are useful for studies of peptide loading (i.e., in
XX CC vaccine development) and to the development of diagnostics. With the
XX CC secreted MHC molecules, naturally loaded peptides can be eluted from the
XX CC MHC molecule and characterised. The secreted MHC molecules allow the
XX CC assessment of structural and functional impact of HLA class I
XX CC polymorphism. The molecules are also useful to generate ligands and hence
XX CC ligand maps from the peptide pools extracted from series of distinct yet
XX CC related class I HLA-B15 allotypes; compare the different ligand maps to
XX CC identify potentially shared elements; and characterise the elements
XX CC identified to positively or negatively validate the occurrence of
XX CC overlapping ligands. The truncated version of (MHC) can be produced in
XX CC mammalian or insect/bacterial cells such that milligram or greater
XX CC quantities of an individual class I or class II molecule can be obtained.
XX CC This sequence represents a HLA (human leukocyte antigen) peptide
XX CC ligand.
XX SQ Sequence 7 AA;
Query Match 26.7%; Score 4; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 12 PPFV 15
QY

DB 3 PPFV 6
RESULT 43
AAU80592
ID AAU80592 standard; peptide; 7 AA.
XX AC AAU80592;
XX DT 26-MAR-2002 (first entry)
XX DE Javelin peptide #22 for conjugation to multi-component viral particles.
XX KW Immunogenic complex; non-pathogenic multi-component viral particle;
XX KW Javelin; heat shock protein; humoral immunity; cellular immunity;
XX KW anti-viral immune response; viral infection; hepatitis; influenza;
XX KW mumps; HIV infection; human immunodeficiency virus; polio;
XX KW tick-borne encephalitis; ebola virus infection.
XX OS Synthetic.
XX PN WO200178772-A1.
XX PD 25-OCT-2001.
XX PF 17-APR-2001; 2001WO-US12568.
XX PR 17-APR-2000; 2000US-197462P.
XX PA (MOJA-) MOJAVE THERAPEUTICS INC.
XX PI Hoe M, Landsberger F;
XX DR WPI; 2002-049177/06.
XX PT New heat shock protein-based viral vaccines, useful for enhancing
XX PT anti-viral immune response in an organism, particularly as a vaccine
XX PT for preventing or ameliorating viral infections, e.g. hepatitis,
XX PT influenza or HIV infection -
XX PS Disclosure; Page 10; 75pp; English.
XX CC The present invention relates to the use of an immunogenic complex,
XX CC comprising a non-pathogenic multi-component viral particle covalently
XX CC linked to a Javelin molecule (preferably a peptide) that selectively
XX CC binds to a heat shock protein. The immunogenic complex is useful for
XX CC inducing both humoral and cellular immunity, especially for enhancing
XX CC the anti-viral immune response, in a human or non-human subject. The
XX CC immunogenic complex is particularly useful as a vaccine for preventing
XX CC HIV (human immunodeficiency virus) infection, polio, tick-borne
XX CC encephalitis or ebola virus infection. AAU80571-AAU80734 represent
XX CC Javelin peptides which may be covalently conjugated to multi-component
XX CC viral particles.
XX SQ Sequence 7 AA;
Query Match 26.7%; Score 4; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 MPVL 7
DB 4 MPVL 7
RESULT 44
AAR58331
ID AAR58331 standard; peptide; 8 AA.
XX AC AAR58331;
XX XX

DT 22-SEP-1994 (first entry)
 XX Hypotensive polypeptide.
 XX Hypotensive; antioxidant; calcium absorption; salt; food;
 XX pharmaceuticals; physiologically active agents.
 XX Lactobacillus helveticus.
 XX JP06041191-A.
 XX 15-FEB-1994.
 XX 03-MAR-1993; 93JP-0043047.
 XX 04-MAR-1992; 92JP-0047340.
 XX (CALV) CALPIS SHOKUHIN KOGYO KK.
 XX WPI; 1994-089332/11.
 XX New polypeptide - used in physiologically active agents having
 XX e.g. hypotensive antioxidant and calcium absorption promoting
 XX activity
 XX Claim 1-2; Page 8; 10pp; Japanese.
 XX Sequences (AA58319-341) are used in conjunction with
 XX physiologically active agents showing a property such as
 XX hypotensive activity, calcium absorption promoting activity and
 XX antioxidant activity. The peptides are non-toxic and can be
 XX used in physiologically active agents.
 XX SQ Sequence 8 AA;
 Query Match 26.7%; Score 4; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 VLPV 9
 DB 3 VLPV 6
 RESULT 45
 AAW05539
 ID AAW05539 standard; peptide; 8 AA.
 AC AAW05539;
 XX 17-JUN-1997 (first entry)
 DT Peptide fragment #1 of aminopeptidase of the invention.
 DE Aminopeptidase; aspergillus oryzae; enzyme; protein hydrolysate; gluten;
 KW protease; N-terminus.
 XX Aspergillus oryzae.
 XX WO9628542-A1.
 XX 19-SEP-1996.
 XX 15-MAR-1996; 96WO-DK00104.
 XX 16-MAR-1995; 95DK-000262.
 XX (NOVO) NOVO-NORDISK AS.
 XX Danbmann C, Halkier T, Kauppinen S, Ostergaard PR;
 PI Si JQ, Spendler T;
 XX WPI; 1996-464617/46.

XX Enzyme with aminopeptidase activity - used in bread or
 PT dough-improving compans., and to reduce the bitter taste of proteins
 PT or protein hydrolysates for foodstuffs, partic. cheese or cocoa
 XX Claim 7; Page 56; 75pp; English.
 XX AAW05538-W05543 represent fragments of the Aspergillus oryzae
 CC aminopeptidase (see AAW05589) of the invention. Aminopeptidases are
 CC capable of removing one or more amino terminal residues from
 CC polypeptides. The enzyme is used in a preparation to reduce the bitter
 CC taste of proteins or protein hydrolysates for foodstuffs, particularly
 CC cheese or cocoa, so improving their flavour. It is also useful in a bread
 CC or dough-improving composition, and in the preparation of baked products
 CC from a flour dough or frozen dough. The enzyme is also useful to improve
 CC dough stickiness, crumb structure or crust colour of a baked product. The
 CC enzyme preparation can also be used to clean contact lenses and in
 CC brewing. The enzyme does not degrade the network of the gluten normally
 CC seen when proteases are used in the preparation of baked products. Thus,
 XX the dough characteristics and crumb structure are unaffected.
 XX SQ Sequence 8 AA;
 Query Match 26.7%; Score 4; DB 17; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 VEPP 12
 DB 4 VEPP 7
 RESULT 46
 AAW36802
 ID AAW36802 standard; peptide; 8 AA.
 AC AAW36802;
 XX 20-APR-1998 (first entry)
 DT Synthetic peptide p2Ca.
 DE Immune response; modulation; regulation; T-cell receptor;
 KW immunoglobulin; selective; target.
 XX Synthetic.
 OS WO9735991-A1.
 XX 02-OCT-1997.
 XX 28-MAR-1997; 97WO-US04694.
 XX 28-MAR-1996; 96US-0014367.
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA O'Herrin S, Schneek JP;
 PI WPI; 1997-489652/45.
 XX New soluble recombinant divalent and multivalent proteins - used for
 PT modulating immune responses for treating e.g. transplant rejection,
 PT auto-immune disorders, tumours or viral infection
 XX Example 4; Page 38; 80pp; English.
 XX Peptides AAW36802-W36810 are used in a novel method which regulates the
 CC immune response and involves a soluble recombinant divalent or
 CC multivalent protein composition comprising the extracellular domains of
 CC a heterodimeric protein operatively linked to immunoglobulin heavy and
 CC light chain polypeptides. Peptide p2Ca is loaded into H-2 Ld on RMA-S Ld
 CC cells and used to assay the reactivity of the soluble divalent TCR

CC chimera 2C TCR/Ig. The protein compositions are capable of specifically
 CC binding target molecules and can selectively increase or decrease
 CC cellular activation, proliferation, anergy or deletion of specific
 CC T cell subsets. They can also be used for selectively inhibiting or
 CC decreasing an immune response. If the heterodimeric protein is a MHC
 CC class II molecule comprising an antigenic peptide, the protein
 CC compositions can be used for stimulating an antigen-specific T-cell
 CC response. If the protein is a T cell receptor (TCR) molecule it can be
 CC used for identifying and purifying an unknown peptide/MHC complex. The
 CC compositions can also be used for destroying viral-infected or tumour
 CC cells and for treating autoimmune diseases. The compositions have high
 CC affinity for their target molecules and allows selective immune
 CC modulation without compromising the general performance of the immune
 CC system.
 XX
 XX Sequence 8 AA;

Query Match 26.7%; Score 4; DB 18; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PPF 14
 Db 3 PPF 6

RESULT 47
 AAW59334
 ID AAW59334 standard; peptide; 8 AA.

XX AC AAW59334;

XX DT 24-SEP-1998 (first entry)

XX DE Non-polio enterovirus peptide fragment 73A.

XX KW Non-polio enterovirus; NPEV; enteroviral disease; aseptic meningitis;
 KW vaccination.

XX OS Enterovirus sp.

XX PN WO9814611-A2.

XX PD 09-APR-1998.

XX PF 01-OCT-1997; 97WO-US17734.

XX PR 02-OCT-1996; 96US-0027353.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kilpatrick D;

XX WPI; 1998-240106/21.

XX PT Identifying non-polio enteroviruses - using primers which hybridise
 XX to sense and antisense strands that encode conserved non-polio
 XX enterovirus peptide sequences

XX PS Claim 4; Page 23; 47pp; English.

XX CC The peptide sequences AAW59298-W59344 are amplified by primers to detect
 CC the presence of a non-polio enterovirus (NPEV) in a sample. The primers
 CC and assays are used to detect NPEVs in a sample, to serotype these
 CC viruses, to diagnose enteroviral diseases and medical conditions, and to
 CC correlate (or disprove a correlation between) specific symptoms or
 CC combinations of symptoms with the presence of a particular enterovirus.
 CC They can be used for diseases such as aseptic meningitis. The detection
 CC of NPEV infections and their correlation with medical conditions will
 CC make possible vaccines and methods of treatment.
 XX
 XX Sequence 8 AA;

Query Match 26.7%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 26.7%; Score 4; DB 19; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVL 7
 Db 3 MPVL 6

RESULT 48

AAW98148

ID AAW98148 standard; Peptide; 8 AA.

XX AC AAW98148;

XX DT 24-JAN-2002 (first entry)

XX DE Human peptide #1423 encoded by a SNP oligonucleotide.

XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.

XX OS Homo sapiens.

XX PN WO200147944-A2.

XX PD 05-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US35498.

XX PR 28-DEC-1999; 99US-0173419.

XX PR 27-DEC-2000; 2000US-0173419.

XX PA (CURA-) CURAGEN CORP.

XX PI Shinkets RA, Leach M;

XX WPI; 2001-465210/50.

XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 XX oncogenes and histones, useful for diagnosing and treating, e.g.
 XX cancer, autoimmune diseases and infections -

XX PS Disclosure; Page 3980; 4143pp; English.

XX CC The present invention relates to oligonucleotides (see AAL26793-AAJ34659)
 XX encoding polymorphic variants of proteins related to amylases, amyloid
 XX proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 XX polymerase, oncogenes, histones, kinases, colony stimulating factors,
 XX complement related proteins, cytochromes, kinesins, cytokines,
 XX interferons, interleukins, G-protein coupled receptors and thioesterases.
 XX The present sequence is a peptide encoded by one such oligonucleotide.
 XX The oligonucleotides and the peptides encoded by them may be used in the
 XX prevention, diagnosis and treatment of diseases associated with
 XX inappropriate expression of the proteins listed above. Disorders that may
 XX be prevented, diagnosed and/or treated include multifactorial diseases
 XX with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 XX arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 XX CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 XX brain, breast, colon and kidney, leukaemia), diseases of the nervous
 XX system and an infection of pathogenic organisms.

XX Sequence 8 AA;

Query Match 26.7%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY      7 LPVE 10
Db      ||||
        4 LPVE 7

RESULT 49
AAM98149
ID      AAM98149 standard; Peptide; 8 AA.
XX
AC
XX
XX
DT      24-JAN-2002 (first entry)
XX
DE      Human peptide #1424 encoded by a SNP oligonucleotide.
XX
KW      Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW      neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW      amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW      cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW      complement related protein; cytochrome; kinesin; cytokine; interferon;
KW      interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW      multifactorial disease; autoimmune disease; infection;
KW      nervous system disease.
XX
OS      Homo sapiens.
XX
PN      WO200147944-A2.
XX
PD      05-JUL-2001.
XX
PF      28-DEC-2000; 2000WO-US35498.
XX
PR      28-DEC-1999; 99US-0173419.
XX
PR      27-DEC-2000; 2000US-0173419.
XX
PA      (CURA-) CURAGEN CORP.
XX
PI      Shimkets RA, Leach M;
XX
DR      WPT; 2001-465210/50.
XX
PT      Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT      oncogenes and histones, useful for diagnosing and treating, e.g.
PT      cancer, autoimmune diseases and infections -
XX
PS      Disclosure; Page 3980; 4143pp; English.
XX
CC      The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC      encoding polymorphic variants of proteins related to amylases, amyloid
CC      proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC      polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC      complement related proteins, cytochromes, kinesins, cytokines,
CC      interferons, interleukins, G-protein coupled receptors and thioesterases.
CC      The present sequence is a peptide encoded by one such oligonucleotide.
CC      The oligonucleotides and the peptides encoded by them may be used in the
CC      prevention, diagnosis and treatment of diseases associated with
CC      inappropriate expression of the proteins listed above. Disorders that may
CC      be prevented, diagnosed and/or treated include multifactorial diseases
CC      with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC      arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC      and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC      brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC      system and an infection of pathogenic organisms.
XX
SQ      Sequence      8 AA;
        Query Match      26.7%; Score 4; DB 22; Length 8;
        Best Local Similarity 100.0%; Pred. No. 9.3e+05;
        Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

OY      7 LPVE 10
Db      ||||
        4 LPVE 7

RESULT 51
AAU05399
ID      AAU05399 standard; peptide; 8 AA.
XX
AC      AAU05399;
XX
XX
DT      24-OCT-2001 (first entry)

```

XX DE Peptide released from alphaKG after cleavage of peptide P1.
 XX KW Heat shock protein; hsp; CD8+ cytotoxic T lymphocyte; alphaKG;
 XX KW CTL; CD4+ T cell; AIDS; acquired immunodeficiency syndrome; murine;
 XX KW human immunodeficiency virus; HIV; pathogen; cancer;
 XX KW alpha-ketoglutaraldehyde dehydrogenase.
 XX OS Mus sp.
 XX PN WO200151081-A1.
 XX PD 19-JUL-2001.
 XX PF 01-DEC-2000; 2000WO-US32831.
 XX PR 14-JAN-2000; 2000US-0176143.
 XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX PI Huang Q; Richmond JFL, Cho BK, Palliser D, Chen J, Eisen HN;
 XX PI Young RA;
 XX DR WPI; 2001-451815/48.
 XX PT Inducing a CD8+ cytotoxic T lymphocyte immune response in an individual
 XX PT for treating diseases such as HIV involves administering a fusion
 XX PT molecule comprising a heat shock protein -
 XX PS Disclosure; Page 4; 59pp; English.
 XX CC The present sequence represents a naturally occurring murine peptide
 XX CC which is released from alpha-ketoglutaraldehyde dehydrogenase (alphaKG)
 XX CC upon cleavage of peptide P1 (AAU05397). The present sequence is described
 XX CC in an invention relating to a novel method of inducing a CD8+ cytotoxic
 XX CC T lymphocyte (CTL) response to a molecule in an individual by
 XX CC administering a fusion molecule joined to a hsp, or an adenosine
 XX CC triphosphate (ATP) binding domain of a hsp. The method is particularly
 XX CC useful in inducing a CD8+ CTL response in an individual deficient in
 XX CC CD4+ T cells e.g. for treating an AIDS acquired immunodeficiency
 XX CC syndrome patient carrying the human immunodeficiency virus (HIV). The
 XX CC method is also useful for treating diseases that are caused by or
 XX CC associated with intracellular pathogens, and for treating cancer.
 XX SQ Sequence 8 AA;
 Query Match 26.7%; Score 4; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 PFPF 14
 Db 3 PFPF 6
 RESULT 52
 ABG73074
 ID ABG73074 standard; peptide; 8 AA.
 AC ABG73074;
 XX ABG73074;
 DT 02-APR-2003 (first entry)
 DE MHC Class I peptide p2Ca.
 XX Antigen-specific T lymphocyte; MHC-antigen complex; MHC Class I peptide;
 KW major histocompatibility complex; tumour-specific killer T cell;
 KW virus-specific killer T cell; cytostatic; virucide; p2Ca.
 XX Synthetic.
 XX OS
 XX PN US2002151690-A1.
 XX PD

XX PD 17-OCT-2002.
 XX PF 05-NOV-1999; 99US-0434965.
 XX PR 12-AUG-1997; 97US-0909549.
 XX PA (LUKE/) LUXEMBURG A T.
 XX PA (JACK/) JACKSON M R.
 XX PA (PETE/) PETER P A.
 XX PI Luxembourg AT, Jackson MR, Peter PA;
 XX DR WPI; 2003-182532/18.
 XX PT Enriching antigen-specific T lymphocytes, for purifying or expanding in
 XX PT vitro tumour- or virus-specific killer T cells for cell therapy,
 XX PT comprises capture of the lymphocytes on a substrate coated with
 XX PT antigenic peptide-MHC complexes -
 XX PS Example 2; Page 5; 40pp; English.
 XX CC The invention relates to a method for enriching antigen-specific T
 XX CC lymphocytes, comprising contacting a heterogeneous population of
 XX CC antigen-specific T lymphocytes with a matrix comprising MHC-antigen
 XX CC complexes for a period of time sufficient to allow the antigen-specific T
 XX CC lymphocytes to interact with the matrix, and eluting the antigen-specific
 XX CC T lymphocytes from the matrix to provide an enriched population of
 XX CC antigen-specific T lymphocytes. The MHC-antigen complexes comprise one or
 XX CC more antigens. Also claimed is a matrix for capturing antigen-specific T
 XX CC lymphocytes, comprising a support having on its surface an immobilised
 XX CC Class I peptide and a predetermined amount of an antigen, or for
 XX CC capturing antigens, comprising a support having on its surface an
 XX CC immobilised empty Class I peptide which is capable of binding one or more
 XX CC antigens, and isolating antigen-specific T lymphocytes from a
 XX CC heterogeneous population of cells from a patient. The methods are useful
 XX CC for enriching antigen-specific T lymphocytes to purify and expand in
 XX CC vitro tumour- and virus-specific killer T cells for cell therapy. The
 XX CC methods are also useful for isolating or preparing a population of
 XX CC antigen-specific T lymphocytes from a patient for treatment of the
 XX CC patient's disease or condition. This sequence represents an MHC Class I
 XX CC peptide used in the method of the invention.
 XX SQ Sequence 8 AA;
 Query Match 26.7%; Score 4; DB 24; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 PFPF 14
 Db 3 PFPF 6
 RESULT 53
 AAU07056
 ID AAU07056 standard; peptide; 9 AA.
 AC AAU07056;
 XX AAU07056;
 DT 21-JAN-1997 (first entry)
 DE Synthetic peptide used in GalNac-transferase activity SPA.
 XX SPA; scintillation proximity assay; antigen; bead coating; capture;
 KW antibody; N-acetyl galactosamine transferase; GalNac transferase;
 KW activity; enzyme; O-linked glycosylation.
 XX Synthetic.
 XX OS
 XX PN WO9615258-A1.
 XX PD 23-MAY-1996.

XX PF 08-NOV-1995; 95WO-US13483.
 XX PR 16-NOV-1994; 94US-0340283.
 XX PA (UPJO) UPJOHN CO.
 XX PI Elhammer AP;
 XX DR WPI; 1996-268220/27.
 XX PT Scintillation proximity assay for N-acetyl-galactosaminyl activity
 PT - esp. for large scale screening of cpds. for their effect on enzyme
 PT activity
 XX PS Claim 14; Page 17; 29pp; English.
 XX AAW06985-W07180 are antigenic peptides derived from either the
 CC product of the human c-myc oncogene or the FLAG peptide (DYKDDPK).
 CC The peptides are useful for coating beads used in a scintillation
 CC proximity assay for N-acetylgalactosamine (GalNAc)-transferase (GNT)
 CC activity. The assay involves fewer steps than known assays and is
 CC quicker, producing excellent signal-to-noise ratios. The
 CC assay is capable of screening large numbers of cpds. for their
 CC ability to affect GNT activity and is thus useful for identifying
 CC inhibitors and promoters of glycosylation (in partic. O-linked
 CC glycosylation).
 XX SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 17; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLIP 8
 DB 1 PVLIP 4

RESULT 54
 AAW36803
 ID AAW36803 standard; peptide; 9 AA.
 XX AC AAW36803;
 XX DT 20-APR-1998 (first entry)
 XX DE Synthetic peptide QL9.
 XX KW Immune response; modulation; regulation; T-cell receptor;
 KW immunoglobulin; selective; target.
 XX OS Synthetic.
 XX PN WO9735991-A1.
 XX PD 02-OCT-1997.
 XX PP 28-MAR-1997; 97WO-US04694.
 XX PR 28-MAR-1996; 96US-0014367.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI O'Herrin S, Schneck JP;
 XX DR WPI; 1997-489652/45.
 XX PT New soluble recombinant divalent and multivalent proteins - used for
 PT modulating immune responses for treating e.g. transplant rejection,
 PT auto-immune disorders, tumours or viral infection
 XX PS Example 4; Page 38; 80pp; English.

XX Peptides AAW36802-W36810 are used in a novel method which regulates the
 CC immune response and involves a soluble recombinant divalent or
 CC multivalent protein composition comprising the extracellular domains of
 CC a heterodimeric protein operatively linked to immunoglobulin heavy and
 CC light chain polypeptides. Peptide Q99 is loaded into H-2 Ld on RMA-S Ld
 CC cells and used to assay the reactivity of the soluble divalent ICR
 CC chimera 2C TCR/1g. The protein compositions are capable of specifically
 CC binding target molecules and can selectively increase or decrease
 CC cellular activation, proliferation, anergy, or deletion of specific
 CC T cell subsets. They can also be used for selectively inhibiting or
 CC decreasing an immune response. If the heterodimeric protein is a MHC
 CC class II molecule comprising an antigenic peptide, the protein
 CC compositions can be used for stimulating an antigen-specific T-cell
 CC response. If the protein is a T cell receptor (TCR) molecule it can be
 CC used for identifying and purifying an unknown peptide/MHC complex. The
 CC compositions can also be used for destroying viral-infected or tumour
 CC cells and for treating autoimmune diseases. The compositions have high
 CC affinity for their target molecules and allows selective immune
 CC modulation without compromising the general performance of the immune
 CC system.
 XX SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 18; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPPF 14
 DB 4 PPPF 7

RESULT 55
 AAW36804
 ID AAW36804 standard; peptide; 9 AA.

XX AC AAW36804;
 XX DT 20-APR-1998 (first entry)
 XX DE Synthetic peptide SL9.
 XX KW Immune response; modulation; regulation; T-cell receptor;
 KW immunoglobulin; selective; target.
 XX OS Synthetic.
 XX PN WO9735991-A1.
 XX PD 02-OCT-1997.
 XX PP 28-MAR-1997; 97WO-US04694.
 XX PR 28-MAR-1996; 96US-0014367.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI O'Herrin S, Schneck JP;
 XX DR WPI; 1997-489652/45.
 XX PT New soluble recombinant divalent and multivalent proteins - used for
 PT modulating immune responses for treating e.g. transplant rejection,
 PT auto-immune disorders, tumours or viral infection
 XX PS Example 4; Page 38; 80pp; English.

XX Peptides AAW36802-W36810 are used in a novel method which regulates the
 CC immune response and involves a soluble recombinant divalent or
 CC multivalent protein composition comprising the extracellular domains of
 CC a heterodimeric protein operatively linked to immunoglobulin heavy and
 CC light chain polypeptides. Peptide S99 is loaded into H-2 Ld on RMA-S Ld

CC cells and used to assay the reactivity of the soluble divalent TCR
 CC chimera 2C TCR/Ig. The protein compositions are capable of specifically
 CC binding target molecules and can selectively increase or decrease
 CC cellular activation, proliferation, energy, or deletion of specific
 CC T cell subsets. They can also be used for selectively inhibiting or
 CC decreasing an immune response. If the heterodimeric protein is a MHC
 CC class II molecule comprising an antigenic peptide, the protein
 CC compositions can be used for stimulating an antigen-specific T-cell
 CC response. If the protein is a T cell receptor (TCR) molecule it can be
 CC used for identifying and purifying an unknown peptide/MHC complex. The
 CC compositions can also be used for destroying viral-infected or tumour
 CC cells and for treating autoimmune diseases. The compositions have high
 CC affinity for their target molecules and allows selective immune
 CC modulation without compromising the general performance of the immune
 CC system.

XX
 XX
 SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 18; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PFPF 14
 | | | |
 DB 3 PFPF 6

RESULT 56
 AAB47585
 ID AAB47585 standard; peptide; 9 AA.
 XX
 AC AAB47585;
 DT 13-DEC-2001 (first entry)
 XX
 XX Ag85 complex derived peptide #16.
 XX
 XX Antigen 85; CD8 T-cell; vaccine; mycobacterium; detection; epitope;
 KW lysis.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WC200170991-Al.
 XX
 PD 27-SEP-2001.
 XX
 XX 20-MAR-2001; 2001WO-GB01210.
 XX
 XX 20-MAR-2000; 2000GB-0006693.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 PA
 XX Klein MR;
 PI
 XX WPI; 2001-611506/70.
 XX
 XX Use of a polypeptide comprising CD8 T-cell groups derived from
 PT Mycobacterium tuberculosis antigen 85 in manufacture of a medicament
 PT for vaccinating prophylactically or therapeutically against
 PT mycobacterial infection -
 XX
 XX Disclosure; Fig 1; 56pp; English.

CC The sequences given in AAB47570-86 are polypeptides derived from M.
 CC tuberculosis antigen 85 which can be recognized by a CD8 T-cell and
 CC which may be used in the manufacture of agent for vaccinating
 CC prophylactically or therapeutically against infection by a
 CC mycobacterium by stimulating a CD8 T cell response.
 CC These polypeptides are useful for vaccinating a pre-selected host to
 CC stimulate a CD8 T cell response against a Mycobacterial infection. They
 CC are also useful for detecting in a population of T cells the presence or
 CC absence of CD8 T cells that recognize an epitope sequence, by contacting
 CC the population of cells comprising CD8 T-cells with the peptide in

CC question and detecting whether the CD8 T-cells recognize the peptide,
 CC by detecting the expression of a substance by the T cell which indicates
 CC that the T cell have recognized the peptide or by detecting lysis by T
 CC cells of cells that present the peptide on their surface, the detection
 CC of lysis indicating that the T cells have recognized the peptide.

XX
 SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LPVE 10
 | | | |
 DB 4 LPVE 7

RESULT 57
 AAM99364
 ID AAM99364 standard; Peptide; 9 AA.
 XX
 AC AAM99364;
 XX
 DT 07-DEC-2001 (first entry)
 XX
 XX Vaccine related MHC ligand peptide SEQ ID NO:467.
 XX
 XX Glutamic acid; glutamine; vaccine; major histocompatibility complex;
 KW MHC; immunomodulator; antiallergic; endocrine; neuroprotectant;
 KW virucidal; bactericidal; antiparasitic; fungicidal; cytostatic;
 KW medicine; pharmaceutical; immune disorder; immune deficiency;
 KW autoimmune; hypersensitivity; allergy; graft rejection; infection;
 KW hormonal disorder; central nervous system disease; cancer; melanoma;
 KW anti-melanoma vaccine; human immunodeficiency virus.
 XX
 OS Mus musculus.
 XX
 PN WO200170772-A2.
 XX
 PD 27-SEP-2001.
 XX
 XX 22-MAR-2001; 2001WO-FR00872.
 XX
 XX 23-MAR-2000; 2000FR-0003711.
 XX
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 XX Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;
 FI WPI; 2001-611470/70.
 DR
 XX Stabilized pharmaceutical containing N-terminal glutamic acid or
 PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
 PT with strong acid -
 XX
 XX Claim 9; Page 111; 149pp; French.

CC The present invention describes a pharmaceutical compound (I) that
 CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue
 CC in the form of an addition salt with a strong, physiologically
 CC acceptable acid (II), also described are: (a) a pharmaceutical
 CC composition containing at least one (I); (b) a vaccine containing at
 CC least one (I) where this is a major histocompatibility complex (MHC)
 CC ligand (Ia); (c) a method for in vitro diagnosis of diseases associated
 CC with the presence of (Ia); (d) a kit for method (c) that includes a (Ia);
 CC and (e) a process for preparing (I). (I) has immunomodulator, endocrine,
 CC antiallergic, neuroprotectant, virucidal, bactericidal, antiparasitic,
 CC fungicidal and cytostatic activities. (I) are useful, in human or
 CC veterinary medicine, in pharmaceutical compositions (for treating immune
 CC disorders, e.g. immune deficiency, autoimmune states, hypersensitivity,
 CC allergy, graft rejection, infection, hormonal disorders and central
 CC nervous system diseases), also, where (I) is a MHC ligand (Ia), in
 CC vaccines for treatment or prevention of: (i) viral, bacterial, parasitic

CC or fungal infections; or (ii) of cancers. A particular application is in
 CC anti-melanoma vaccines. (i) are also useful for in vitro diagnosis of
 CC diseases associated with interactions between MHC and (i), e.g. melanoma
 CC and human immunodeficiency virus infection. AAM9898 to AAM99592
 CC represent peptides which can be used in pharmaceutical compounds from
 CC the present invention.

XX Sequence 9 AA;
 CC Query Match 26.7%; Score 4; DB 22; Length 9;
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPF 14
 DB 4 PPF 7

RESULT 58
 AAB82787
 ID AAB82787 standard; Peptide; 9 AA.

XX AAB82787;
 AC
 XX 29-OCT-2001 (first entry)
 DT
 XX Epitope of mycobacterial antigen 85A.
 DE
 XX Mycobacterial antigen 85A; Ag85A; infection; vaccine; diagnosis;
 KW therapy.

XX Mycobacterium tuberculosis.

OS WO200158461-A1.

XX 16-AUG-2001.

PD 12-FEB-2001; 2001WO-GB00561.

XX 10-FEB-2000; 2000GB-0003082.

PR (GLAX) GLAXO GROUP LTD.

XX Dockrell HM, Smith SM, Brookes R;

PI WPI; 2001-536505/59.

XX Use of polypeptides comprising groups of mycobacterial antigen 85A
 CC protein and expression vectors comprising polynucleotides encoding the
 CC polypeptide for vaccination against Mycobacterium infection -

XX Disclosure; Page 5; 49pp; English.

XX The present sequence is that of an epitope peptide comprising amino
 CC acid residues 48-56 of Mycobacterium tuberculosis antigen 85A
 CC (Ag85A). Epitopes, including the present sequence, have been
 CC found in Ag85A which cause the generation of a strong CD8 T-cell
 CC response in humans. The CD8 T-cells which recognise the epitopes
 CC are able to lyse macrophages infected with live Mycobacterium
 CC tuberculosis. A polypeptide which comprises an epitope structure
 CC of Ag85A, or an expression vector comprising a polynucleotide
 CC encoding such a polypeptide, is used in the manufacture of a
 CC medicament for vaccinating prophylactically or therapeutically
 CC against infection by a mycobacterium stimulating a CD8 T-cell
 CC response. The polypeptide or expression vector may be within an
 CC antigen-presenting cell. A claimed vaccine composition comprises
 CC the polypeptide or expression vector and an adjuvant or delivery
 CC system capable of stimulating a CD8 T-cell response. Also claimed
 CC are methods of detecting in a population of T-cells the presence
 CC or absence of CD8 T-cells that recognise the epitope sequence, a
 CC method of diagnosing mycobacterial infection or of testing the
 CC effectiveness of a vaccination, and a method of treating a
 CC mycobacterium infection by administering T-cells capable of

CC recognising the epitope.

XX Sequence 9 AA;

CC Query Match 26.7%; Score 4; DB 22; Length 9;
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LEVE 10
 DB 2 LEVE 5

RESULT 59

AAE07191
 ID AAE07191 standard; peptide; 9 AA.

XX AAE07191;

AC AAE07191;
 XX 06-NOV-2001 (first entry)

DT Colostrinin peptide 7.

DE Colostrinin peptide 7.

XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;

XX antiviral.

XX Unidentified.

OS WO200155199-A1.

XX 02-AUG-2001.

PD 26-JAN-2001; 2001WO-GB00329.

XX 26-JAN-2000; 2000GB-0001825.

PR (REG-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of
 CC the immune system and the central nervous system comprises ten
 CC amino-terminal amino acid sequence derived from peptides present in
 CC Colostrinin -

XX Claim 1; Page 15; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC in persons dependent on stimulants. Colostrinin peptides are used to
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is colostrinin peptide 7 related to the invention.
 CC Colostrinin peptide 7 corresponds to position 182-200 of beta-caesin.

```
XX Sequence 9 AA;
SQ Query Match 26.7%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9
Db 4 VLPV 7

RESULT 60
AAB75912
ID AAB75912 standard; Peptide; 9 AA.
XX
AC AAB75912;
XX
DT 10-APR-2001 (first entry)
XX
DE Hepatitis B virus env HLA-A2 binding peptide.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
KW HLA binding peptide; immune response; glycoprotein; cytostatic;
KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;
KW human immunodeficiency virus; protozoacide; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
KW renal carcinoma; cervical carcinoma; lymphoma; malaria;
KW condyloma acuminatum.
XX
OS Hepatitis B virus.
XX
PN WO200100225-A1.
XX
PD 04-JAN-2001.
XX
PF 28-JUN-2000; 2000WO-US17842.
XX
PR 29-JUN-1999; 99US-0141422.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S;
XX
DR WPI; 2001-112389/12.
XX
PT Composition comprising human leukocyte antigen binding peptide which
PT comprises isolated, prepared epitope useful for treating viral
PT infections such as acquired immunodeficiency syndrome, and cancer -
XX
PS Claim 1; Page 43; 58pp; English.
XX
CC The present invention describes a composition (I) which comprises at
CC least one human leukocyte antigen (HLA) binding peptide comprising an
CC isolated, prepared epitope comprising one of 547 8-11 residue amino acid
CC sequences (SI), given in AAB75803 to AAB76349. (I) has cytostatic,
CC virucide, hepatotropic, antiinflammatory, anti-HIV (human
CC immunodeficiency virus) and protozoacide activities, which can be used
CC in vaccine production and is an inducer of cytotoxic T-cell response.
CC (I) is useful for inducing a cytotoxic T cell response against a
CC preselected antigen in a patient expressing a specific major
CC histocompatibility complex (MHC) class I allele, by contacting cytotoxic
CC T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to
CC treat and/or prevent viral infection and cancer such as prostate cancer,
CC hepatitis B, hepatitis C, human papilloma virus (HPV) infection,
CC cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal
CC carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
CC acuminatum.
XX
SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVLV 8
Db 1 PVLV 4

RESULT 61
AAB75913
ID AAB75913 standard; Peptide; 9 AA.
XX
AC AAB75913;
XX
DT 10-APR-2001 (first entry)
XX
DE Hepatitis B virus env HLA-A2 binding peptide.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
KW HLA binding peptide; immune response; glycoprotein; cytostatic;
KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;
KW human immunodeficiency virus; protozoacide; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
KW renal carcinoma; cervical carcinoma; lymphoma; malaria;
KW condyloma acuminatum.
XX
OS Hepatitis B virus.
XX
PN WO200100225-A1.
XX
PD 04-JAN-2001.
XX
PF 28-JUN-2000; 2000WO-US17842.
XX
PR 29-JUN-1999; 99US-0141422.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S;
XX
DR WPI; 2001-112389/12.
XX
PT Composition comprising human leukocyte antigen binding peptide which
PT comprises isolated, prepared epitope useful for treating viral
PT infections such as acquired immunodeficiency syndrome, and cancer -
XX
PS Claim 1; Page 43; 58pp; English.
XX
CC The present invention describes a composition (I) which comprises at
CC least one human leukocyte antigen (HLA) binding peptide comprising an
CC isolated, prepared epitope comprising one of 547 8-11 residue amino acid
CC sequences (SI), given in AAB75803 to AAB76349. (I) has cytostatic,
CC virucide, hepatotropic, antiinflammatory, anti-HIV (human
CC immunodeficiency virus) and protozoacide activities, which can be used
CC in vaccine production and is an inducer of cytotoxic T-cell response.
CC (I) is useful for inducing a cytotoxic T cell response against a
CC preselected antigen in a patient expressing a specific major
CC histocompatibility complex (MHC) class I allele, by contacting cytotoxic
CC T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to
CC treat and/or prevent viral infection and cancer such as prostate cancer,
CC hepatitis B, hepatitis C, human papilloma virus (HPV) infection,
CC cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal
CC carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
CC acuminatum.
XX
SQ Sequence 9 AA;
```


QY 5 PVLIP 8
 Db 1 PVLIP 4

RESULT 62
 AAU99719 ID AAU99719 standard; Peptide; 9 AA.
 XX AC AAU99719;
 XX DT 07-OCT-2002 (first entry)
 XX DE Mouse MHC Ld/beta2m specific peptide sequence.
 XX KW Mutant major histocompatibility complex class I chimeric protein; MHC;
 KW lymphocyte; T-cell receptor; tissue sample; biopsy material; pathogen;
 KW bodily fluid; T lymphocyte; neoplastic cell; tumour cell; MHC antigen;
 KW virus; protozoan; bacteria; fungi; nematode; immune response; activator;
 KW enhancer; T cell activator; mouse; recombinant yeast cell; Kb; OVA; Ld;
 KW beta2m; dEV8.
 XX OS Mus sp..
 XX PN WC200246399-A2.
 XX PD 13-JUN-2002.
 XX PF 10-DEC-2001; 2001WO-US47817.
 XX PR 08-DEC-2000; 2000US-254495P.
 XX PA (UNII) UNIV ILLINOIS FOUND.
 XX PI Krantz DM, Brophy S;
 XX DR WPI; 2002-527916/56.
 XX PT New isolated mutant major histocompatibility complex class I chimeric
 PT protein displayed on surfaces of recombinant yeast cells, has improved
 PT stability, and is useful for activating immune response -
 XX PS Disclosure; Page 7; 96pp; English.
 XX CC The present invention relates to a new mutant major histocompatibility
 CC complex (MHC) class I chimeric protein. The protein of the invention
 CC comprises a portion mediating binding to surfaces of recombinant yeast
 CC cells and a portion comprising peptide binding region of MHC class I
 CC protein, where the invention is improved in stability as compared with
 CC MHC class I chimeric protein which is not a mutant chimeric protein.
 CC The protein, further comprising a detectable label, is useful for
 CC detecting a lymphocyte having a T-cell receptor protein in a biological
 CC sample such as cells, tissue sample, biopsy material or bodily fluids.
 CC The method is useful for detecting a T lymphocyte that is specific for
 CC a neoplastic cell, a tumour cell, a virus-infected cell, a protozoan-
 CC infected cell, a bacterium-infected cell or a fungus-infected cell. The
 CC protein of the invention can be used to directly activate T cells, in
 CC order to identify/screen for peptide-MHC antigens. The protein is also
 CC useful in activating T cells that participate in the removal of target
 CC cells including neoplastic cells and cells infected with pathogenic
 CC agents including viruses, protozoans, bacteria, fungi or nematodes.
 CC The invention is improved in stability as compared with MHC class I
 CC protein which is not a mutant chimeric protein. The present amino acid
 CC sequence represents a mouse MHC peptide of the invention, as described
 CC above.
 XX SQ Sequence 9 AA;
 Query Match 26.7%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 BPFF 14
 Db 4 BPFF 7

RESULT 63
 ABP61737 ID ABP61737 standard; Peptide; 9 AA.
 XX AC ABP61737;
 XX DT 02-OCT-2002 (first entry)
 XX DE Human KRPI tryptic digest peptide #170.
 XX KW Human; tryptic digest peptide; KRPI; kidney response; KR; nephrotropic
 KW kidney response-associated protein isoform; gene therapy; renal failure;
 KW antitense therapy; kidney function; tubular nephritis; renal failure;
 KW nephron cell metabolic pathway modulation; glomerular necrosis;
 KW papillary necrosis.
 XX OS Homo sapiens.
 XX PN WC200254081-A2.
 XX PD 11-JUL-2002.
 XX PF 24-DEC-2001; 2001WO-GB05777.
 XX PR 29-DEC-2000; 2000US-260392P.
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX PI Holt GD, Kelly MD, Kennedy SJ, Moyses C;
 XX DR WPI; 2002-583637/62.
 XX PT Screening, diagnosis or prognosis of kidney response in subject, by
 PT detecting kidney response-associated features or kidney
 PT response-associated protein isoforms in body fluid or tissue from
 PT subject -
 XX PS Disclosure; Page 46; 169pp; English.
 XX CC The invention relates to a novel method for the screening, diagnosis or
 CC prognosis of kidney response (KR). The method of the invention has
 CC nephrotropic activity, and may have a use in gene therapy or antitense
 CC therapy. The method is useful for the screening, diagnosis or prognosis
 CC of KR in a subject, for determining the stage or severity of KR in a
 CC subject, for identifying a subject at risk of developing KR, or for
 CC monitoring the effect of therapy administered to a subject with KR. An
 CC alternative method of the invention is useful for screening agents that
 CC interact with one or more of the kidney response-associated protein
 CC isoforms (KRPIs). The kidney response includes alterations in kidney
 CC function, any phase of nephron cell metabolic pathway modulation,
 CC glomerular/proximal tubular nephritis, glomerular/papillary necrosis,
 CC acute and chronic renal failure, and end stage renal disease. The
 CC sequences shown in ABP61514-ABP61787 represent tryptic digest peptides of
 CC the KRPIs of the invention.
 XX SQ Sequence 9 AA;
 Query Match 26.7%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVE 10
 Db 2 LPVE 5

RESULT 64
 AAU98288

ID AAU98288 standard; peptide; 9 AA.
 XX AAU98288;
 AC
 DT 15-AUG-2002 (first entry)
 XX
 DE M. tuberculosis Ag85 derived immunodominant T cell epitope #15.
 XX
 KW Ag85; epitope; vaccine; tuberculosis; mycolyltransferase; HLA-A*02001;
 KW Mycobacterium tuberculosis; Mycobacterium leprae; Mycobacterium bovis;
 KW Mycobacterium ulcerans; Mycobacterium avium; antibacterial;
 KW MHC class I-restricted CD8+ T cell; human leukocyte antigen.
 XX
 OS Mycobacterium tuberculosis.
 XX
 XX Key Location/Qualifiers
 XX Region 2
 FT /note= "Amino acid contributing to the HLA-A*02001
 FT binding motif"
 FT 9
 FT Region
 FT /note= "Amino acid contributing to the HLA-A*02001
 FT binding motif"
 FT
 FT EP1211260-A1.
 XX
 XX 05-JUN-2002.
 XX
 XX 30-NOV-2000; 2000EP-0204268.
 XX
 XX 30-NOV-2000; 2000EP-0204268.
 XX
 XX (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
 XX
 XX Ottenhof THM, Geluk A;
 PI
 XX WPI; 2002-464923/50.
 DR
 XX
 XX Peptide of 8-11 amino acids derived from the Ag85 protein of
 PT mycobacterium induce proliferation of MHC class I-restricted CD8+ T
 PT cells and are useful to vaccinate against infection by mycobacterium
 XX
 XX Claim 1; Page 7; 20pp; English.
 XX
 CC The invention relates to peptide (P1) derived from an Ag85 protein of
 CC mycobacterium (which is associated with mycolyltransferase activity
 CC and is involved in cell wall synthesis), comprising 8-11 amino acids, and
 CC capable of inducing proliferation of MHC class I-restricted CD8+ T cells
 CC in vivo. Also included are (1) a peptide comprising P1 flanked by amino
 CC acids representing antigen processing sites; (2) a polypeptide comprising
 CC at least two of the peptides in (1); (3) a nucleic acid encoding one of
 CC the claimed peptides or polypeptides; (4) a vector comprising the above
 CC nucleic acid; (5) a host cell comprising the above nucleic acid or
 CC vector; and (6) detecting and/or enumerating CD8+ T cells against
 CC mycobacterium, comprising tetrameric complexes of MHC (major
 CC histocompatibility group) class I and one of the claimed peptides or
 CC polypeptides. The molecules of the invention are used to prepare a
 CC vaccine against mycobacterium (e.g. Mycobacterium tuberculosis,
 CC Mycobacterium leprae, Mycobacterium bovis, Mycobacterium ulcerans,
 CC Mycobacterium avium) and thus protect against diseases such as
 CC tuberculosis. The present sequence is an M. tuberculosis Ag85
 CC derived immunogenic peptide of the invention binding to HLA-A*02001
 CC (human leukocyte antigen).
 XX
 SQ Sequence 9 AA;
 Query Match 26.7%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 LPVE 10
 DB 2 LPVE 5

RESULT 65
 AAU94070
 ID AAU94070 standard; Peptide; 9 AA.
 XX
 AC AAU94070;
 DT 02-JUL-2002 (first entry)
 XX
 DE Human novel protein CatrP2E11 HLA binding peptide #3.
 XX
 KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CatrP2E11;
 KW calcium transport protein; cancer; prostate cancer; cytostatic;
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
 XX
 OS Homo sapiens.
 XX
 XX WO200214361-A2.
 XX
 XX 21-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-US25782.
 XX
 XX 17-AUG-2000; 2000US-226329P.
 XX
 XX (AGEN-) AGENSYS INC.
 XX
 XX Raitano AB, Challita-Bid PM, Faris M, Saffran DC, Afar DEH;
 PI Levin B, Hubert RS, Ge W, Jakobovits A;
 XX
 XX WPI; 2002-269179/31.
 DR
 XX
 XX Monitoring 83P2H3 gene products for monitoring the presence of cancer
 PT in a subject, comprises determining the status of 83P2H3 gene products
 PT in a tissue sample from the subject and comparing it to a normal sample
 PT
 XX
 XX Example 11; Page 164; 270pp; English.
 PS
 CC The invention relates to monitoring 83P2H3 (a calcium transport
 CC protein whose gene is located on chromosome 7q34) gene products in a
 CC biological sample from a patient who has or is suspected of having
 CC cancer (especially prostate cancer), comprises: (a) determining the
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from
 CC an individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3
 CC function or status, generating antibodies/immune response against
 CC 83P2H3 (or related, protein CatrP2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding
 CC peptides derived from the protein, delivering a cytotoxic agent to
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
 CC antibody, a recombinant protein comprising an antigen-binding region of
 CC the antibody, a non-human transgenic animal that produces the recombinant
 CC protein, a hybridoma that produces the recombinant protein, a single-
 CC chain monoclonal antibody that comprises the variable domains of the
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell, respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
 CC treating cancer and the vector is useful for treating a patient with a
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence

CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CaTrF2E11.
 XX
 SQ Sequence 9 AA;
 Query Match 26.7%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 DLEM 4
 |||||
 Db 1 DLEM 4
 |||||
 RESULT 66
 AAU94117
 ID AAU94117 standard; Peptide; 9 AA.
 XX
 AC AAU94117;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human novel protein CaTrF2E11 HLA binding peptide #50.
 XX
 KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
 KW calcium transport protein; cancer; prostate cancer; cytostatic;
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
 XX
 OS Homo sapiens.
 XX
 FN WO200214361-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-US25782.
 XX
 PR 17-AUG-2000; 2000US-226329P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Raitano AB, Challita-Bid PM, Faris M, Saffran DC, Afar DEH;
 PI Levin E, Hubert RS, Ge W, Jakobovits A;
 XX
 DR WPI; 2002-269179/31.
 XX
 Monitoring 83P2H3 gene products for monitoring the presence of cancer
 PT in a subject, comprises determining the status of 83P2H3 gene products
 PT in a tissue sample from the subject and comparing it to a normal sample
 PT -
 XX
 Example 11; Page 166; 270pp; English.
 CC
 The invention relates to monitoring 83P2H3 (a calcium transport
 CC protein whose gene is located on chromosome 7q34) gene products in a
 CC biological sample from a patient who has or is suspected of having
 CC cancer (especially prostate cancer), comprises: (a) determining the
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from
 CC an individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3
 CC function or status, generating antibodies/immune response against
 CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding
 CC peptides derived from the protein, delivering a cytotoxic agent to
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
 CC antibody, a recombinant protein comprising an antigen-binding region of
 CC the antibody, a non-human transgenic animal that produces the recombinant
 CC protein, a hybridoma that produces the recombinant protein, a single-
 CC chain monoclonal antibody that comprises the variable domains of the
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell, respectively. The method

CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
 CC treating cancer and the vector is useful for treating a patient with a
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CaTrF2E11.
 XX
 SQ Sequence 9 AA;
 Query Match 26.7%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 DLEM 4
 |||||
 Db 3 DLEM 6
 |||||
 RESULT 67
 AAU94489
 ID AAU94489 standard; Peptide; 9 AA.
 XX
 AC AAU94489;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human novel protein CaTrF2E11 HLA binding peptide #222.
 XX
 KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
 KW calcium transport protein; cancer; prostate cancer; cytostatic;
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
 XX
 OS Homo sapiens.
 XX
 FN WO200214361-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-US25782.
 XX
 PR 17-AUG-2000; 2000US-226329P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Raitano AB, Challita-Bid PM, Faris M, Saffran DC, Afar DEH;
 PI Levin E, Hubert RS, Ge W, Jakobovits A;
 XX
 DR WPI; 2002-269179/31.
 XX
 Monitoring 83P2H3 gene products for monitoring the presence of cancer
 PT in a subject, comprises determining the status of 83P2H3 gene products
 PT in a tissue sample from the subject and comparing it to a normal sample
 PT -
 XX
 Example 11; Page 179; 270pp; English.
 CC
 The invention relates to monitoring 83P2H3 (a calcium transport
 CC protein whose gene is located on chromosome 7q34) gene products in a
 CC biological sample from a patient who has or is suspected of having
 CC cancer (especially prostate cancer), comprises: (a) determining the
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from
 CC an individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3
 CC function or status, generating antibodies/immune response against

CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding
 CC peptides derived from the protein, delivering a cytotoxic agent to
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
 CC antibody, a recombinant protein comprising an antigen-binding region of
 CC the antibody, a non-human transgenic animal that produces the recombinant
 CC protein, a hybridoma that produces the recombinant protein, a single-
 CC chain monoclonal antibody that comprises the variable domains of the
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell, respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
 CC treating cancer and the vector is useful for treating a patient with a
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotype antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CaTrF2E11.

XX Sequence 9 AA;
 SQ

Query Match 26.7%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLEM 4
 Db 1 DLEM 4

RESULT 68

ID AAU94707 standard; Peptide; 9 AA.

AC AAU94707;

DT 02-JUL-2002 (first entry)

DE Human novel protein CaTrF2E11 HLA binding peptide #340.

KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
 KW calcium transport protein; cancer; prostate cancer; cytostatic;
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.

XX Homo sapiens.

XX WO200214361-A2.

XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-US25782.

XX 17-AUG-2000; 2000US-226329P.

XX (AGEN-) AGENSYS INC.

XX Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
 XX Levin E, Hubert RS, Ge W, Jakobovits A;
 XX WPI; 2002-269179/31.

XX Monitoring 83P2H3 gene products for monitoring the presence of cancer

PT in a subject, comprises determining the status of 83P2H3 gene products

PT in a tissue sample from the subject and comparing it to a normal sample
 PS Example 11; Page 187; 270pp; English.

XX The invention relates to monitoring 83P2H3 (a calcium transport
 CC protein whose gene is located on chromosome 7q34) gene products in a
 CC biological sample from a patient who has or is suspected of having the
 CC cancer (especially prostate cancer), comprises: (a) determining the
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from
 CC an individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3
 CC function or status, generating antibodies/immune response against
 CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding
 CC peptides derived from the protein, delivering a cytotoxic agent to
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
 CC antibody, a recombinant protein comprising an antigen-binding region of
 CC the antibody, a non-human transgenic animal that produces the recombinant
 CC protein, a hybridoma that produces the recombinant protein, a single-
 CC chain monoclonal antibody that comprises the variable domains of the
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell, respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
 CC treating cancer and the vector is useful for treating a patient with a
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotype antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CaTrF2E11.

XX Sequence 9 AA;

Query Match 26.7%; Score 4; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLEM 4

Db 1 DLEM 4

RESULT 69

ID AAU95042 standard; Peptide; 9 AA.

AC AAU95042;

DT 02-JUL-2002 (first entry)

DE Human novel protein CaTrF2E11 HLA binding peptide #475.

KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
 KW calcium transport protein; cancer; prostate cancer; cytostatic;
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.

XX Homo sapiens.

XX WO200214361-A2.

XX 21-FEB-2002.

XX Monitoring 83P2H3 gene products for monitoring the presence of cancer

PT in a subject, comprises determining the status of 83P2H3 gene products

PF 17-AUG-2001; 2001WO-US25782.
 XX
 PR 17-AUG-2000; 2000US-226329P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Raitano AB, Challita-Eid PM, Faris M, Safran DC, Afar DBH;
 PI Levin E, Hubert RS, Ge W, Jakobovits A;
 XX
 DR WPI; 2002-269179/31.
 XX
 XX Monitoring 83P2H3 gene products for monitoring the presence of cancer
 PT in a subject, comprises determining the status of 83P2H3 gene products
 PT in a tissue sample from the subject and comparing it to a normal sample
 PT
 XX
 PS Example 11; Page 201; 270pp; English.
 XX
 CC The invention relates to monitoring 83P2H3 (a calcium transport
 CC protein whose gene is located on chromosome 7q34) gene products in a
 CC biological sample from a patient who has or is suspected of having
 CC cancer (especially prostate cancer), comprises: (a) determining the
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from
 CC an individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3
 CC function or status, generating antibodies/immune response against
 CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding
 CC peptides derived from the protein, delivering a cytotoxic agent to
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3
 CC antibody, a recombinant protein comprising an antigen-binding region of
 CC the antibody, a non-human transgenic animal that produces the recombinant
 CC protein, a hybridoma that produces the recombinant protein, a single-
 CC chain monoclonal antibody that comprises the variable domains of the
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell, respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
 CC treating cancer and the vector is useful for treating a patient with a
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CaTrF2E11.
 XX
 SQ Sequence 9 AA;
 Query Match 26.7%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLEM 4
 DB 5 DLEM 8
 RESULT 70
 ABR10368
 ID ABR10368 standard; Peptide; 9 AA.
 XX
 AC ABR10368;
 XX
 DT 19-MAY-2003 (first entry)

XX Human cancer-related protein 154P2A8 HLA peptide #3.
 DE
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 XX 10-APR-2002; 2002WO-US11654.
 PF
 XX 10-APR-2001; 2001US-282739P.
 PR
 PR 10-APR-2001; 2001US-283112P.
 PR
 PR 25-APR-2001; 2001US-286630P.
 XX
 XX (AGEN-) AGENSYS INC.
 PA
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients
 XX
 PS Claim 13; Page 216; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 26.7%; Score 4; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 VLPV 9
 DB 4 VLPV 7
 RESULT 71
 ABR10399
 ID ABR10399 standard; Peptide; 9 AA.
 XX
 AC ABR10399;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 XX Human cancer-related protein 154P2A8 HLA peptide #34.
 DE
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX

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PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US11654.
XX
XX 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX Claim 13; Page 216; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
XX Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 6 VLPV 9
DB |||||
6 VLPV 9

RESULT 72
ABR10408
ID ABR10408 standard; Peptide; 9 AA.
AC ABR10408;
XX
XX 19-MAY-2003 (first entry)
XX
XX Human cancer-related protein 154P2A8 HLA peptide #43.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US11654.
XX
XX 10-APR-2001; 2001US-282739P.
XX
XX 10-APR-2001; 2001US-283112P.
XX
XX 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
XX Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX (AGEN-) AGENSYS INC.
XX

```

PS Claim 13; Page 216; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and

CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or

CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention.

XX SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9

Db 3 VLPV 6

RESULT 74

ABR10455

ID ABR10455 standard; Peptide; 9 AA.

XX AC ABR10455;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 154P2A8 HLA peptide #90.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;

XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WQ200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of

XX PT proteins and polynucleotides, useful for therapeutic, prognostic and

XX PT diagnostic reagents for eliciting cellular or humoral immune response

XX PT in cancer patients -

XX PS Claim 13; Page 216; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and

CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or

CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention.

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention.

XX SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9

Db 1 VLPV 4

RESULT 75

ABR10580

ID ABR10580 standard; Peptide; 9 AA.

XX AC ABR10580;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 154P2A8 HLA peptide #215.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;

XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WQ200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of

XX PT proteins and polynucleotides, useful for therapeutic, prognostic and

XX PT diagnostic reagents for eliciting cellular or humoral immune response

XX PT in cancer patients -

XX PS Claim 13; Page 218; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and

CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or

CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention.

XX SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9
| | |
Db 3 VLPV 6

Search completed: November 25, 2003, 18:15:45
Job time : 50.5904 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 : Search time 29.8404 Seconds
(without alignments)
92.715 Million cell updates/sec

Title: US-09-641-801-5

Perfect score: 15

Sequence: 1 DLEMPVLVPEFFPV 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 18443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

Published Applications AA.*
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2: /cgn2_6/ptodata/1/pubaa/PCT_NEW PUB.pdb.*
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5: /cgn2_6/ptodata/1/pubaa/US07_NEW PUB.pdb.*
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13: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pdb.*
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15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pdb.*
16: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pdb.*
17: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pdb.*
18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	15	US-10-281-652-5
2	5	33.3	18	15	US-10-281-652-22
3	4	26.7	5	11	US-09-788-006-138
4	4	26.7	5	11	US-09-788-006-140
5	4	26.7	7	9	US-09-997-900-11
6	4	26.7	7	12	US-10-052-578-170
7	4	26.7	7	12	US-10-022-066-506
8	4	26.7	7	12	US-10-053-520-170
9	4	26.7	7	12	US-10-118-708-2
10	4	26.7	7	12	US-10-053-498B-170
11	4	26.7	7	16	US-10-305-346-8
12	4	26.7	8	10	US-09-954-166-12
13	4	26.7	8	10	US-09-761-534A-3
14	4	26.7	8	10	US-09-434-965-2
15	4	26.7	8	12	US-10-266-463A-46

16	4	26.7	8	15	US-10-145-396-2	Sequence 2, Appli
17	4	26.7	8	15	US-10-046-801-25	Sequence 28, Appl
18	4	26.7	8	15	US-10-046-801-28	Sequence 26, Appl
19	4	26.7	8	15	US-10-046-801-33	Sequence 33, Appl
20	4	26.7	9	10	US-09-954-166-13	Sequence 13, Appl
21	4	26.7	9	10	US-09-954-166-14	Sequence 14, Appl
22	4	26.7	9	10	US-09-434-965-1	Sequence 1, Appli
23	4	26.7	9	10	US-09-434-965-3	Sequence 3, Appli
24	4	26.7	9	12	US-09-932-165-53	Sequence 53, Appl
25	4	26.7	9	12	US-09-932-165-100	Sequence 100, App
26	4	26.7	9	12	US-09-932-165-472	Sequence 472, App
27	4	26.7	9	12	US-09-932-165-690	Sequence 690, App
28	4	26.7	9	12	US-09-932-165-1025	Sequence 1025, Ap
29	4	26.7	9	12	US-10-266-463A-47	Sequence 47, Appl
30	4	26.7	9	12	US-10-062-109A-4	Sequence 4, Appli
31	4	26.7	9	12	US-10-062-109A-44	Sequence 44, Appl
32	4	26.7	9	12	US-10-239-313A-467	Sequence 467, App
33	4	26.7	9	12	US-10-005-480A-4	Sequence 4, Appli
34	4	26.7	9	12	US-10-005-480A-44	Sequence 44, Appl
35	4	26.7	9	14	US-10-093-200A-13	Sequence 13, Appl
36	4	26.7	9	15	US-10-015-535-4	Sequence 4, Appli
37	4	26.7	9	15	US-10-046-801-29	Sequence 29, Appl
38	4	26.7	9	15	US-10-093-248-13	Sequence 13, Appl
39	4	26.7	10	9	US-09-220-920-111	Sequence 111, App
40	4	26.7	10	12	US-09-932-165-154	Sequence 154, App
41	4	26.7	10	12	US-09-932-165-785	Sequence 785, App
42	4	26.7	10	12	US-10-062-109A-55	Sequence 55, Appl
43	4	26.7	10	12	US-10-062-109A-71	Sequence 71, Appl
44	4	26.7	10	12	US-10-005-480A-55	Sequence 55, Appl
45	4	26.7	10	12	US-10-005-480A-71	Sequence 71, Appl
46	4	26.7	10	15	US-10-062-710-199	Sequence 199, App
47	4	26.7	11	9	US-09-780-662A-14	Sequence 14, Appl
48	4	26.7	11	12	US-10-182-303-14	Sequence 14, Appl
49	4	26.7	11	15	US-10-082-710-173	Sequence 173, App
50	4	26.7	12	11	US-09-934-385-146	Sequence 146, App
51	4	26.7	12	11	US-09-934-385-319	Sequence 319, App
52	4	26.7	12	12	US-10-214-867A-17	Sequence 17, Appl
53	4	26.7	12	12	US-10-118-708-5	Sequence 5, Appli
54	4	26.7	12	15	US-10-057-789-142	Sequence 142, App
55	4	26.7	12	15	US-10-212-628-142	Sequence 142, App
56	4	26.7	12	15	US-10-254-446A-157	Sequence 157, App
57	4	26.7	13	9	US-09-113-924-14	Sequence 14, Appl
58	4	26.7	13	10	US-09-897-107-72	Sequence 72, Appl
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60	4	26.7	13	15	US-10-116-846B-5	Sequence 5, Appli
61	4	26.7	13	15	US-10-116-846B-45	Sequence 45, Appl
62	4	26.7	14	9	US-09-113-924-13	Sequence 13, Appl
63	4	26.7	15	9	US-09-934-385-146	Sequence 9, Appli
64	4	26.7	15	9	US-09-934-385-319	Sequence 9, Appli
65	4	26.7	15	9	US-09-947-770-15	Sequence 15, Appl
66	4	26.7	15	10	US-09-813-333-18	Sequence 18, Appl
67	4	26.7	15	10	US-09-953-510-37	Sequence 37, Appl
68	4	26.7	15	10	US-09-953-510-38	Sequence 38, Appl
69	4	26.7	15	11	US-09-880-505-22	Sequence 22, Appl
70	4	26.7	15	11	US-09-880-505-24	Sequence 24, Appl
71	4	26.7	15	12	US-10-349-023-18	Sequence 18, Appl
72	4	26.7	15	12	US-10-147-255-37	Sequence 37, Appl
73	4	26.7	15	12	US-10-147-255-38	Sequence 38, Appl
74	4	26.7	15	12	US-10-161-791-312	Sequence 312, App
75	4	26.7	15	14	US-10-044-703-18	Sequence 18, Appl
76	4	26.7	15	14	US-10-051-643-22	Sequence 22, Appl
77	4	26.7	15	14	US-10-051-643-24	Sequence 24, Appl
78	4	26.7	15	15	US-10-100-957A-104	Sequence 104, App
79	4	26.7	15	15	US-10-186-867-36	Sequence 36, Appl
80	4	26.7	16	11	US-09-880-748-2228	Sequence 2228, Ap
81	4	26.7	16	11	US-09-880-748-2334	Sequence 2334, Ap
82	4	26.7	16	12	US-10-094-407A-36	Sequence 36, Appl
83	4	26.7	16	12	US-10-161-791-200	Sequence 200, App
84	4	26.7	16	12	US-10-161-791-202	Sequence 202, App
85	4	26.7	16	12	US-10-161-791-406	Sequence 406, App
86	4	26.7	16	15	US-10-043-487-442	Sequence 442, App
87	4	26.7	16	15	US-10-034-934-141	Sequence 141, App
88	4	26.7	16	15	US-10-211-088-27	Sequence 27, Appl

89 4 26.7 16 15 US-10-028-075B-4 Sequence 4, Appli
 90 4 26.7 16 15 US-10-029-206A-4 Sequence 4, Appli
 91 4 26.7 17 9 US-09-864-761-34508 Sequence 34508, A
 92 4 26.7 17 11 US-09-996-069-30 Sequence 30, Appl
 93 4 26.7 17 11 US-09-996-069-31 Sequence 31, Appl
 94 4 26.7 17 12 US-10-161-791-362 Sequence 362, App
 95 4 26.7 17 15 US-10-091-724-39 Sequence 39, Appl
 96 4 26.7 17 15 US-10-225-567A-1000 Sequence 1000, Ap
 97 4 26.7 18 9 US-09-864-761-42763 Sequence 42763, A
 98 4 26.7 19 11 US-09-880-505-23 Sequence 23, Appl
 99 4 26.7 19 12 US-10-348-190-9 Sequence 9, Appli
 100 4 26.7 19 14 US-10-051-643-23 Sequence 23, Appl

ALIGNMENTS

RESULT 1
 US-10-281-652-5
 ; Sequence 5, Application US/10281652
 ; Publication No. US20030091606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; FILE REFERENCE: 265.00220101
 ; CURRENT APPLICATION NUMBER: US/10/281.652
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: US/09/641.803
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide
 US-10-281-652-5

Query Match 100.0%; Score 15; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.2e-09; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLPVPPFPV 15
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 Db 1 DLEMPVLPVPPFPV 15

RESULT 2
 US-10-281-652-22
 ; Sequence 22, Application US/10281652
 ; Publication No. US20030091606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; FILE REFERENCE: 265.00220101
 ; CURRENT APPLICATION NUMBER: US/10/281.652
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: US/09/641.803
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide
 US-10-281-652-22

Query Match 33.3%; Score 5; DB 15; Length 18;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEPFF 12
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 Db 10 PVEPFF 14

RESULT 3
 US-09-788-006-138
 ; Sequence 138, Application US/09788006
 ; Publication No. US20030036093A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Floudas, Christopher A.
 ; APPLICANT: Klepeis, John L.
 ; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
 ; FILE REFERENCE: PU-0007
 ; CURRENT APPLICATION NUMBER: US/09/788,006
 ; CURRENT FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 138
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 ; TYPE: PRT
 ; ORGANISM: Hordeum vulgare
 US-09-788-006-138

Query Match 26.7%; Score 4; DB 11; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
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QY 6 VLPV 9
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 Db 2 VLPV 5

RESULT 4
 US-09-788-006-140
 ; Sequence 140, Application US/09788006
 ; Publication No. US20030036093A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Floudas, Christopher A.
 ; APPLICANT: Klepeis, John L.
 ; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
 ; FILE REFERENCE: PU-0007
 ; CURRENT APPLICATION NUMBER: US/09/788,006
 ; CURRENT FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 140
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Hordeum vulgare
 US-09-788-006-140

Query Match 26.7%; Score 4; DB 11; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
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Db 1 VLPV 4

RESULT 5

US-09-997-900-11
; Sequence 11, Application US/09997900
; Patent No. US20020053098A1
; GENERAL INFORMATION:
; APPLICANT: Kakefuda, Genichi
; APPLICANT: Costello, Colleen
; APPLICANT: Sun, Ming
; APPLICANT: Hu, Weiming
; TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
; FILE REFERENCE: 043753/241148 (5849-20A)
; CURRENT APPLICATION NUMBER: US/09/997,900
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/106,239
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 09/426,568
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(7)
; OTHER INFORMATION: N-terminal of AHAS small subunit peptide from
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Thrombin cleavage site
US-09-997-900-11

Query Match 26.7%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
Db 3 VEPF 6

RESULT 6

US-10-052-578-170
; Sequence 170, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; PRIOR FILING DATE: 2002-01-17
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 170
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage

US-10-052-578-170

Query Match 26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPVL 7
Db 4 MPVL 7

RESULT 7

US-10-022-066-506
; Sequence 506, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: FRILLMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 506
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-022-066-506

Query Match 26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PEPV 15
Db 3 PEPV 6

RESULT 8

US-10-053-520-170
; Sequence 170, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 170

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; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-520-170

Query Match      26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 MPVL 7
Db      4 MPVL 7

RESULT 9
US-10-118-708-2
; Sequence 2, Application US/10118708
; Publication No. US20030165991A1
; GENERAL INFORMATION:
; APPLICANT: Hart, L P
; APPLICANT: Pestka, James J
; APPLICANT: Yuan, Qiaoping
; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
; FILE REFERENCE: MSU 4.1-447
; CURRENT APPLICATION NUMBER: US/10/118,708
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/146,643
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DONPEP.2
; OTHER INFORMATION: peptide mimotope of deoxynivalenol
US-10-118-708-2

Query Match      26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 PPPP 14
Db      4 PPPP 7

RESULT 10
US-10-053-498B-170
; Sequence 170, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouefelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 170

; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-498B-170

Query Match      26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 MPVL 7
Db      4 MPVL 7

RESULT 11
US-10-305-346-8
; Sequence 8, Application US/10305346
; Publication No. US20030130195A1
; GENERAL INFORMATION:
; APPLICANT: AMIOT, Jean
; TITLE OF INVENTION: ENZYMATIC HYDROLYSATE OF MILK PROTEINS
; FILE REFERENCE: 6013-57"US"-1
; CURRENT APPLICATION NUMBER: US/10/305,346
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide from enzymatic hydrolyseate of milk proteins
US-10-305-346-8

Query Match      26.7%; Score 4; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 VLPV 9
Db      1 VLPV 4

RESULT 12
US-09-954-166-12
; Sequence 12, Application US/09954166
; Patent No. US2002012731A1
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; Heterodimeric Analogs of Proteins
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/954,166
; FILING DATE: 18-Sep-2001
; CLASSIFICATION: <Unknown>
```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/828,712
 FILING DATE: 28-MAR-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Kagan, Sarah A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 01107.73713
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)508-9100
 TELEFAX: (202)508-9299
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: peptide p2Ca
 SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Query Match 26.7%; Score 4; DB 10; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 11 PFPF 14
 Db 3 PFPF 6

RESULT 13
 US-09-761-534A-3
 Sequence 3, Application US/09761534A
 Patent No. US20020146426A1
 GENERAL INFORMATION:
 APPLICANT: Huang, Qian
 APPLICANT: Richmond, Joan F.L.
 APPLICANT: Cho, Bryan K.
 APPLICANT: Palliser, Deborah
 APPLICANT: Chen, Jianzhu
 APPLICANT: Eisen, Herman N.
 APPLICANT: Young, Richard A.
 TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
 TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
 TITLE OF INVENTION: CD4+T Cell-Independent
 FILE REFERENCE: 0399.2006-003
 CURRENT APPLICATION NUMBER: US/09/761,534A
 CURRENT FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: PCT/US00/32831
 PRIOR FILING DATE: 2000-12-01
 PRIOR APPLICATION NUMBER: US 60/176,143
 PRIOR FILING DATE: 2000-01-14
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 3
 LENGTH: 8
 TYPE: PPT
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Alpha KG Peptide
 US-09-761-534A-3

Query Match 26.7%; Score 4; DB 10; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 11 PFPF 14
 Db 3 PFPF 6

RESULT 14
 US-09-434-965-2
 Sequence 2, Application US/09434965
 Patent No. US20020151690A1
 GENERAL INFORMATION:
 APPLICANT: Luxembourg, Alain T.
 APPLICANT: Jackson, Michael R.
 APPLICANT: Peterson, Per A.
 TITLE OF INVENTION: PURIFICATION OF ANTIGEN-SPECIFIC T CELLS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Johnson & Johnson
 STREET: One Johnson & Johnson Plaza
 CITY: New Brunswick
 STATE: NJ
 COUNTRY: USA
 ZIP: 08933-7003
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/434,965
 FILING DATE: 05-No. US20020151690A1-1999
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Wallen, John W.
 REGISTRATION NUMBER: 35,403
 REFERENCE/DOCKET NUMBER: ORT-841
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 732-524-2806
 TELEFAX: 732-524-2808
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ANTI-SENSE: NO
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-434-965-2

Query Match 26.7%; Score 4; DB 10; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 11 PFPF 14
 Db 3 PFPF 6

RESULT 15
 US-10-266-463A-46
 Sequence 46, Application US/10266463A
 Publication No. US20030138946A1
 GENERAL INFORMATION:
 APPLICANT: CAI, Zeling
 APPLICANT: SPRENT, Jonathan
 APPLICANT: BRUNMARK, Anders
 APPLICANT: JACKSON, Michael
 APPLICANT: PETERSON, Per A.
 APPLICANT: LUXEMBOURG, Alain
 APPLICANT: LETURCO, Didier Jean
 APPLICANT: MORIARTY, Ann M.
 TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
 TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS
 FILE REFERENCE: TSRI 471.1 Div. 1
 CURRENT APPLICATION NUMBER: US/10/266,463A
 CURRENT FILING DATE: 2002-10-08
 PRIOR APPLICATION NUMBER: US 08/913,612
 PRIOR FILING DATE: 1997-09-08

Qy 11 PFPF 14
Db 3 PFPF 6

RESULT 20

US-09-954-166-13
; Sequence 13, Application US/09954166
; Patent No. US20020127231A1
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; Heterodimeric Analogs of Proteins
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/954,166
; FILING DATE: 18-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,712
; FILING DATE: 28-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide QL9
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-954-166-13

Query Match 26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 11 PFPF 14
Db 4 PFPF 7

RESULT 21

US-09-954-166-14
; Sequence 14, Application US/09954166
; Patent No. US20020127231A1
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; Heterodimeric Analogs of Proteins

; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/954,166
; FILING DATE: 18-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,712
; FILING DATE: 28-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide SL9
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-954-166-14

Query Match 26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 11 PFPF 14
Db 3 PFPF 6

RESULT 22

US-09-434-965-1
; Sequence 1, Application US/09434965
; Patent No. US20020151690A1
; GENERAL INFORMATION:
; APPLICANT: Luxembourg, Alain T.
; Jackson, Michael R.
; Peterson, Per A.
; TITLE OF INVENTION: PURIFICATION OF ANTIGEN-SPECIFIC T CELLS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/434,965

;; FILING DATE: 05-NO. US20020151690A1-1999
;; CLASSIFICATION: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wallen, John W.
;; REGISTRATION NUMBER: 35,403
;; REFERENCE/DOCKET NUMBER: ORT-841
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 732-524-2806
;; TELEFAX: 732-524-2808
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; ANTI-SENSE: NO
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-434-965-1

Query Match 26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 11 PFPF 14
Db 4 PFPF 7

RESULT 23
US-09-434-965-3
; Sequence 3, Application US/09434965
; Patent No. US20020151690A1
; GENERAL INFORMATION:
; APPLICANT: Luxembourg, Alain T.
; Jackson, Michael R.
; Peterson, Per A.
; TITLE OF INVENTION: PURIFICATION OF ANTIGEN-SPECIFIC T CELLS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/434,965
; FILING DATE: 05-NO. US20020151690A1-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: ORT-841
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-524-2806
; TELEFAX: 732-524-2808
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-434-965-3

Query Match 26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 11 PFPF 14
Db 2 PFPF 5

RESULT 24
US-09-932-165-53
; Sequence 53, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AVA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CAT-F2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-53

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DLEM 4
Db 1 DLEM 4

RESULT 25
US-09-932-165-100
; Sequence 100, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AVA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CAT-F2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508


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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-100

Query Match          26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
   ||||
Db 3 DLEM 6

RESULT 26
US-09-932-165-472
; Sequence 472, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 472
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-472

Query Match          26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
   ||||
Db 1 DLEM 4

RESULT 27
US-09-932-165-690
; Sequence 690, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 472
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-472

Query Match          26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
   ||||
Db 1 DLEM 4

RESULT 28
US-09-932-165-1025
; Sequence 1025, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1025
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1025

Query Match          26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
   ||||
Db 5 DLEM 8

RESULT 29
US-10-266-463A-47
; Sequence 47, Application US/10266463A
; Publication No. US20030138946A1
; GENERAL INFORMATION:

```

```

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 690
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-690

Query Match          26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
   ||||
Db 1 DLEM 4

RESULT 28
US-09-932-165-1025
; Sequence 1025, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1025
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1025

Query Match          26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
   ||||
Db 5 DLEM 8

RESULT 29
US-10-266-463A-47
; Sequence 47, Application US/10266463A
; Publication No. US20030138946A1
; GENERAL INFORMATION:

```

; APPLICANT: CAI, Zeling
 ; APPLICANT: SPRENT, Jonathan
 ; APPLICANT: BRUNMARK, Anders
 ; APPLICANT: JACKSON, Michael
 ; APPLICANT: PETERSON, Per A.
 ; APPLICANT: LUXENBOURG, Alain
 ; APPLICANT: LETURCO, Didier Jean
 ; APPLICANT: MORIARTY, Ann M.
 ; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
 ; FILE REFERENCE: TSRI 471.1 Div. 1
 ; CURRENT APPLICATION NUMBER: US/10/266.463A
 ; PRIOR FILING DATE: 2002-10-08
 ; PRIOR APPLICATION NUMBER: US 08/913.612
 ; PRIOR FILING DATE: 1997-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US96/03249
 ; PRIOR FILING DATE: 1996-03-08
 ; PRIOR APPLICATION NUMBER: US 08/400.338
 ; PRIOR FILING DATE: 1995-03-08
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 47
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Mus musculus
 US-10-266-463A-47

Query Match 26.7%; Score 4; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPF 14
 Db 4 PPF 7

RESULT 30

US-10-062-109A-4
 ; Sequence 4, Application US/10062109A
 ; Publication No. US20030165505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys
 ; APPLICANT: Challita-Bid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 ; FILE REFERENCE: 51158-20062.01
 ; CURRENT APPLICATION NUMBER: US/10/062.109A
 ; CURRENT FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 10/005.480
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 765
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-062-109A-4

Query Match 26.7%; Score 4; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
 Db 4 VEPF 7

RESULT 31

US-10-062-109A-44
 ; Sequence 44, Application US/10062109A
 ; Publication No. US20030165505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys
 ; APPLICANT: Challita-Bid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 ; FILE REFERENCE: 51158-20062.01
 ; CURRENT APPLICATION NUMBER: US/10/062.109A
 ; CURRENT FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 10/005.480
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 765
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 44
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-062-109A-44

Query Match 26.7%; Score 4; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
 Db 2 VEPF 5

RESULT 32

US-10-239-313A-467
 ; Sequence 467, Application US/10239313A
 ; Publication No. US20030175285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KLINGUER - HAMOUR, Christine
 ; APPLICANT: CORVAIA, Nathalie
 ; APPLICANT: BECK, Alain
 ; APPLICANT: GOETSCH, Liliane
 ; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
 ; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
 ; FILE REFERENCE: 343 727 US
 ; CURRENT APPLICATION NUMBER: US/10/239.313A
 ; CURRENT FILING DATE: 2002-09-19
 ; PRIOR APPLICATION NUMBER: FR 00/03711
 ; PRIOR FILING DATE: 2000-03-23
 ; PRIOR APPLICATION NUMBER: PCT 01/70772
 ; PRIOR FILING DATE: 2001-03-22
 ; NUMBER OF SEQ ID NOS: 697
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 467
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-239-313A-467

Query Match 26.7%; Score 4; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPF 14
 Db 4 PPF 7

```

RESULT 33
US-10-005-480A-4
; Sequence 4, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Rya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-4

Query Match      26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
Db 4 VEPF 7

RESULT 34
US-10-005-480A-4
; Sequence 44, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Rya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-4

Query Match      26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
Db 2 VEPF 5

RESULT 35
US-10-005-480A-4
; Sequence 13, Application US/10093200A
; Publication No. US20020187521A1
; GENERAL INFORMATION:
; APPLICANT: Duesbery, Nicholas
; APPLICANT: Webb, Craig
; APPLICANT: Leppia, Stephen
; APPLICANT: Vande Woude, George
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the Department
; APPLICANT: of Health and Human Services
; TITLE OF INVENTION: Anthrax Lethal Factor is a MAPK Kinase Protease
; FILE REFERENCE: 015280-345200US
; CURRENT APPLICATION NUMBER: US/10/093,200A
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/080,330
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: WO PCT/US99/07126
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 09/623,104
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:N-terminal
; OTHER INFORMATION: amino acid residues 1-9 of MAPKK2
US-10-093-200A-13

Query Match      26.7%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLP 8
Db 6 PVLP 9

RESULT 36
US-10-015-535-4
; Sequence 4, Application US/10015535
; Publication No. US20030036506A1
; GENERAL INFORMATION:
; APPLICANT: Kratz, David M.
; APPLICANT: Baskay, Susan
; TITLE OF INVENTION: Mutated Class I Major Histocompatibility proteins and
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: 100-00
; CURRENT APPLICATION NUMBER: US/10/015,535
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/254,495
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-015-535-4

Query Match      26.7%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPFF 14
Db 4 PPFF 7

```

```

RESULT 37
US-10-046-801-29
; Sequence 29, Application US/10046801
; Publication No. US20030054027A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/10/046,801
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/540,448
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/935,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
US-10-046-801-29

Query Match      26.7%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 PFPF 14
      |||||
Db      2 PFPF 5

RESULT 38
US-10-093-248-13
; Sequence 13, Application US/10093248
; Publication No. US20030096333A1
; GENERAL INFORMATION:
; APPLICANT: Duesbery, Nicholas
; APPLICANT: Webb, Craig
; APPLICANT: Leppla, Stephen
; APPLICANT: Vande Woude, George
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the Department
; APPLICANT: of Health and Human Services
; TITLE OF INVENTION: Anthrax Lethal Factor is a MAPK Kinase Protease
; FILE REFERENCE: 015280-345200US
; CURRENT APPLICATION NUMBER: US/10/093,248
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/080,330
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: WO PCT/US99/07126
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 09/623,104
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:N-terminal
; OTHER INFORMATION: amino acid residues 1-9 of MAPKK2
US-10-093-248-13

Query Match      26.7%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PVLV 8

```

```

Db      |||||
      6 PVLV 9

RESULT 39
US-09-220-920-111
; Sequence 111, Application US/09220920
; Patent No. US20020002269A1
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. US20020002269A1el Neurotrophic Factor
; FILE REFERENCE: 6029-7996
; CURRENT APPLICATION NUMBER: US/09/220,920
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-220-920-111

Query Match      26.7%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 VLPV 9
      |||||
Db      2 VLPV 5

RESULT 40
US-09-932-165-154
; Sequence 154, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CATEP2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51156-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 154
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-154

Query Match      26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 DLEM 4
 ||||
 Db 1 DLEM 4

RESULT 41

US-09-932-165-785
 ; Sequence 785, Application US/09932165
 ; Publication No. US20030134784A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RAITANO, ARTHUR
 ; APPLICANT: CHALLITA-BID, PIA M.
 ; APPLICANT: PARIS, MARY
 ; APPLICANT: SAFFRAN, DOUGLAS
 ; APPLICANT: AFAR, DANIEL
 ; APPLICANT: LEVIN, ELANA
 ; APPLICANT: HUBERT, RENE
 ; APPLICANT: GE, WANGMAO
 ; APPLICANT: JAKOBOWITS, AYA
 ; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
 ; TITLE OF INVENTION: 83P2H3 AND CATIF2E11 USEFUL IN TREATMENT AND
 ; FILE REFERENCE: 51158-20014.00
 ; CURRENT APPLICATION NUMBER: US/09/932,165
 ; CURRENT FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: 60/226,329
 ; PRIOR FILING DATE: 2000-08-17
 ; NUMBER OF SEQ ID NOS: 1508
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 785
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
 US-09-932-165-785

Query Match 26.7%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
 ||||
 Db 2 DLEM 5

RESULT 42

US-10-062-109A-55
 ; Sequence 55, Application US/10062109A
 ; Publication No. US20030165505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys
 ; APPLICANT: Challita-Bid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 ; FILE REFERENCE: 51158-20062.01
 ; CURRENT APPLICATION NUMBER: US/10/062,109A
 ; CURRENT FILING DATE: 2002-01-31
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 765
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 55
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 26.7%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-062-109A-55

Query Match 26.7%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
 ||||
 Db 2 VEPF 5

RESULT 43

US-10-062-109A-71
 ; Sequence 71, Application US/10062109A
 ; Publication No. US20030165505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys
 ; APPLICANT: Challita-Bid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 ; FILE REFERENCE: 51158-20062.01
 ; CURRENT APPLICATION NUMBER: US/10/062,109A
 ; CURRENT FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 10/005,480
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 765
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 71
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-062-109A-71

Query Match 26.7%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
 ||||
 Db 4 VEPF 7

RESULT 44

US-10-005-480A-55
 ; Sequence 55, Application US/10005480A
 ; Publication No. US20030191073A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys
 ; APPLICANT: Challita-Bid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Jakobovits, Aya
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 ; FILE REFERENCE: 51158-20062.00
 ; CURRENT APPLICATION NUMBER: US/10/005,480A
 ; CURRENT FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 765
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 55
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-005-480A-55

Query Match 26.7%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Query Match      26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEPF 12
Db 2 VEPF 5
   ||||

RESULT 45
US-10-005-480A-71
; Sequence 71, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eld, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 1612P10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-71

Query Match      26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEPF 12
Db 4 VEPF 7
   ||||

RESULT 46
US-10-062-710-199
; Sequence 199, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-09-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T Cell epitopes
US-10-062-710-199

Query Match      26.7%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;

```

```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVL 8
Db 1 PVL 4
   ||||

RESULT 47
US-09-780-662A-14
; Sequence 14, Application US/09780662A
; Patent No. US20020076741A1
; GENERAL INFORMATION:
; APPLICANT: Burroughs-Tencza, Sarah
; TITLE OF INVENTION: Biosensor for Anthrax
; FILE REFERENCE: MHB00-126-A
; CURRENT APPLICATION NUMBER: US/09/780,662A
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic peptide sequence
US-09-780-662A-14

Query Match      26.7%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVL 8
Db 4 PVL 7
   ||||

RESULT 48
US-10-182-303-14
; Sequence 14, Application US/10182303
; Publication No. US20030166028A1
; GENERAL INFORMATION:
; APPLICANT: Burroughs-Tencza, Sarah
; TITLE OF INVENTION: Biosensor for Anthrax
; FILE REFERENCE: MHB00-126-US
; CURRENT APPLICATION NUMBER: US/10/182,303
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic peptide sequence
US-10-182-303-14

Query Match      26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVL 8
Db 4 PVL 7
   ||||

RESULT 49
US-10-062-710-173
; Sequence 173, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.

```

```

; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062.710
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV B Cell Epitopes
US-10-062-710-173

```

```

Query Match      26.7%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred.No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      8 PVEP 11
      |||||
DB      1 PVEP 4

```

```

RESULT 50
US-09-954-385-146
; Sequence 146: Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Wintzky, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954.385
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-146

```

```

Query Match      26.7%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      5 PVL P 8
      |||||
DB      8 PVL P 11

```

```

RESULT 51
US-09-954-385-319
; Sequence 319: Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.

```

```

; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Wintzky, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954.385
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-319

```

```

Query Match      26.7%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      11 PFPF 14
      |||||
DB      7 PFPF 10

```

```

RESULT 52
US-10-214-867A-17
; Sequence 17: Application US/10214867A
; Publication No. US20030148444A1
; GENERAL INFORMATION:
; APPLICANT: KANAI, YOSHIKATSU
; APPLICANT: ENDOU, HITOSHI
; TITLE OF INVENTION: SODIUM-INDEPENDENT SMALL NEUTRAL AMINO ACID
; TITLE OF INVENTION: TRANSPORTERS TRANSPORTING L- AND D-AMINO ACIDS AND
; FILE REFERENCE: 57783 (71526)
; CURRENT APPLICATION NUMBER: US/10/214.867A
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00031
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: JP 2000-28822
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligopeptide
US-10-214-867A-17

```

```

Query Match      26.7%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      12 FPFV 15
      |||||
DB      8 FPFV 11

```

```

RESULT 53
US-10-118-708-5
; Sequence 5: Application US/10118708
; Publication No. US2003016591A1
; GENERAL INFORMATION:
; APPLICANT: Hart, L P
; APPLICANT: Pestka, James J
; APPLICANT: Yuan, Qiaoping

```

; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: MSU 4.1-447
; CURRENT APPLICATION NUMBER: US/10/118,708
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/146,643
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C430, the
; OTHER INFORMATION: DONPEP.2 with a structurally flexible linker and a
; OTHER INFORMATION: cysteine residue
US-10-118-708-5

Query Match 26.7%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PEPF 14
Db 4 PEPF 7

RESULT 54
US-10-057-789-142

; Sequence 142, Application US/10057789
; Publication No. US20030082522A1
; GENERAL INFORMATION:
; APPLICANT: Paul Haynes
; APPLICANT: Jing Wei
; APPLICANT: John Yates
; APPLICANT: Nancy Andon
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE
; TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES
; FILE REFERENCE: NADII 022A
; CURRENT APPLICATION NUMBER: US/10/057,789
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/264,576
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/305,232
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-057-789-142

Query Match 26.7%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEPF 12
Db 2 VEPF 5

RESULT 55

US-10-212-628-142
; Sequence 142, Application US/10212628
; Publication No. US20030087329A1
; GENERAL INFORMATION:
; APPLICANT: Paul Haynes

; APPLICANT: Jing Wei
; APPLICANT: John Yates
; APPLICANT: Nancy Andon
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE
; TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES
; FILE REFERENCE: NADII 022CPI
; CURRENT APPLICATION NUMBER: US/10/212,628
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/264,576
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/305,232
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/057,789
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-212-628-142

Query Match 26.7%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEPF 12
Db 2 VEPF 5

RESULT 56

US-10-254-446A-157
; Sequence 157, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Esther
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 157
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopam
US-10-254-446A-157

Query Match 26.7%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EPFF 13
Db 1 EPFF 4

RESULT 57

US-09-113-924-14
; Sequence 14, Application US/09113924
; Patent No. US20010007019A1

GENERAL INFORMATION:
APPLICANT: Brigstock, David R.
APPLICANT: Harding, Paul H.
TITLE OF INVENTION: HEPARIN BINDING GROWTH FACTOR (HBGF)
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,924
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/308,526
FILING DATE: 07-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A., Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08766/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
LENGTH: 13 amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-113-924-14

Query Match 26.7%; Score 4; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LEVE 10
DB 8 LEVE 11

RESULT 58

US-09-897-107-72

Sequence 72, Application US/09897107

Patent No. US20020137094A1

GENERAL INFORMATION:

APPLICANT: YAMAGISHI, Akihiko

TITLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HAVING

TITLE OF INVENTION: THERMOSTABILITY IMPROVED BY THE METHOD AND NUCLEIC ACIDS ENCODING

FILE REFERENCE: 210383US0

CURRENT APPLICATION NUMBER: US/09/897,107

PRIOR FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: JP2000-201920

PRIOR FILING DATE: 2000-07-04

PRIOR APPLICATION NUMBER: JP2001-164332

PRIOR FILING DATE: 2001-05-31

NUMBER OF SEQ ID NOS: 104

SOFTWARE: PatentIn version 3.1

SEQ ID NO 72

LENGTH: 13

TYPE: PRT

ORGANISM: Thermus thermophilus

US-09-897-107-72

Query Match 26.7%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LEVE 10
DB 8 LEVE 11

RESULT 59

US-09-943-692-29

Sequence 29, Application US/09943692

Patent No. US20020152496A1

GENERAL INFORMATION:

APPLICANT: FISCHHOFF, DAVID A.

APPLICANT: FUCHS, ROY L.

APPLICANT: LAVRIK, PAUL B.

APPLICANT: MCPHERSON, SYLVIA A.

APPLICANT: PERLAK, FREDERICK J.

TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS

FILE REFERENCE: MOBT:195--1

CURRENT APPLICATION NUMBER: US/09/943,692

CURRENT FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: 09/027,998

PRIOR FILING DATE: 1998-02-23

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PatentIn version 3.1

SEQ ID NO 29

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Chimeric toxin
US-09-943-692-29

Query Match 26.7%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PFFV 15
DB 7 PFFV 10

RESULT 60

US-10-116-846B-5

Sequence 5, Application US/10116846B

Publication No. US20030073102A1

GENERAL INFORMATION:

APPLICANT: KWOK, William

APPLICANT: NEPOM, Gerald

APPLICANT: GEBE, John

APPLICANT: REIJONEN, Helena

APPLICANT: LIU, Andrew

TITLE OF INVENTION: METHODS OF MHC CLASS II EPITOPE MAPPING, DETECTION OF AUTOIMMUNE

FILE REFERENCE: 20149-000520US

CURRENT APPLICATION NUMBER: US/10/116,846B

CURRENT FILING DATE: 2002-09-15

PRIOR APPLICATION NUMBER: US 60/282,328

PRIOR FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: US 60/308,962

PRIOR FILING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5

LENGTH: 13

TYPE: PRT

ORGANISM: Herpes Simplex Virus 2

US-10-116-846B-5

Query Match 26.7%; Score 4; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PFFV 15
DB 7 PFFV 10

QY 1 DLEM 4
 |||||
Db 2 DLEM 5

RESULT 61

US-10-116-846B-45
; Sequence 45, Application US/10116846B
; Publication No. US20030073102A1
; GENERAL INFORMATION:
; APPLICANT: KWOK, William
; APPLICANT: NEPOM, Gerald
; APPLICANT: GEBER, John
; APPLICANT: REIJONEN, Helena
; APPLICANT: LIU, Andrew
; TITLE OF INVENTION: METHODS OF MHC CLASS II EPTIPE MAPPING, DETECTION OF AUTOIMMUNE
; FILE REFERENCE: 20149-000520US
; CURRENT APPLICATION NUMBER: US/10/116,846B
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/282,328
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/308,962
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 45
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Herpes simplex Virus 2
US-10-116-846B-45

Query Match 26.7%; Score 4; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 DLEM 4
 |||||
Db 2 DLEM 5

RESULT 62

US-09-113-924-13
; Sequence 13, Application US/09113924
; Patent No. US20010007019A1
; GENERAL INFORMATION:
; APPLICANT: Brigstock, David R.
; APPLICANT: Harding, Paul H.
; TITLE OF INVENTION: HEPARIN BINDING GROWTH FACTOR (HBGF)
; NUMBER OF SEQUENCES: 22
; TITLE OF INVENTION: POLYPEPTIDES
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,924
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/908,526
; FILING DATE: 07-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A., Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08/66/003001

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-113-924-13

Query Match 26.7%; Score 4; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.8e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 7 LPVE 10
 |||||
Db 9 LPVE 12

RESULT 63

US-08-996-140-9
; Sequence 9, Application US/08996140
; Publication No. US20030190318A1
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: USHIO, Shimpei
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,140
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 356,426/1996
; FILING DATE: 26-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 52,526/1997
; FILING DATE: 21-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 163,490/1997
; FILING DATE: 6-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,490/1997
; FILING DATE: 28-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
US-08-996-140-9

```

Query Match          26.7%; Score 4; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VLPV 9
        |||||
Db      11 VLPV 14

RESULT 64
US-09-759-010-9
; Sequence 9, Application US/09759010
; Patent No. US20010034042A1
; GENERAL INFORMATION:
; APPLICANT: Strivastava, Pramod K.
; TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
; FILE REFERENCE: 8449-135
; CURRENT APPLICATION NUMBER: US/09/759,010
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Vesicular stomatitis virus
US-09-759-010-9

Query Match          26.7%; Score 4; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DLEM 4
        |||||
Db      7 DLEM 10

RESULT 65
US-09-947-770-15
; Sequence 15, Application US/09947770
; Patent No. US20020068713A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Ruiz, Pedro
; APPLICANT: Garren, Hideki
; TITLE OF INVENTION: DNA Vaccination for Treatment of
; FILE REFERENCE: STAN123CIP
; CURRENT APPLICATION NUMBER: US/09/947,770
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/06233
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/267,590
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HSPV16 P45
US-09-947-770-15

Query Match          26.7%; Score 4; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DLEM 4
        |||||
Db      12 DLEM 15

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```

RESULT 66
US-09-813-333-18
; Sequence 18, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-18

Query Match          26.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LPVE 10
        |||||
Db      1 LPVE 4

RESULT 67
US-09-953-510-37
; Sequence 37, Application US/09953510
; Patent No. US20020131975A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Abundant Extracellular
; CORRESPONDENCE ADDRESS: Products and Methods for Their Production and Use
; ADDRESSEE: Kurt A. MacLean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,510
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids

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; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-953-510-38

Query Match          26.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 7 LPVE 10
    ||||
Db 1 LPVE 4

RESULT 69
US-09-880-505-22
; Sequence 22, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-880-505-22

Query Match          26.7%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 7 LPVE 10
    ||||
Db 6 LPVE 9

RESULT 70
US-09-880-505-24
; Sequence 24, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-880-505-24

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Query Match 26.7%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 7 LPVE 10
|
|
|
|
Db 6 LPVE 9

RESULT 71

US-10-349-023-18
; Sequence 18, Application US/10349023
; Publication No. US20030133919A1
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; OKURA, Takahori
; KURIMOTO, Koushi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,023
; FILING DATE: 23-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/556,972
; FILING DATE: 24-Apr-2000
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-Dec-1997
; APPLICATION NUMBER: JP 74,697/1997
; FILING DATE: 12-Mar-1997
; APPLICATION NUMBER: JP 215,488/1997
; FILING DATE: 28-Jul-1997
; APPLICATION NUMBER: JP 291,837/1997
; FILING DATE: 09-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-349-023-18

Query Match 26.7%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 6 VLPV 9
|
|
|
|
Db 11 VLPV 14

RESULT 72

US-10-147-255-37

; Sequence 37, Application US/10147255
; Publication No. US20030152584A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Abundant Extracellular
; Products and Methods for Their Production and Use
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. MacLean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0,
; Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/147,255
; FILING DATE: 15-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,539A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-147-255-37

Query Match 26.7%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVE 10
|
|
|
|
Db 6 LPVE 9

RESULT 73
US-10-147-255-38
; Sequence 38, Application US/10147255
; Publication No. US20030152584A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Abundant Extracellular
; Products and Methods for Their Production and Use

```

;
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. MacLean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; CURRENT APPLICATION DATA: Version #1.30
; APPLICATION NUMBER: US/10/147,255
; FILING DATE: 15-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,539A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
;
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-147-255-38
;
; Query Match 26.7%; Score 4; DB 12; Length 15;
; Best Local Similarity 100.0%; Pred. No. 7.2e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 7 LPVE 10
; Db 1 LPVE 4
;
; RESULT 74
; US-10-161-791-312
; Sequence 312, Application US/10161791
; Publication No.: US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME

```

```

;
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mastrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-312
;
; Query Match 26.7%; Score 4; DB 12; Length 15;
; Best Local Similarity 100.0%; Pred. No. 7.2e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 5 PVLP 8
; Db 8 PVLP 11
;
; RESULT 75
; US-10-044-703-18
; Sequence 18, Application US/10044703
; Publication No.: US20020192235A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PPT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-18
;
; Query Match 26.7%; Score 4; DB 14; Length 15;
; Best Local Similarity 100.0%; Pred. No. 7.2e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 7 LPVE 10
; Db 1 LPVE 4

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Wed Nov 26 09:08:36 2003

us-09-641-801-5.oligo.rapb

Page 23

Search completed: November 25, 2003, 20:25:31
Job time : 31.8404 secs

ALIGNMENTS

```
RESULT 1
US-09-641-803-5
; Sequence 5, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-5
Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLVFPFPPFV 15
DB 1 DLEMPVLVFPFPPFV 15

RESULT 2
US-08-687-956A-7
; Sequence 7, Application US/08687956A
; Patent No. 5861157
; GENERAL INFORMATION:
; APPLICANT: BURNIE, JAMES P
; APPLICANT: MATTHEWS, RUTH C
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP
; STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,956A
; FILING DATE: 29-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9401689.6
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N
; REGISTRATION NUMBER: 16,773
```

```
REFERENCE/DOCKET NUMBER: 50885/222892
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/861-3000
; TELEFAX: 202/822-0944
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus sobrinus
; STRAIN: Streptococcus sobrinus MUCOB 263
US-08-687-956A-7
Query Match 33.3%; Score 5; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVEPF 11
DB 10 LPVEPF 14

RESULT 3
US-09-641-803-22
; Sequence 22, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-22
Query Match 33.3%; Score 5; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEPF 12
DB 10 PVEPF 14

RESULT 4
US-08-261-206A-22
; Sequence 22, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
```

;; TITLE OF INVENTION: with Thrombin
;; NUMBER OF SEQUENCES: 80
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Birch, Stewart, Kolasch & Birch
;; STREET: 301 N. Washington St.
;; CITY: Falls Church
;; STATE: Virginia
;; COUNTRY: USA
;; ZIP: 22046-0747
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/261,206A
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/740,492
;; FILING DATE: 03-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Svensson, Leonard R.
;; REGISTRATION NUMBER: 30330
;; REFERENCE/DOCKET NUMBER: 216-275P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-241-1300
;; TELEFAX: 703-241-2848
;; TELEX: 248345
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-261-206A-22

Query Match 26.7%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEP 11
Db 2 PVEP 5

RESULT 5
US-09-147-933-17
;; Sequence 17 Application US/09147933A
;; Patent No. 6168917
;; GENERAL INFORMATION:
;; APPLICANT: Kilpatrick, David
;; TITLE OF INVENTION: DETECTION AND IDENTIFICATION OF
;; FILE OF INVENTION: NON-POLIO ENTEROVIRUSES
;; FILE REFERENCE: 62242/US
;; CURRENT APPLICATION NUMBER: US/09/147,933A
;; CURRENT FILING DATE: 1999-07-09
;; EARLIER APPLICATION NUMBER: PCT/US97/17734
;; EARLIER FILING DATE: 1997-10-01
;; EARLIER APPLICATION NUMBER: U. S. 60/027,353
;; EARLIER FILING DATE: 1996-10-02
;; NUMBER OF SEQ ID NOS: 96
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 17
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: peptide
US-09-147-933-17

Query Match 26.7%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 MPVL 7
Db 1 MPVL 4

RESULT 6
US-09-365-581A-2
;; Sequence 2 Application US/09365581A
;; Patent No. 6287776
;; GENERAL INFORMATION:
;; APPLICANT: Hart, L. P
;; APPLICANT: Pestka, James J
;; APPLICANT: Yuan, Qiaoping
;; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
;; TITLE OF INVENTION: THEREOF
;; FILE REFERENCE: MSU 4.1-447
;; CURRENT APPLICATION NUMBER: US/09/365,581A
;; CURRENT FILING DATE: 2000-07-27
;; PRIOR APPLICATION NUMBER: 60/146,643
;; PRIOR FILING DATE: 1999-07-30
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: DONPRP.2
;; OTHER INFORMATION: Peptide mimotope of deoxynivalenol
US-09-365-581A-2

Query Match 26.7%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFPF 14
Db 4 PFPF 7

RESULT 7
US-09-426-568A-11
;; Sequence 11 Application US/09426568A
;; Patent No. 638843
;; GENERAL INFORMATION:
;; APPLICANT: Kakefuda, Genichi
;; APPLICANT: Costello, Colleen
;; APPLICANT: Sun, Ming
;; APPLICANT: Hu, Weiming
;; TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
;; FILE OF INVENTION: in Plants
;; FILE REFERENCE: 008103/195497
;; CURRENT APPLICATION NUMBER: US/09/426,568A
;; CURRENT FILING DATE: 1999-10-22
;; PRIOR APPLICATION NUMBER: 60/106,239
;; PRIOR FILING DATE: 1998-10-29
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 11
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Arabidopsis sp.
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (1)..(7)
;; OTHER INFORMATION: N-terminal of AHAS small subunit peptide from
;; OTHER INFORMATION: plasmid F3
;; NAME/KEY: SITE
;; LOCATION: (1)..(2)
;; OTHER INFORMATION: Thrombin cleavage site
US-09-426-568A-11

Query Match 26.7%; Score 4; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 9 VEPF 12
 ||||
 Db 3 VEPF 6

RESULT 8
 US-09-492-766-8
 ; Sequence 8, Application US/09492766
 ; Patent No. 6506732
 ; GENERAL INFORMATION:
 ; APPLICANT: AMIOT, Jean
 ; TITLE OF INVENTION: ENZYMIC HYDROLYSATE OF MILK PROTEINS
 ; FILE REFERENCE: 6013-57"US"
 ; CURRENT APPLICATION NUMBER: US/09/492,766
 ; CURRENT FILING DATE: 2000-01-27
 ; EARLIER APPLICATION NUMBER: 60/117,661
 ; EARLIER FILING DATE: 1999-01-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk
 ; OTHER INFORMATION: proteins
 US-09-492-766-8

Query Match 26.7%; Score 4; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 6 VLPV 9
 ||||
 Db 1 VLPV 4

RESULT 9
 US-09-626-821A-2
 ; Sequence 2, Application US/09626821A
 ; Patent No. 657762
 ; GENERAL INFORMATION:
 ; APPLICANT: Hart, L P
 ; APPLICANT: Pestka, James J
 ; TITLE OF INVENTION: PEPTIDE
 ; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
 ; FILE REFERENCE: MSU 4.1-447
 ; CURRENT APPLICATION NUMBER: US/09/626,821A
 ; CURRENT FILING DATE: 2000-07-27
 ; PRIOR APPLICATION NUMBER: 60/146,643
 ; PRIOR FILING DATE: 1999-07-30
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: DONPEP.2
 ; OTHER INFORMATION: peptide mimotope of deoxynivalenol
 US-09-626-821A-2

Query Match 26.7%; Score 4; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 11 PFPF 14

Db 4 PFPF 7
 ||||

RESULT 10
 US-08-360-239B-2
 ; Sequence 2, Application US/08360239B
 ; Patent No. 5801222
 ; GENERAL INFORMATION:
 ; APPLICANT: Pettit, George R.
 ; APPLICANT: Tan, Rui
 ; TITLE OF INVENTION: Isolation and Structure of
 ; TITLE OF INVENTION: the Human Cancer Cell Growth Inhibitory Cyclic
 ; TITLE OF INVENTION: Octapeptides Phakellistatin 10 and 11
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Richard R. Mybeck
 ; STREET: 8010 East Morgan Trail, #10
 ; CITY: Scottsdale
 ; STATE: Arizona
 ; COUNTRY: USA
 ; ZIP: 85258-1234
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: DOS 5
 ; SOFTWARE: Microsoft Word for Windows
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/360,239B
 ; FILING DATE: 12/20/94
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Richard R. Mybeck
 ; REGISTRATION NUMBER: 17,886
 ; REFERENCE/DOCKET NUMBER: 4997
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (602)-483-1285
 ; TELEFAX: (602)-483-7452
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acid residues
 ; TYPE: amino acid
 ; TOPOLOGY: Cyclic
 ; MOLECULE TYPE: Cyclooctapeptide
 ; DESCRIPTION: Phakellistatin 11
 ; DESCRIPTION: Phakellistatin 11
 ; HYPOTHETICAL: no
 ; ANTI-SENSE: no
 ; FRAGMENT TYPE: circular
 ; ORIGINAL SOURCE:
 ; ORGANISM: Phakellia sp.
 ; DEVELOPMENTAL STAGE: whole organism
 ; FEATURE:
 ; NAME/KEY: phakellistatin 11
 ; NAME/KEY: amino acid analysis, high resolution
 ; NAME/KEY: nuclear magnetic resonance and mass
 ; NAME/KEY: spectral MS/MS techniques
 ; OTHER INFORMATION: Phakellistatin is a
 ; OTHER INFORMATION: cell growth inhibitory peptide with
 ; OTHER INFORMATION: activity in murine lymphocytic leukemia
 ; OTHER INFORMATION: cell line of 0.20 mg/ml.
 US-08-360-239B-2

Query Match 26.7%; Score 4; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 11 PFPF 14
 ||||
 Db 3 PFPF 6

RESULT 11

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US-08-929-922B-7
; Sequence 7, Application US/0892922B
; Patent No. 5994113
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Si, Joan Qi
; APPLICANT: Spendler, Tina
; APPLICANT: Dambmann, Claus
; APPLICANT: Halkier, Torben
; APPLICANT: stergaard, Peter Rahbek
; APPLICANT: Packat, Shankant Anant
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 59941130 No. 5994113disk of No. 5994113th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,922B
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4355.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-08-929-922B-7
; Query Match 26.7%; Score 4; DB 2; Length 8;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 9 VEPF 12
;
Db 4 VEPF 7
;
RESULT 12
US-08-828-712-12
; Sequence 12, Application US/08828712
; Patent No. 6015884
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; APPLICANT: O'Herrin, Sean
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.

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; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,712
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide p2Ca
; US-08-828-712-12
; Query Match 26.7%; Score 4; DB 3; Length 8;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 11 PFPF 14
;
Db 3 PFPF 6
;
RESULT 13
US-08-993-165-25
; Sequence 25, Application US/08993165A
; Patent No. 6123923
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Wu, Yunqiu
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1224
; CURRENT APPLICATION NUMBER: US/08/993,165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el Sequence
; US-08-993-165-25
; Query Match 26.7%; Score 4; DB 3; Length 8;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 11 PFPF 14
;
Db 3 PFPF 6
;
RESULT 14
US-08-993-165-28
; Sequence 28, Application US/08993165A
; Patent No. 6123923
; GENERAL INFORMATION:

```

; APPLICANT: Unger, Evan C
; APPLICANT: Wu, Yungui
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1224
; CURRENT APPLICATION NUMBER: US/08/993,165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
US-08-993-165-28

Query Match 26.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPPF 14
|||
Db 3 PPPF 6

RESULT 15
US-08-993-165-30
; Sequence 30, Application US/08993165A
; Patent No. 6123923
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Wu, Yungui
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1224
; CURRENT APPLICATION NUMBER: US/08/993,165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
US-08-993-165-30

Query Match 26.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPPF 14
|||
Db 3 PPPF 6

RESULT 16
US-08-993-165-34
; Sequence 34, Application US/08993165A
; Patent No. 6123923
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Wu, Yungui
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1224
; CURRENT APPLICATION NUMBER: US/08/993,165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923e1 Sequence
US-08-993-165-34

Query Match 26.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPPF 14
|||
Db 3 PPPF 6

RESULT 17
US-08-993-276-12
; Sequence 12, Application US/09063276
; Patent No. 6140113
; GENERAL INFORMATION:
; APPLICANT: Schneek, Jonathan
; APPLICANT: O'Herrin, Sean
; TITLE OF INVENTION: Molecular Complexes Which
; TITLE OF INVENTION: Modify Immune Responses
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,276
; FILING DATE: 21-APR-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,712
; FILING DATE: 28-MAR-1997
; APPLICATION NUMBER: 60/014,367
; FILING DATE: 28-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.74154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6140113e
US-09-063-276-12

Query Match 26.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPPF 14
|||
Db 3 PPPF 6

RESULT 18
US-09-342-394-7
; Sequence 7, Application US/09342394
; Patent No. 6143546

```
;
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Si, Joan Qi
; APPLICANT: Spendler, Tina
; APPLICANT: Dammann, Claus
; APPLICANT: Halkier, Torben
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Pakkar, Shamkant Anant
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6143546o No. 6143546disk of No. 6143546th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/342,394
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,922
; FILING DATE: 15-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4355.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-09-342-394-7

Query Match 26.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
DB 4 VEPF 7

RESULT 19
US-09-580-064-7
; Sequence 7, Application US/09580064
; Patent No. 6200792
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Si, Joan Qi
; APPLICANT: Spendler, Tina
; APPLICANT: Dammann, Claus
; APPLICANT: Halkier, Torben
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Pakkar, Shamkant Anant
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
```

```
;
; ADDRESSEE: No. 6200792o No. 6200792disk of No. 6200792th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,064
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/929,922
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4355.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-09-580-064-7

Query Match 26.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
DB 4 VEPF 7

RESULT 20
US-09-540-448-25
; Sequence 25, Application US/09540448
; Patent No. 6403056
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGRI592
; CURRENT APPLICATION NUMBER: US/09/540,448
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el Sequence
; US-09-540-448-25

Query Match 26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14
|||||
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; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-496-761-1

Query Match 26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14
Db 3 PFPF 6

RESULT 25
US-09-496-761-4
; Sequence 4, Application US/09496761
; Patent No. 6444660
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; APPLICANT: Shen, De Kang
; TITLE OF INVENTION: No. 6444660el Lipid Soluble Steroid Prodrugs
; FILE REFERENCE: UNGR-1586
; CURRENT APPLICATION NUMBER: US/09/496,761
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 08/851,780
; PRIOR FILING DATE: 1997-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-496-761-4

Query Match 26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14
Db 3 PFPF 6

RESULT 26
US-09-496-761-6
; Sequence 6, Application US/09496761
; Patent No. 6444660
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; APPLICANT: Shen, De Kang
; TITLE OF INVENTION: No. 6444660el Lipid Soluble Steroid Prodrugs
; FILE REFERENCE: UNGR-1586
; CURRENT APPLICATION NUMBER: US/09/496,761
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 08/851,780
; PRIOR FILING DATE: 1997-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-496-761-6

Query Match 26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14

Db 3 PFPF 6

RESULT 27
US-09-496-761-10
; Sequence 10, Application US/09496761
; Patent No. 6444660
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; APPLICANT: Shen, De Kang
; TITLE OF INVENTION: No. 6444660el Lipid Soluble Steroid Prodrugs
; FILE REFERENCE: UNGR-1586
; CURRENT APPLICATION NUMBER: US/09/496,761
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 08/851,780
; PRIOR FILING DATE: 1997-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-496-761-10

Query Match 26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14
Db 3 PFPF 6

RESULT 28
US-09-324-782-12
; Sequence 12, Application US/09324782
; Patent No. 6448071
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; APPLICANT: O'Heslin, Sean
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/324,782
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,712
; FILING DATE: 28-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 12:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; INDIVIDUAL ISOLATE: peptide p2Ca
US-09-324-782-12

Query Match 26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 11 PFPF 14
|||||

Db 3 PFPF 6

RESULT 29
US-09-668-143-12
; Sequence 12, Application US/09668143
; Patent No. 6458354
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; APPLICANT: O'Herrin, Sean
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/668,143
; FILING DATE: 25-SEP-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,712
; FILING DATE: 28-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A. 32,141
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide p2Ca
US-09-668-143-12

Query Match 26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 11 PFPF 14
|||||

Db 3 PFPF 6

RESULT 30
US-08-913-612A-46
; Sequence 46, Application US/08913612A
; Patent No. 6461867
; GENERAL INFORMATION:
; APPLICANT: Cai, Zeling
; APPLICANT: Brunmark, Anders
; APPLICANT: Jackson, Michael
; APPLICANT: Peterson, Per A.
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
; TITLE OF INVENTION: ACTIVATION OF T-CELLS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Olson & Hierl, Ltd.
; STREET: 20 No. 6461867th Wacker Drive, 36th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,612A
; FILING DATE: 08-SEP-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cepuritis, Talivaldis
; REGISTRATION NUMBER: 20,818
; REFERENCE/DOCKET NUMBER: 471.1 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 580-1180
; TELEFAX: (312) 580-1189
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-913-612A-46

Query Match 26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 11 PFPF 14
|||||

Db 3 PFPF 6

RESULT 31
US-08-929-847-26
; Sequence 26, Application US/08929847
; Patent No. 6548047
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
; FILE REFERENCE: BMS0441
; CURRENT APPLICATION NUMBER: US/08/929,847
; CURRENT FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 26

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; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-26

Query Match          26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 PFPF 14
        ||||
Db       3 PFPF 6

RESULT 32
US-08-929-847-29
; Sequence 29, Application US/08929847
; Patent No. 6548047
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
; FILE REFERENCE: BMS0441
; CURRENT APPLICATION NUMBER: US/08/929,847
; CURRENT FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-29

Query Match          26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 PFPF 14
        ||||
Db       3 PFPF 6

RESULT 33
US-08-929-847-34
; Sequence 34, Application US/08929847
; Patent No. 6548047
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
; FILE REFERENCE: BMS0441
; CURRENT APPLICATION NUMBER: US/08/929,847
; CURRENT FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-34

Query Match          26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 PFPF 14
        ||||
Db       3 PFPF 6

RESULT 34
US-08-340-283-81
; Sequence 81, Application US/08340283
; Patent No. 5861318
; GENERAL INFORMATION:
; APPLICANT: Elhammer, Ake P.
; TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
; TITLE OF INVENTION: N-ACETYL GALACTOSAMINYLTRANSFERASE ACTIVITY
; NUMBER OF SEQUENCES: 205
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia and Upjohn, Inc., Intellect. Prop. Law
; ADDRESS: (1920-32-1)
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,283
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Wootton, Thomas A.
; REGISTRATION NUMBER: 35,004
; REFERENCE/DOCKET NUMBER: 4828
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (616) 385-7914
; TELEFAX: (616) 385-6897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-340-283-81

Query Match          26.7%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PVLV 8
        ||||
Db       1 PVLV 4

RESULT 35
US-08-828-712-13
; Sequence 13, Application US/08828712
; Patent No. 6015884
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; APPLICANT: O'Herrin, Sean
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
```

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,712
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide QL9
US-08-828-712-13

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14
DB 4 PFPF 7

RESULT 36
US-08-828-712-14
; Sequence 14, Application US/08828712
; Patent No. 6015884
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,712
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
```

```
;
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide SL9
US-08-828-712-14

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14
DB 3 PFPF 6

RESULT 37
US-08-993-165-29
; Sequence 29, Application US/08993165A
; Patent No. 6123923
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Wu, Yunqiu
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1224
; CURRENT APPLICATION NUMBER: US/08/993,165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el Sequence
US-08-993-165-29

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14
DB 2 PFPF 5

RESULT 38
US-09-063-276-13
; Sequence 13, Application US/09063276
; Patent No. 6140113
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan
; APPLICANT: O'Herrin, Sean
; TITLE OF INVENTION: Molecular Complexes Which
; TITLE OF INVENTION: Modify Immune Responses
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,276
; FILING DATE: 21-APR-1998
```

```
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,712
; FILING DATE: 28-MAR-1997
; APPLICATION NUMBER: 60/014,367
; FILING DATE: 28-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.74154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6140113e
US-09-063-276-13

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PPPP 14
Db 4 PPPP 7

RESULT 39
US-09-063-276-14
; Sequence 14, Application US/09063276
; Patent No. 6140113
; GENERAL INFORMATION:
; APPLICANT: Schneek, Jonathan
; APPLICANT: O'Herrin, Sean
; TITLE OF INVENTION: Molecular Complexes Which
; TITLE OF INVENTION: Modify Immune Responses
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 21-APR-1998
; APPLICATION NUMBER: US/09/063,276
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,712
; FILING DATE: 28-MAR-1997
; APPLICATION NUMBER: 60/014,367
; FILING DATE: 28-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.74154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6140113e
US-09-063-276-14

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PPPP 14
Db 2 PPPP 5

RESULT 40
US-09-540-448-29
; Sequence 29, Application US/09540448
; Patent No. 6403056
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/09/540,448
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056e1 Sequence
US-09-540-448-29

Query Match 26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PPPP 14
Db 2 PPPP 5

RESULT 41
US-09-496-761-5
; Sequence 5, Application US/09496761
; Patent No. 644660
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; APPLICANT: Shen, De Kang
; TITLE OF INVENTION: No. 6444660e1 Lipid Soluble Steroid Prodrugs
; FILE REFERENCE: UNGR-1586
; CURRENT APPLICATION NUMBER: US/09/496,761
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 08/851,780
; PRIOR FILING DATE: 1997-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-496-761-5

Query Match 26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 11 PFPF 14
|
|
|
|
Db 2 PFPF 5

RESULT 42
US-09-324-782-13
; Sequence 13, Application US/09324782
; Patent No. 6448071
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; APPLICANT: O'Herrin, Sean
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/324,782
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,712
; FILING DATE: 28-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide QL9

US-09-324-782-13
Query Match 26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 11 PFPF 14
|
|
|
|
Db 4 PFPF 7

RESULT 43
US-09-324-782-14
; Sequence 14, Application US/09324782
; Patent No. 6448071
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; APPLICANT: O'Herrin, Sean
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins
; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/324,782
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,712
; FILING DATE: 28-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide SL9

US-09-324-782-14
Query Match 26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 11 PFPF 14
|
|
|
|
Db 3 PFPF 6

RESULT 44
US-09-668-143-13
; Sequence 13, Application US/09668143
; Patent No. 6458354
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; APPLICANT: O'Herrin, Sean
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/668,143
; FILING DATE: 25-SEP-2000
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/828,712
FILING DATE: 28-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.73713
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)508-9100
TELEFAX: (202)508-9299
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL ISOLATE: peptide QL9
US-09-668-143-13

Query Match 26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 11 PFPF 14
Db 4 PFPF 7

RESULT 45

US-09-668-143-14
Sequence 14, Application US/09668143
Patent No. 6458354
GENERAL INFORMATION:
APPLICANT: Schneek, Jonathan P.
APPLICANT: O'Herrin, Sean
TITLE OF INVENTION: Soluble Divalent and Multivalent
TITLE OF INVENTION: Heterodimeric Analogs of Proteins
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/668,143
FILING DATE: 25-SEP-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,712
FILING DATE: 28-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.73713
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)508-9100
TELEFAX: (202)508-9299

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO

ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide SL9
US-09-668-143-14

Query Match 26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 11 PFPF 14
Db 3 PFPF 6

RESULT 46

US-08-913-612A-47
Sequence 47, Application US/08913612A
Patent No. 6461867
GENERAL INFORMATION:
APPLICANT: Cal, Zeling
APPLICANT: Sprent, Jonathan
APPLICANT: Brunmark, Anders
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A.
TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
TITLE OF INVENTION: ACTIVATION OF T-CELLS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Olson & Hierl, Ltd.
STREET: 20 No. 6461867th Wacker Drive, 36th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,612A
FILING DATE: 08-SEP-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cepuritis, Talivaldis
REGISTRATION NUMBER: 20,818
REFERENCE/DOCKET NUMBER: 471.1 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-913-612A-47

Query Match 26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 11 PFPF 14
Db 4 PFPF 7

RESULT 47

US-08-929-847-30
Sequence 30, Application US/08929847

```

; Patent No. 6548047
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
; FILE REFERENCE: BMS0441
; CURRENT APPLICATION NUMBER: US/08/929,847
; CURRENT FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-30

Query Match      26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 PPPP 14
Db      2 PPPP 5

RESULT 48
US-09-001-984C-92
; Sequence 92, Application US/09001984C
; Patent No. 6245331
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: NYU-011
; CURRENT APPLICATION NUMBER: US/09/001,984C
; CURRENT FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: 60/034,003
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-001-984C-92

Query Match      26.7%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LPVE 10
Db      6 LPVE 9

RESULT 49
US-09-001-984C-97
; Sequence 97, Application US/09001984C
; Patent No. 6245331
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: NYU-011
; CURRENT APPLICATION NUMBER: US/09/001,984C
; CURRENT FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: 60/034,003
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-001-984C-92

Query Match      26.7%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LPVE 10
Db      6 LPVE 9

RESULT 50
US-09-001-984C-101
; Sequence 101, Application US/09001984C
; Patent No. 6245331
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: NYU-011
; CURRENT APPLICATION NUMBER: US/09/001,984C
; CURRENT FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: 60/034,003
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-001-984C-101

Query Match      26.7%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LPVE 10
Db      6 LPVE 9

RESULT 51
US-09-220-528-111
; Sequence 111, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Balch, Robert H.
; TITLE OF INVENTION: Artemin, A No. 6284540e1 Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-220-528-111

Query Match      26.7%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LPVE 10
Db      6 LPVE 9

RESULT 52
US-09-220-528-111
; Sequence 111, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Balch, Robert H.
; TITLE OF INVENTION: Artemin, A No. 6284540e1 Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-220-528-111

Query Match      26.7%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LPVE 10
Db      6 LPVE 9

```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
 ||||
 Db 2 VLPV 5

RESULT 52

US-09-396-347F-92
 ; Sequence 92, Application US/09396347F
 ; Patent No. 6506384
 ; GENERAL INFORMATION:
 ; APPLICANT: Laal, Suman
 ; APPLICANT: Zolla-Pazner, Susan
 ; APPLICANT: Belisle, John T
 ; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
 ; FILE REFERENCE: 32004-169276
 ; CURRENT APPLICATION NUMBER: US/09/396,347F
 ; PRIOR FILING DATE: 1999-09-14
 ; PRIOR APPLICATION NUMBER: 09/001,984
 ; PRIOR FILING DATE: 1997-12-31
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 92
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Mycobacterium tuberculosis strain H37Rv
 US-09-396-347F-92

Query Match 26.7%; Score 4; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVE 10
 ||||
 Db 6 LPVE 9

RESULT 53

US-09-396-347F-97
 ; Sequence 97, Application US/09396347F
 ; Patent No. 6506384
 ; GENERAL INFORMATION:
 ; APPLICANT: Laal, Suman
 ; APPLICANT: Zolla-Pazner, Susan
 ; APPLICANT: Belisle, John T
 ; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
 ; FILE REFERENCE: 32004-169276
 ; CURRENT APPLICATION NUMBER: US/09/396,347F
 ; PRIOR FILING DATE: 1999-09-14
 ; PRIOR APPLICATION NUMBER: 09/001,984
 ; PRIOR FILING DATE: 1997-12-31
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 97
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Mycobacterium tuberculosis strain H37Rv
 US-09-396-347F-97

Query Match 26.7%; Score 4; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVE 10
 ||||
 Db 6 LPVE 9

RESULT 54

US-09-396-347F-101
 ; Sequence 101, Application US/09396347F
 ; Patent No. 6506384

; GENERAL INFORMATION:
 ; APPLICANT: Laal, Suman
 ; APPLICANT: Zolla-Pazner, Susan
 ; APPLICANT: Belisle, John T
 ; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
 ; FILE REFERENCE: 32004-169276
 ; CURRENT APPLICATION NUMBER: US/09/396,347F
 ; PRIOR FILING DATE: 1999-09-14
 ; PRIOR APPLICATION NUMBER: 09/001,984
 ; PRIOR FILING DATE: 1997-12-31
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 101
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Mycobacterium tuberculosis strain H37Rv
 US-09-396-347F-101

Query Match 26.7%; Score 4; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVE 10
 ||||
 Db 6 LPVE 9

RESULT 55

US-08-338-992B-29
 ; Sequence 29, Application US/08338992B
 ; Patent No. 5736524
 ; GENERAL INFORMATION:
 ; APPLICANT: CONTENT, JEAN
 ; APPLICANT: HUYGEN, KRIS
 ; APPLICANT: LIU, MARGARET A.
 ; APPLICANT: MONTGOMERY, DONNA
 ; APPLICANT: ULMER, JEFFREY
 ; TITLE OF INVENTION: A POLYNUCLEOTIDE TUBERCULOSIS VACCINE
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.
 ; STREET: 125 E. LINCOLN AVE., - P.O. BOX 2000
 ; CITY: RAHWAY
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07065-0900
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/338,992B
 ; FILING DATE: 14-NOV-1994
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: YABLONSKY, MICHAEL D.
 ; REGISTRATION NUMBER: 40,407
 ; REFERENCE/DOCKET NUMBER: 19342
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 908-594-4678
 ; TELEFAX: 908-594-4720
 ; INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: N-terminal
 US-08-338-992B-29

Query Match

26.7%; Score 4; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.6e+02; Indels 0; Gaps 0; Mismatches 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVE 10
|
|
|
|
Db 8 LPVE 11

RESULT 56
US-08-637-759B-103
; Sequence 103, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS: 501
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-103

Query Match 26.7%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVL 7
|
|
|
|
Db 7 MPVL 10

RESULT 57
US-08-871-355A-103
; Sequence 103, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,355A
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-103

Query Match 26.7%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVL 7
|
|
|
|
Db 7 MPVL 10

RESULT 58
US-09-365-581A-5
; Sequence 5, Application US/09365581A
; Patent No. 6287776
; GENERAL INFORMATION:
; APPLICANT: Hart, L P
; APPLICANT: Pestka, James J
; APPLICANT: Yuan, Qiaoping
; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: MSU 4.1-447
; CURRENT APPLICATION NUMBER: US/09/365,581A
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,643
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C430, the
; OTHER INFORMATION: DONPEP.2 with a structurally flexible linker and a
; OTHER INFORMATION: cysteine residue
US-09-365-581A-5

Query Match 26.7%; Score 4; DB 3; Length 12;

```

Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14
Db 4 PFPF 7

RESULT 59
US-09-147-208-55
; Sequence 55, Application US/09147208
; Patent No. 633303
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antiviral Ricin-Like Proteins
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/147,208
; FILING DATE: 02-MAR-1999
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Rudolph, John R.
; REGISTRATION NUMBER: 38,003
; REFERENCE/DOCKET NUMBER: 7841-76
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-147-208-55

Query Match 26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
Db 5 VLPV 8

RESULT 60
US-09-201-945-103
; Sequence 103, Application US/09201945
; Patent No. 6342315
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Fabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450

US-09-147-208-55
; Sequence 55, Application US/09147208
; Patent No. 633303
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Antiviral Ricin-Like Proteins
; FILE REFERENCE: 10447-108
; CURRENT APPLICATION NUMBER: US/09/550,117A
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/147,208
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PAP-205/PAP-206 linker
US-09-550-117A-55

Query Match 26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
Db 5 VLPV 8

RESULT 62
US-09-626-821A-5
; Sequence 5, Application US/09626821A

```

Patent No. 6537762
GENERAL INFORMATION:
APPLICANT: Hart, L P
APPLICANT: Pestka, James J
APPLICANT: Yuan, Qiaoping
TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
FILE REFERENCE: MSU 4.1-447
CURRENT APPLICATION NUMBER: US/09/626,821A
CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/146,643
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 5
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: C430, the
OTHER INFORMATION: DORPP.2 with a structurally flexible linker and a
OTHER INFORMATION: cysteine residue
US-09-626-821A-5

Query Match 26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 11 PFPF 14
Db 4 PFPF 7

RESULT 63
US-07-794-288D-22
Sequence 22, Application US/07794288D
Patent No. 5580953
GENERAL INFORMATION:
APPLICANT: ELISABETH ALBRECHT,
APPLICANT: HOWARD JONES,
APPLICANT: LAURA S.L. GAETA,
APPLICANT: KATHRYN S. PRICKETT and
APPLICANT: KEVIN BEKIMONT
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: First Interstate World
STREET: Center
STREET: 633 West Fifth Street,
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM M.S. DOS (Version
OPERATING SYSTEM: 5.0)
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/794,288D
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/794,288
FILING DATE: 19-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Duff, Bradford, J.
REGISTRATION NUMBER: 32,219

REFERENCE/DOCKET NUMBER: 193/153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
FEATURE:
OTHER INFORMATION:
US-07-794-288D-22

Query Match 26.7%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 5 PVLV 8
Db 1 PVLV 4

RESULT 64
US-08-471-033-11
Sequence 11, Application US/08471033
Patent No. 5770696
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Malini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,033
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: P-40,403
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SOLv3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
ORGANISM: Bacillus thuringiensis
US-08-471-033-11

Query Match 26.7%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 9 VEPP 12
DB 6 VEPP 9

RESULT 65

US-08-471-044-11
Sequence 11, Application US/08471044
Patent No. 5840868

GENERAL INFORMATION:

APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J

TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,044
FILING DATE: 06-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483

FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594

FILING DATE: 09-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018

FILING DATE: 23-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057

FILING DATE: 25-MAR-1993

ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.

REGISTRATION NUMBER: 40,403

REFERENCE/DOCKET NUMBER: CGC 1695/cip3/div6 - SOLv3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8582

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
US-08-471-044-11

Query Match 26.7%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 9 VEPP 12
DB 6 VEPP 9

RESULT 66

US-08-463-483A-11
Sequence 11, Application US/08463483A
Patent No. 5849870

GENERAL INFORMATION:

APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J

TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,483A
FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594

FILING DATE: 09-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018

FILING DATE: 23-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057

FILING DATE: 25-MAR-1993

ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray

REGISTRATION NUMBER: 32,943

REFERENCE/DOCKET NUMBER: CGC 1695/cip3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8615

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

ORIGINAL SOURCE:

ORGANISM: Bacillus thuringiensis

US-08-463-483A-11

Query Match 26.7%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
|
|
|
|
Db 6 VEPF 9

RESULT 67
US-08-471-046A-11
; Sequence 11, Application US/08471046A
; Patent No. 5866326
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Kozziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: Method For Isolating Vegetative Insecticidal
; TITLE OF INVENTION: Protein Genes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5866326artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION NUMBER: US/08/471,046A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV8 - SOLV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis

Query Match 26.7%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 VEPF 12
|
|
|
|
Db 6 VEPF 9

RESULT 68
US-08-470-566B-11
; Sequence 11, Application US/08470566B
; Patent No. 5872212
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Kozziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5872212el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5872212artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION NUMBER: US/08/470,566B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV4 - SOLV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis

Query Match 26.7%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12

Db ||||
6 VEPF 9

RESULT 69
US-08-908-526-14
; Sequence 14, Application US/08908526
; Patent No. 5876730
; GENERAL INFORMATION:
; APPLICANT: Briggs, David R.
; APPLICANT: Harding, Paul H.
; TITLE OF INVENTION: HEPARIN BINDING GROWTH FACTOR (HBGF)
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,526
; FILING DATE: 07-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A., Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08766/003002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-908-526-14

Query Match 26.7%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 7 LPVE 10
Db ||||
8 LPVE 11

RESULT 70
US-08-838-219B-11
; Sequence 11, Application US/08838219B
; Patent No. 5877012
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: A No. 5877012el Class of Proteins for the
; TITLE OF INVENTION: Control of Plant Pests
; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,219B
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; US-08-838-219B-11

Query Match 26.7%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 9 VEPF 12
Db ||||
6 VEPF 9

RESULT 71
US-08-469-334-11
; Sequence 11, Application US/08469334
; Patent No. 5990383
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5990383el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive

```

; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,334
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463,483
; FILING DATE:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; ORIGINAL SOURCE:
; US-08-469-334-11

```

```

Query Match          26.7%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred.No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      9 VEPF 12
        |||||
Db      6 VEPF 9

```

```

RESULT 72
US-09-300-529-11
; Sequence 11, Application US/09300529
; Patent No. 6066783
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: Genes Encoding Insecticidal Proteins
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6066783artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,529
; FILING DATE: TBA
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,334
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19506L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; ORIGINAL SOURCE:
; US-09-300-529-11

```

```

Query Match          26.7%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred.No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      9 VEPF 12
        |||||
Db      6 VEPF 9

```

```

RESULT 73
US-09-233-336A-11
; Sequence 11, Application US/09233336A
; Patent No. 6107279
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: A No. 6107279el Class of Proteins for the
; CONTROL OF PLANT PESTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA

```

ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/233,336A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/838,219
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/314,594
 FILING DATE: 09-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/218,018
 FILING DATE: 23-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/037,057
 FILING DATE: 25-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pace, Gary M.
 REGISTRATION NUMBER: 40,403
 REFERENCE/DOCKET NUMBER: CGC 1925
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8582
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ORGANISM: Bacillus thuringiensis
 US-09-233-336A-11

Query Match 26.7%; Score 4; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEPF 12
 Db 6 VEPF 9

RESULT 74
 US-09-233-752A-11
 Sequence 11, Application US/09233752A
 Patent No. 6137033
 GENERAL INFORMATION:
 APPLICANT: Warren, Gregory W
 APPLICANT: Kosiel, Michael G
 APPLICANT: Mullins, Martha A
 APPLICANT: Nye, Gordon J
 APPLICANT: Carr, Brian
 APPLICANT: Desai, Nalini M
 APPLICANT: Kostichka, N. Kristy
 APPLICANT: Duck, Nicholas B
 TITLE OF INVENTION: A No. 6137033el Class of Proteins for the
 CONTROL OF PLANT PESTS
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESS: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: NY
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/233,752A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/838,219
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/314,594
 FILING DATE: 09-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/218,018
 FILING DATE: 23-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/037,057
 FILING DATE: 25-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pace, Gary M.
 REGISTRATION NUMBER: 40,403
 REFERENCE/DOCKET NUMBER: CGC 1925
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8582
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ORGANISM: Bacillus thuringiensis
 US-09-233-752A-11

Query Match 26.7%; Score 4; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEPF 12
 Db 6 VEPF 9

RESULT 75
 US-09-027-998A-29
 Sequence 29, Application US/09027998A
 Patent No. 6284949
 GENERAL INFORMATION:
 APPLICANT: Fischhoff, David A
 APPLICANT: Fuchs, Roy L
 APPLICANT: Perlak, Frederick J
 TITLE OF INVENTION: Insect Resistant Plants
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold White and Durkee
 STREET: PO Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210-4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/027,998A
 FILING DATE: 23-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:


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; NAME: Patterson, Melinda L
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
US-09-027-998A-29

Query Match      26.7%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 PPFV 15
        ||||
Db       7 PPFV 10
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Search completed: November 25, 2003, 20:16:01
Job time : 17.3564 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 10.1223 Seconds
(without alignments)
104.507 Million cell updates/sec

Title: US-09-641-801-6

Perfect score: 11

Sequence: 1 MPQNFYKLPQM 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	12	2 PH1454	T-cell receptor al
2	4	36.4	13	2 PH0787	T-cell receptor al
3	3	27.3	6	2 A17765	hypothetical prote
4	3	27.3	8	2 S16324	hypothetical prote
5	3	27.3	8	2 I49404	prealbumin - weste
6	3	27.3	11	2 A38590	transforming prote
7	3	27.3	11	2 F33098	214K exoantigen (v
8	3	27.3	12	2 E45691	probable minor cap
9	3	27.3	12	2 PA0047	protein QAL00045 -
10	3	27.3	13	2 S01119	photosystem II pro
11	3	27.3	13	2 S29488	GTP-binding protei
12	3	27.3	14	2 B36079	hypothetical prote
13	3	27.3	14	2 S29486	GTP-binding protei
14	3	27.3	14	2 JS0272	hypothetical 1.5K
15	3	27.3	14	2 PC4382	dehydrin 4.5K poly
16	3	27.3	15	2 IS2734	gene c-Ki-ras prot
17	3	27.3	15	2 PH1782	T cell receptor al
18	3	27.3	15	2 PQ0073	T-cell receptor be
19	3	27.3	15	2 I65478	c-Ki-ras - hamster
20	3	27.3	15	2 S08282	cytochrome P450K-2
21	3	27.3	16	2 C39509	mannose-specific 1
22	3	27.3	16	2 S22040	cob protein - comm
23	3	27.3	16	2 PH1778	T cell receptor al
24	3	27.3	16	2 I46275	hemoglobin beta-x
25	3	27.3	17	2 I42753	interferon alpha (
26	3	27.3	18	2 PN0149	beta-Gliadine 13 -
27	3	27.3	18	2 B44995	alkanal monooxygen
28	3	27.3	18	2 S33971	alpha-macroglobuli
29	3	27.3	18	2 S39009	oviductin - golden

30	3	27.3	19	2 S60633	Ha-transporting tw
31	3	27.3	19	2 S59486	cell wall protein,
32	3	27.3	20	2 S08605	hypothetical prote
33	3	27.3	20	2 A34859	heliothermine - Mex
34	3	27.3	20	2 S10876	hypothetical prote
35	3	18.2	3	3 I78890	tyrosine protein k
36	2	18.2	3	3 S68328	blood cell protein
37	2	18.2	4	2 T46627	hypothetical prote
38	2	18.2	5	1 HOR08A	proctolin - Americ
39	2	18.2	5	2 JN0860	peptidyl-dipectida
40	2	18.2	5	2 C41225	copper resistance
41	2	18.2	5	2 E42364	flagellar protein
42	2	18.2	5	2 A60411	proctolin - Atlant
43	2	18.2	5	2 S53595	hypothetical prote
44	2	18.2	5	2 B44823	synaptosomal-assoc
45	2	18.2	6	2 S11556	hydrogensulfite re
46	2	18.2	6	2 PC4127	hypothetical 6 pro
47	2	18.2	6	2 I48126	alpha-tubulin 6 ch
48	2	18.2	6	2 B33532	alpha-tubulin D reg
49	2	18.2	6	2 I67345	IG mu chain D regi
50	2	18.2	6	2 I49424	MHC H2-K-K cell su
51	2	18.2	6	2 A43129	cytotoxic T-lympho
52	2	18.2	6	2 A35039	neuropeptide GNFRP
53	2	18.2	7	1 XEYDGD	hypothetical colla
54	2	18.2	7	1 NYPG7	galactose oxidase
55	2	18.2	7	2 JN0859	hypothalamic hepta
56	2	18.2	7	2 ECMUCR	peptidyl-dipectida
57	2	18.2	7	2 PT0087	catch-relaxing pep
58	2	18.2	7	2 S71299	ribulose-bisphosph
59	2	18.2	7	2 S33246	ICL2 protein - Par
60	2	18.2	7	2 B44787	neuromodulatory pe
61	2	18.2	7	2 B39040	calliPRFamide 11
62	2	18.2	7	2 E33932	calsequestrin, fas
63	2	18.2	7	2 EX0008	IG mu chain D regi
64	2	18.2	7	2 S68442	glucuronosyltransf
65	2	18.2	7	2 S45648	glutathione S-tran
66	2	18.2	7	2 S15597	Nat-transporting A
67	2	18.2	7	2 A61348	orf 4 rara 5'-regi
68	2	18.2	8	2 A28004	red pigment-concen
69	2	18.2	8	2 S08995	adipokinetic hormo
70	2	18.2	8	2 S10596	hypertrehalosemic
71	2	18.2	8	2 A49823	adipokinetic hormo
72	2	18.2	8	2 A43976	neuropeptide led-C
73	2	18.2	8	2 B43976	hypertrehalosemic
74	2	18.2	8	2 S55310	adipokinetic hormo
75	2	18.2	8	2 A58420	adipokinetic hormo
76	2	18.2	8	2 B24749	neuropeptide B - b
77	2	18.2	8	2 S43971	tumor-associated a
78	2	18.2	8	2 S43972	tumor-associated a
79	2	18.2	8	2 P40184	cagid protein vp
80	2	18.2	8	2 S70727	ipgf protein - Shi
81	2	18.2	8	2 S63493	disimilatory sulf
82	2	18.2	8	2 S68802	nitrate reductase
83	2	18.2	8	2 A05169	neuropeptide M-I -
84	2	18.2	8	2 JS0318	leucokinin VIII -
85	2	18.2	8	2 A14683	aspartate transami
86	2	18.2	8	2 I57018	enamelin f - bovin
87	2	18.2	8	2 S10783	gene Cfr protein
88	2	18.2	8	2 S65381	cytochrome-c oxida
89	2	18.2	8	2 I57532	MHC class I histoc
90	2	18.2	8	2 A59028	oxytocin - hippopo
91	2	18.2	9	2 A91466	oxytocin - spotted
92	2	18.2	9	2 A92774	oxytocin - finback
93	2	18.2	9	2 A33147	oxytocin - Austral
94	2	18.2	9	2 A33408	oxytocin - rabbit
95	2	18.2	9	2 S90667	ribosomal protein
96	2	18.2	9	2 S35538	calsequestrin, car
97	2	18.2	9	2 A61230	translation elonga
98	2	18.2	9	2 D58503	
99	2	18.2	9	2	
100	2	18.2	9	2	

ALIGNMENTS

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1
PHI454
T-cell receptor alpha chain (clone A3/72.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1454
R/Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1454
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 36.4%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNFY 6
|||
Db 7 QNFY 10

RESULT 2
PH0787
T-cell receptor alpha chain (F8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0787
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-2
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0787
A:Molecule type: mRNA
A:Residues: 1-13 <CAS>
A:Cross-references: EMBL:X60891
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 36.4%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNFY 6
|||
Db 8 QNFY 11

RESULT 3
A37765
hypotheical protein (csmA 5' region) - Chloroflexus aurantiacus (fragment)
C:Species: Chloroflexus aurantiacus
C>Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 30-Sep-1993
C:Accession: A37765
R/Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.
J. Bacteriol. 172, 4497-4504, 1990
A:Title: Gene encoding the 5.7-kilodalton chlorosome protein of Chloroflexus aurantiacus
A:Reference number: A37765; MUID:90330558; PMID:2376566
A:Accession: A37765
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <THL>
A:Cross-references: GB:M33964

Query Match 27.3%; Score 3; DB 2; Length 6;

QY 9 PQM 11
|||
Db 1 PQM 3

RESULT 4
SI6324
hypotheical protein 2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C:Accession: SI6324
R/Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A:Title: A novel class of plant proteins containing a homeodomain with a closely linked
A:Reference number: SI6323; MUID:91266907; PMID:1675603
A:Accession: SI6324
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <RUB>
A:Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 27.3%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
|||
Db 3 YKL 5

RESULT 5
I49404
prealbumin - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49404
R/Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49404
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <RES>
A:Cross-references: EMBL:U05689; NID:g497008; PIDN:AAB60461.1; PID:g642825

Query Match 27.3%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4
|||
Db 6 PQN 8

RESULT 6
A38590
transforming protein (Ddras) - slime mold (Dictyostelium discoideum) (fragment)
C:Species: Dictyostelium discoideum
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 30-Sep-1993
C:Accession: A38590
R/Esch, R.K.; Firtel, R.A.
Genes Dev. 5, 9-21, 1991
A:Title: cAMP and cell sorting control the spatial expression of a developmentally essen
A:Reference number: A38590; MUID:91115102; PMID:1703508
A:Accession: A38590
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <ESC>
A:Cross-references: GB:Z11804; GB:K02114; GB:X58190

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
|||
Db 4 YKL 6

RESULT 7
F33098
214K exoantigen (version 3) - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: F33098
R:Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: F33098
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <NIC>

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
|||
Db 3 LPQ 5

RESULT 8
E45691
probable minor capsid protein R117a [similarity] - Lactobacillus delbrueckii subsp. lact
C:Species: Lactobacillus delbrueckii subsp. lactis phage LL-H
C>Date: 24-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 28-Jul-2000
C:Accession: E45691
R:Vasala, A.; Dupont, L.; Baumann, M.; Ritzenthaler, P.; Alatosava, T.
J. Virol. 67, 3061-3068, 1993
A:Title: Molecular comparison of the structural proteins encoding gene clusters of two
A:Reference number: A45691; MUID:93267750; PMID:8497043
A:Accession: E45691
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <VAS>
A>Note: sequence extracted from NCBI backbone (NCBIN:132363, NCBIPI:132373)

Query Match 27.3%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
|||
Db 2 KLP 4

RESULT 9
PA0047
protein QA100045 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0047
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JPIB, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A:Reference number: PA0001
A:Accession: PA0047
A:Molecule type: Protein
A:Residues: 1-12 <KAM>

Query Match 27.3%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
|||
Db 7 KLP 9

RESULT 10
S01119
photosystem II protein psbK - spinach chloroplast (fragment)
C:Species: chloroplast Spinacia oleracea (spinach)
C>Date: 30-Jun-1989 #sequence_revision 31-Dec-1990 #text_change 19-Jan-1996
C:Accession: S01119
R:Murata, N.; Miyao, M.; Hayaashida, N.; Hidaka, T.; Sugiura, M.
FEBS Lett. 235, 283-288, 1988
A:Title: Identification of a new gene in the chloroplast genome encoding a low-molecular
A:Reference number: S01119
A:Accession: S01119
A:Molecule type: protein
A:Residues: 1-13 <MUR>
C:Genetics:
A:Gene: psbK
A:Genome: chloroplast
C:Superfamily: photosystem II protein psbK
C:Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem II; th

Query Match 27.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
|||
Db 1 KLP 3

RESULT 11
S29488
GTP-binding protein o-rab3 - marbled electric ray (fragment)
C:Species: Torpedo marmorata (marbled electric ray)
C>Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C:Accession: S29488
R:Volkmann, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.
PMAS Lett. 317, 53-56, 1993
A:Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic
A:Reference number: S29485; MUID:93154521; PMID:8428634
A:Accession: S29488
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <VOL>

Query Match 27.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNF 5
|||
Db 6 QNF 8

RESULT 12

B36079
hypothetical protein insulin-like growth factor I 5'-region - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Nov-1990 #sequence_revision 13-Sep-1991 #text_change 18-Aug-2000
C:Accession: B36079
R:Kajimoto, Y.; Rotwein, P.
Mol. Endocrinol. 4, 217-226, 1990
A:Title: Evolution of insulin-like growth factor I (IGF-I): structure and expression of
A:Reference number: A36079; MUID:90231335; PMID:2330002
A:Accession: B36079
A:Molecule type: mRNA
A:Residues: 1-14 <KAJ>

A;Cross-References: GB:M29857; NID:g214287; PIDN:AAA70329.1; PID:g903887
 A;Note: the authors translated the codon CAG for residue 4 as Gly
 C;Superfamily: unassigned leader peptides

Query Match 27.3%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
 |||
 Db 2 LPQ 4

RESULT 13

S29486
 GTP-binding protein o-rab3 - electric ray (Discothyoe ommata) (fragment)

C;Species: Discothyoe ommata
 C;Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
 C;Accession: S29486

R;Volkmann, W.; Pevsner, J.; Eiferink, L.A.; Scheller, R.H.

FEBS Lett. 317, 53-56, 1993

A;Title: Association of three small GTP-binding proteins with cholinergic synaptic vesicle

A;Reference number: S29486; MUID:93154521; PMID:8428634

A;Accession: S29486

A;Status: Preliminary

A;Molecule type: Protein

A;Residues: 1-14 <VOL>

Query Match 27.3%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNF 5
 |||
 Db 7 QNF 9

RESULT 14

JS0272

hypothetical 1.5K protein - Chinese hamster

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-Apr-1995

C;Accession: JS0272

R;Andrulis, I.L.; Shotwell, M.; Evans-Blackler, S.; Zalkin, H.; Siminovich, L.; Ray, P.

Gene 80, 75-85, 1989

A;Title: Fine structure analysis of the Chinese hamster AS gene encoding asparagine synthetase

A;Reference number: A91619; MUID:90005788; PMID:2477309

A;Accession: JS0272

A;Molecule type: DNA

A;Residues: 1-14 <AND>

A;Experimental source: ovary

C;Comment: This open reading frame is located in the 5'-flanking region of the gene encoding

C;Genetics:

A;Gene: AS

Query Match 27.3%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
 |||
 Db 3 KLP 5

RESULT 15

PC4382

dehydrin 4.5K polypeptide - Soybean (fragment)

N;Alternate names: acid soluble 26K protein

C;Species: Glycine max

C;Date: 06-Nov-1997 #sequence_revision 06-Nov-1997 #text_change 18-Jul-2001

C;Accession: PC4382

R;Moma, M.; Haraguchi, K.; Saito, M.; Chikuni, K.; Harada, K.

Biosci. Biotechnol. Biochem. 61, 1286-1291, 1997

A;Title: Purification and characterization of the acid soluble 26-kDa polypeptide from soybean
 A;Reference number: PC4380; MUID:97446521; PMID:9301109

A;Accession: PC4382

A;Molecule type: protein

A;Residues: 1-14 <MOM>

A;Experimental source: seed

C;Comment: This protein is rich in hydrophilic amino acid, and highly heat stable.

Query Match 27.3%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
 |||
 Db 7 KLP 9

RESULT 16

IS2734

Gene C-Ki-ras protein - hamster (fragment)

C;Species: Cricetinae gen. sp. (hamster)

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 28-May-1999

C;Accession: IS2734

R;Takahashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian, C.

Carcinogenesis 16, 931-939, 1995

A;Title: Differences in molecular biological, biological and growth characteristics between

A;Reference number: IS2734; MUID:95246257; PMID:7728976

A;Accession: IS2734

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-15 <RES>

A;Cross-References: GB:S77068; NID:g914176

C;Genetics:

A;Gene: C-Ki-ras

C;Superfamily: ras transforming protein; translation elongation factor Tu homology

C;Keywords: GTP binding

Query Match 27.3%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
 |||
 Db 4 YKL 6

RESULT 17

PH1762

T cell receptor alpha chain V region (clone 1V alpha 23-1) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: PH1762

R;Porcell, S.; Yockey, C.B.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A;Reference number: PH1754; MUID:93301585; PMID:8391057

A;Accession: PH1762

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-15 <POR>

Query Match 27.3%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
 |||
 Db 10 YKL 12

RESULT 18

PQ0073

```

T-cell receptor beta chain (BTB48) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C:Accession: PQ0073
R:Tanaka, A.; Ishiguro, N.; Shinagawa, M.
submitted to JIPID, May 1990
A:Description: Sequence analysis of bovine T-cell receptor beta chain genes.
A:Reference number: JQ0472
A:Accession: PQ0073
A:Molecule type: mRNA
A:Residues: 1-15 <TAN>
A:Experimental source: T cell
C:Genetics:
A:Gene: BTB48
C:Keywords: receptor

Query Match      27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 QNF 5
      |||
Db      4 QNF 6
      |||

RESULT 19
165478
C:Ki-ras - hamster (fragment)
C:Species: Cricetinae gen. sp. (hamster)
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 28-Feb-1997
C:Accession: 165478
R:Takahashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian,
Carcinogenesis 16, 931-939, 1995
A>Title: Differences in molecular biological, biological and growth characteristics between
A:Reference number: 152734; MUID:95246257; PMID:7728976
A:Accession: 165478
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-15 <RBS>
A:Cross-references: GB:S77069; NID:G914177
C:Genetics:
A:Gene: c-Ki-ras

Query Match      27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 YKL 8
      |||
Db      4 YKL 6
      |||

RESULT 20
S08282
cytochrome P450K-2 - rat (tentative sequence) (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Mar-2000
C:Accession: S08282
R:Imaoka, S.; Nagashima, K.; Funae, Y.
Arch. Biochem. Biophys. 276, 473-480, 1990
A>Title: Characterization of three cytochrome P450s purified from renal microsomes of un
A:Reference number: S08282; MUID:90185442; PMID:2306108
A:Accession: S08282
A:Molecule type: protein
A:Residues: 1-15 <IMA>
C:Keywords: heme; monooxygenase

Query Match      27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 KLP 9
      |||
Db      4 YKL 6
      |||

T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1778
R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A>Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1778
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <FOR>

Query Match      27.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 YKL 8
      |||
Db      3 NFY 5
      |||

mannose-specific lectin B-SUA-II chain b-1, bark - Japanese pagoda tree (fragment)
C:Species: Sophora japonica (Japanese pagoda tree)
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: C39509
R;Ueno, M.; Ogawa, H.; Matsumoto, I.; Seno, N.
J. Biol. Chem. 266, 3146-3153, 1991
A>Title: A novel mannose-specific and sugar specifically aggregatable lectin from the ba
A:Reference number: A39509; MUID:91131618; PMID:1993686
A:Accession: C39509
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <UEN>

Query Match      27.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LPQ 10
      |||
Db      2 LPQ 4
      |||

cob protein - common sunflower
C:Species: Helianthus annuus (common sunflower)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997
C:Accession: S22040
R;Koehler, R.H.
submitted to the EMBL Data Library, October 1991
A:Reference number: S22040
A:Accession: S22040
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <KOE>
A:Cross-references: EMBL:X62592; NID:G12990; PID:G12991

Query Match      27.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 NFY 6
      |||
Db      3 NFY 5
      |||

T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1778
R;Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A>Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1778
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <FOR>

Query Match      27.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 YKL 8
      |||
Db      3 NFY 5
      |||

```

```

Db          12 YKL 14

RESULT 24
146275
hemoglobin beta-x chain - goat (fragment)
C:Species: Capra aegagrus hircus (domestic goat)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46275
R:Haynes, J.R.; Rostock, P.R.; Schon, E.A.; Gallagher, P.M.; Burks, D.J.; Smith, K.; Lin
J.; Biol. Chem. 255:6355-6367, 1980
A>Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumptive
A:Reference number: I46275; MUID:80227766; PMID:6248519
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <HAY>
A:Cross-references: GB:K00659; NID:gl64151; PIDN:AAA30919.1; PID:gl64156

Query Match          27.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 QNF 5
Db          12 QNF 14

RESULT 25
142753
interferon alpha (component 1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 17-Mar-1999
C:Accession: I42753
R:Zoon, K.C.; Miller, D.; Bekisz, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.; Hu,
J.; Biol. Chem. 267, 15210-15216, 1992
A>Title: Purification and characterization of multiple components of human lymphoblastoid
A:Reference number: A42753; MUID:92340576; PMID:1634550
A:Accession: I42753
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <ZOO>

Query Match          27.3%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          8 LPQ 10
Db          3 LPQ 5

RESULT 26
PN0149
beta-Gliadine 13 - Aegilops longissima (fragment)
C:Species: Aegilops longissima
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PN0149
R:Odintsova, T.I.; Egorov, T.A.
Biokhimiya 55, 509-516, 1990
A>Title: N-terminal sequences of omega-gliadins of Aegilops longissima: On the origin of
A:Reference number: PN0146; MUID:90283493; PMID:2354218
A:Accession: PN0149
A:Molecule type: protein
A:Residues: 1-18 <ODI>
A:Experimental source: strain K-202
C:Superfamily: gliadin

Query Match          27.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 PQN 4

us-09-641-801-6.oligo.rpr

Db          10 PQN 12

RESULT 27
B44995
alkanal monooxygenase (PMN-linked) (EC 1.14.14.3) beta chain - flashlight fish symbiont
C:Species: flashlight fish symbiont bacterium
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
C:Accession: B44995
R:Haywood, M.G.
Arch. Microbiol. 154, 496-503, 1990
A>Title: Relationship of the luminous bacterial symbiont of the Caribbean flashlight fis
genes.
A:Reference number: A44995; MUID:91076680; PMID:2256783
A:Accession: B44995
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <HAY>
A:Cross-references: GB:M36597; NID:9213345; PIDN:AAA91214.1; PID:gl204253
C:Keywords: PMN; luminescence; monooxygenase; oxidoreductase

Query Match          27.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 QNF 5
Db          8 QNF 10

RESULT 28
S3971
alpha-macroglobulin proteinase inhibitor - common octopus
C:Species: Octopus vulgaris (common octopus)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S3971
R:Thøgersen, I.B.; Salvesen, G.; Brucato, F.H.; Pizzo, S.V.; Engild, J.J.
Biochem. J. 285, 521-527, 1992
A>Title: Purification and characterization of an alpha-macroglobulin proteinase inhibito
A:Reference number: S23971; MUID:92344633; PMID:1379044
A:Accession: S23971
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <THO>

Query Match          27.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 NPY 6
Db          12 NPY 14

RESULT 29
S39009
oviductin - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 19-Mar-1997 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S39009
R:Malette, B.; Bleau, G.
Biochem. J. 295, 437-445, 1993
A>Title: Biochemical characterization of hamster oviductin as a sulphated zona pellucida
A:Reference number: S39009; MUID:94059881; PMID:8240241
A:Accession: S39009
A:Molecule type: protein
A:Residues: 1-18 <MAL>
C:Keywords: glycoprotein

Query Match          27.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 6 YKL 8
 Db 1 YKL 3

RESULT 30
 S0633
 H-transferring two-sector ATPase (EC 3.6.3.14) protein 8 - brine shrimp mitochondrion
 C:Species: mitochondrion Artemia sp. (brine shrimp)
 A:Variety: Strain La Mata
 C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 03-Jun-2002
 C:Accession: S0633
 R:Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.
 J. Mol. Evol. 38, 156-168, 1994
 A:Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and par
 A:Reference number: S0624; MUID:94223692; PMID:8169960
 A:Accession: S0633
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-19 <PER>
 A:Cross-references: EMBL:X67263; NID:g11210; PIDN:CAA47685.1; PID:g11211
 A:Experimental source: strain La Mata
 A:Note: the source is designated as Artemia parthenogenetica
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
 C:Genetics:
 A:Gene: ATP8
 A:Genome: mitochondrion
 A:Genetic code: SGC4
 C:Superfamily: H-transferring ATP synthase protein 8
 C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi

Query Match 27.3%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PQM 11
 Db 2 PQM 4

RESULT 31
 S59486
 cell wall protein, 22K - kidney bean (fragment)
 C:Species: Phaseolus vulgaris (kidney bean)
 C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C:Accession: S59486
 R:Wojtaszek, P.; Tretowan, J.; Bolwell, G.P.
 Plant Mol. Biol. 28, 1075-1087, 1995
 A:Title: Specificity in the immobilisation of cell wall proteins in response to differ
 A:Reference number: S59481; MUID:96011753; PMID:7548825
 A:Accession: S59486
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-19 <WOJ>

Query Match 27.3%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQM 4
 Db 14 PQM 16

RESULT 32
 S08605
 hypothetical protein 1 estrogen receptor 5'-region - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 18-Aug-2000
 C:Accession: S08605
 R:Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.
 EMBO J. 5, 891-897, 1986

A:Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oes
 A:Reference number: S07192; MUID:86247578; PMID:3755102
 A:Accession: S08605
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-20 <KRU>
 A:Cross-references: EMBL:X03805; NID:g63378; PIDN:CAA27431.1; PID:g63379
 A:Note: the authors translated the codon TTT for residue 5 as Gly and TTC for residue 16
 C:Superfamily: unassigned leader peptides

Query Match 27.3%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQM 4
 Db 12 PQM 14

RESULT 33
 A34859
 helohermine - Mexican beaded lizard (fragment)
 C:Species: Heloderma horridum (Mexican beaded lizard)
 C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 30-Sep-1993
 C:Accession: A34859
 R:Mochca-Morales, J.; Martin, B.M.; Possani, L.D.
 Toxicon 28, 299-309, 1990
 A:Title: Isolation and characterization of helohermine, a novel toxin from Heloderma ho
 A:Reference number: A34859; MUID:90260878; PMID:1693019
 A:Accession: A34859
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <MOC>

Query Match 27.3%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
 Db 5 KLP 7

RESULT 34
 S10876
 hypothetical protein - human
 C:Species: Homo sapiens (man)
 C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Nov-1994
 C:Accession: S10876
 R:Assouline, Z.; Kerbirou-Nabias, D.M.; Pietu, G.; Thomas, N.; Bahnak, B.R.; Meyer, D.
 Biochem. Biophys. Res. Commun. 153, 1159-1166, 1988
 A:Title: The human gene for von Willebrand factor. Identification of repetitive Alu sequ
 A:Reference number: S10876; MUID:88268889; PMID:3260493
 A:Accession: S10876
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-20 <ASS>
 A:Cross-references: EMBL:X07258

Query Match 27.3%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
 Db 8 LPQ 10

RESULT 35
 I78890
 tyrosine protein kinase - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: I78890
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.
Oncogene 9, 3437-3448, 1994
A;Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protease
A;Reference number: I58407; MUID:95060800; PMID:7970703
C;Accession: I78890
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3 <RES>
A;Cross-references: GB:I33339; NID:G609536; PIDN:AAA64432.1; PID:G609538
C;Genetics:
A;Gene: p52ntk

Query Match 18.2%; Score 2; DB 3; Length 3;
Best Local Similarity 100.0%; Pred.No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MP 2
||
Db 1 MP 2

RESULT 36
S68328
blood cell protein A - Molgula manhattensis (fragment)
C;Species: Molgula manhattensis
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: S68328
R;Taylor, S.W.; Ross, M.M.; Waite, J.H.
Arch. Biochem. Biophys. 324, 228-240, 1995
A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from the
A;Reference number: S68325; MUID:96132650; PMID:9554314
A;Accession: S68328
A;Molecule type: protein
A;Residues: 1-3 <YAY>

Query Match 18.2%; Score 2; DB 3; Length 3;
Best Local Similarity 100.0%; Pred.No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FY 6
||
Db 2 FY 3

RESULT 37
T46627
hypothetical protein c4 - loblolly pine
C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: T46627
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
submitted to the EMBL Data Library, July 1995
A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do
A;Reference number: Z23105
A;Accession: T46627
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-4 <CHA>
A;Cross-references: EMBL:U31309; NID:G974285; PID:G974292
A;Experimental source: strain s6PTx56PT3; 8 month seedlings

Query Match 18.2%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred.No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KL 8
||
Db 2 KL 3

RESULT 38
HORCHA

proctolin - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 29-Jul-1991 #sequence_revision 29-Jul-1991 #text_change 23-Aug-1996
C;Accession: A01644
R;Starratt, A.N.; Brown, B.E.
Life Sci. 17, 1253-1256, 1975
A;Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects
A;Reference number: A93048; MUID:76074708; PMID:576
A;Accession: A01644
A;Molecule type: protein
A;Residues: 1-5 <STA>
A;Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmac
R;O'Shea, M.; Adams, M.E.
Science 213, 567-569, 1981
A;Title: Pentapeptide (proctolin) associated with an identified neuron.
A;Reference number: A94260; MUID:91225865; PMID:6113690
A;Contents: annotation; biological source
A;Comment: this peptide is found in the lateral white neurons, which occur in the cockr
innervate the striated hindgut muscles in insects and stimulate contraction of these mus
C;Superfamily: proctolin
C;Keywords: neuropeptide

Query Match 18.2%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LP 9
||
Db 3 LP 4

RESULT 39
JN0860
peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito
C;Species: Sarda orientalis (striped bonito)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: JN0860
R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe
A;Reference number: JN0859; MUID:94080036; PMID:7764272
A;Accession: JN0860
A;Molecule type: protein
A;Residues: 1-5 <MAT>
A;Experimental source: intestine
C;Comment: The carboxyl-terminus is essential for the protein's expression of angiotensi
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 18.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LP 9
||
Db 2 LP 3

RESULT 40
C41225
copper resistance protein - Pseudomonas syringae pv. tomato (fragment)
C;Species: Pseudomonas syringae pv. tomato
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C;Accession: C41225
R;Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 8915-8919, 1992
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer mem
A;Reference number: A41225; MUID:92020961; PMID:1924351
A;Accession: C41225
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CHA>

A;Cross-references: EMBL:X66844

Query Match 18.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MP 2
||
Db 1 MP 2

RESULT 44

B44823
synaptonemal-associated protein SNAP-25 peptide 10A - rabbit (fragment)
N;Alternate names: superprotein peptide 10A
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: B44823
R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A;Reference number: A44823; MUID:92044785; PMID:1941090
A;Accession: B44823
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <LO>
A;Experimental source: visual tissue
A;Note: sequence extracted from NCBI backbone (NCBI:P.64255)
C;Keywords: membrane trafficking

Query Match 18.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QM 11
||
Db 2 QM 3

RESULT 45

S11556
hydrogenulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragment)
N;Alternate names: bisulfite reductase; desulfofuscin
C;Species: Desulfovibrio thermophilus
C;Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998
C;Accession: S11556
R;Faugue, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.; L
Biochim. Biophys. Acta 1040, 112-118, 1990
A;Title: Purification and characterization of bisulfite reductase (desulfofuscin) from
A;Reference number: S11024; MUID:90335276; PMID:2165817
A;Accession: S11556
A;Molecule type: protein
A;Residues: 1-6 <FAU>
C;Keywords: oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YK 7
||
Db 5 YK 6

RESULT 46

PC4127
hypothetical 6 protein - Streptomyces clavuligerus (fragment)
C;Species: Streptomyces clavuligerus
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PC4127
R;Rodriguez-Garcia, A.; Martin, J.F.; Liras, P.
Gene 167, 9-15, 1995
A;Title: The argG gene of Streptomyces clavuligerus has low homology to unstable argG fr

Query Match 18.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8
||
Db 3 KL 4

RESULT 41

E42364
flagellar protein flir - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
C;Accession: E42364
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
J. Bacteriol. 173, 3564-3572, 1991
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seg
A;Reference number: A42364; MUID:91258342; PMID:1646201
A;Accession: E42364
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 <VO>
A;Cross-references: GB:M62408

Query Match 18.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
||
Db 4 LP 5

RESULT 42

A60411
proctolin - Atlantic horseshoe crab
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 17-Mar-1999
C;Accession: A60411
R;Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, D
Peptides 11, 205-211, 1990
A;Title: Identification of proctolin in the central nervous system of the horseshoe crab
A;Reference number: A60411; MUID:90287800; PMID:2356151
A;Accession: A60411
A;Molecule type: protein
A;Residues: 1-5 <GRO>
C;Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horse
C;Keywords: neuropeptide

Query Match 18.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
||
Db 3 LP 4

RESULT 43

S53595
hypothetical protein (upstream of transcription factor, CCAAT-binding) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
C;Accession: S53595
R;Calhoun, C.F.; Bowman, P.R.J.; Snippe, L.; Ab, G.
Nucleic Acids Res. 22, 5540-5547, 1994
A;Title: Translation start site multiplicity of the CCAAT/enhancer binding protein alpha
A;Reference number: S53595; MUID:95140613; PMID:7838705
A;Accession: S53595
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 <CAL>

A:Reference number: JC4548; MUID:96144242; PMID:8566818

A:Accession: FC4127

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-6 <ROD>

A:Cross-references: EMBL:Z49111

Query Match 18.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QN 4

DB 2 QN 3

RESULT 47

148126

alpha-tubulin - Chinese hamster (fragment)

C:Species: Crictetus griseus (Chinese hamster)

C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999

C:Accession: I48126

R:Elliot, E.M.; Sarangi, F.; Henderson, G.; Ling, V.

Can. J. Biochem. Cell Biol. 63, 511-519, 1985

A:Title: Cloning of 11 alpha-tubulin gene sequences from the genome of Chinese hamster

A:Reference number: 148126; MUID:86001952; PMID:2931165

A:Accession: I48126

A:Molecule type: DNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-6 <RES>

A:Cross-references: GB:M25895; NID:g341417; PIDN:AAA74493.1; PID:g516601

C:Genetics:

A:Introns: 3/3

Query Match 18.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8

DB 2 KL 3

RESULT 48

B3932

Ig mu chain D region (D23) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996

C:Accession: B3932

R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.

Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989

A:Title: Two murine natural polyclonal antibodies are encoded by nonmutated germ-

A:Reference number: A33932; MUID:89282823; PMID:2499887

A:Accession: B3932

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-6 <BAC>

A:Cross-references: GB:M27107

C:Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8

DB 2 KL 3

RESULT 49

167345

MHC H2-K-k cell surface glycoprotein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C:Accession: I67345

R:Archibald, A.L.; Thompson, N.A.; Kvist, S.

EMBO J. 5, 957-965, 1986

A:Title: A single nucleotide difference at the 3' end of an intron causes differential s

A:Reference number: I53243; MUID:86247587; PMID:3013627

A:Accession: I67345

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6 <RES>

A:Cross-references: GB:M26859; NID:g199439; PIDN:AAA39612.1; PID:g387458

C:Genetics:

A:Introns: 6/1

C:Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9

DB 1 LP 2

RESULT 50

I49424

cytotoxic T-lymphocyte proteinase 3 (EC 3.4.21.-) - western wild mouse (fragment)

C:Species: Mus spretus (western wild mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: I49424

R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maizaki, Y.; Nadeau, J.H.

Mamm. Genome 5, 349-355, 1994

A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A:Reference number: I48934; MUID:94319082; PMID:8043949

A:Accession: I49424

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6 <RES>

A:Cross-references: EMBL:U05745; NID:9497084; PIDN:AAB60481.1; PID:g642831

C:Keywords: hydrolase; serine proteinase

Query Match 18.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8

DB 4 KL 5

RESULT 51

A43129

neuropeptide GNFRamide - tapeworm (Moniezia expansa)

C:Species: Moniezia expansa

C>Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 14-Nov-1997

C:Accession: A43129

R:Maule, A.; Shaw, C.; Halton, D.; Thim, L.

Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993

A:Title: GNFRamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep t

A:Reference number: A43129; MUID:93312289; PMID:8323531

A:Accession: A43129

A:Molecule type: protein

A:Residues: 1-6 <MAU>

C:Keywords: amidated carboxyl end; neuropeptide

F;6/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5

DB 2 NF 3

RESULT 52
 A35039
 hypothetical collagen alpha 2(I) intron 2 protein 1 - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C:Accession: A35039
 R:Bernmet, V.D.; Adams, S.L.
 J. Biol. Chem. 265, 2223-2230, 1990
 A>Title: Identification of a cartilage-specific promoter within intron 2 of the chick alpha 2(I) collagen gene
 A:Reference number: A35039; PMID:1688851
 A:Accession: A35039
 A:Molecule type: mRNA
 A:Residues: 1-6 <BN>
 A:Cross-references: GB:M33382; NID:g211043
 A>Note: This ORF is not translated in GenBank entry CHKA21CG
 C:Comment: This sequence is the translation of a cartilage specific alternative transcript
 C:Keywords: alternative splicing; cartilage
 Query Match 18.2%; Score 2; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 LP 9
 DB 4 LP 5
 RESULT 53
 XYDGD
 galactose oxidase inhibitor - fungus (Cladobotryum dendroides)
 C:Species: Cladobotryum dendroides
 C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-1993
 C:Accession: A01341
 R:Avigad, G.; Markus, Z.
 Fed. Proc. 31, 447, 1972
 A:Reference number: A01341
 A:Accession: A01341
 A:Molecule type: protein
 A:Residues: 1-7 <AVI>
 C:Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxidase, which is inactivated by the enzyme by binding to its prosthetic copper group.
 C:Superfamily: galactose oxidase inhibitor
 C:Keywords: copper
 Query Match 18.2%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QN 4
 DB 3 QN 4
 RESULT 54
 NYEG7
 hypothalamic heptapeptide - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 23-Aug-1996
 C:Accession: A01417
 R:Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong, H.M. Metab. Res. 13, 228-232, 1981
 A>Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-releasing activity
 A:Reference number: A01417; PMID:81213980; PMID:6263778
 A:Accession: A01417
 A:Molecule type: protein
 A:Residues: 1-7 <CHA>
 C:Superfamily: hypothalamic heptapeptide
 C:Keywords: hypothalamus
 Query Match 18.2%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QN 4
 DB 3 QN 4
 RESULT 55
 JN0859
 peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito
 C:Species: Sarda orientalis (striped bonito)
 C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C:Accession: JN0859
 R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
 A>Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide from the skin of striped bonito
 A:Reference number: JN0859; PMID:94080036; PMID:7764272
 A:Accession: JN0859
 A:Molecule type: protein
 A:Residues: 1-7 <MAT>
 A:Experimental source: intestine
 A:Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin I-converting enzyme inhibitory peptide
 C:Superfamily: bradykinin-potentiating peptide
 C:Keywords: angiotensin-converting enzyme inhibitor
 Query Match 18.2%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KL 8
 DB 4 KL 5
 RESULT 56
 ECMUCR
 catch-relaxing peptide - blue mussel
 N:Alternate names: CARP
 C:Species: Mytilus edulis (blue mussel)
 C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C:Accession: A29342
 R:Hirata, T.; Kubota, I.; Takabatake, I.; Kawahara, A.; Shimamoto, N.; Munesaka, Y.
 Brain Res. 422, 374-376, 1987
 A>Title: Catch-relaxing peptide isolated from Mytilus pedal ganglia.
 A:Reference number: A29342; PMID:88052022; PMID:3676797
 A:Accession: A29342
 A:Molecule type: protein
 A:Residues: 1-7 <HR>
 C:Comment: This peptide exhibits both potentiating (contraction) and inhibitory (relaxation) activities
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end; hormone; retractor muscle
 F:7/Modified site: amidated carboxyl end (Leu) #status experimental
 Query Match 18.2%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MP 2
 DB 2 MP 3
 RESULT 57
 PT0087
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - Arabidopsis thaliana (frag)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Nov-1999
 C:Accession: PT0087
 R:Tsuigita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
 submitted to JIPID, December 1995
 A:Description: Two dimensional electrophoresis of plant proteins and standardization of
 A:Reference number: PNO173
 A:Accession: PT0087

A;Molecule type: protein
A;Residues: 1-7 <TSU>
A;Experimental source: leaf
C;Keywords: acetylated amino end; carbon-carbon lyase; carboxy-lyase
F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQ 3
||
2 PQ 3

Db

RESULT 58
S71299
ICL2 protein - Paramecium tetraurelia (fragment)
C;Species: Paramecium tetraurelia
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
C;Accession: S71299
R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
Eur. J. Biochem. 238, 121-128, 1996
A;Title: Characterization of centrin genes in Paramecium.
A;Reference number: S71298; MUID:96248429; PMID:8665928
A;Accession: S71299
A;Molecule type: Protein
A;Residues: 1-7 <WAD>
A;Experimental source: strain d4-2
C;Genetics:
A;Genetic code: SGC5

Query Match 18.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQ 3
||
5 PQ 6

Db

RESULT 59
S3246
neuromodulatory peptide Wamide-3 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S3246
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t
A;Reference number: S3244; MUID:93265912; PMID:8495720
A;Accession: S3246
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIN>

Query Match 18.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QM 11
||
3 QM 4

Db

RESULT 60
B44787
calliphorinamide 11 - bluebottle fly (Calliphora vomitoria)
C;Species: Calliphora vomitoria
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: B44787
R;Duve, H.; Johnson, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992

A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi-
A;Reference number: A41978; MUID:92196111; PMID:1549595
A;Accession: B44787
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <DUV>
C;Keywords: amidated carboxyl end; neuropeptide
F;7/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
||
3 NF 4

Db

RESULT 61
B39040
calasequestrin, fast skeletal muscle - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C;Accession: B39040
R;Cala, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A;Title: Phosphorylation of cardiac and skeletal muscle calasequestrin isoforms by casein
A;Reference number: A39040; MUID:91093153; PMID:1985907
A;Accession: B39040
A;Status: preliminary
A;Molecule type: Protein
A;Residues: 1-7 <CAL>
C;Keywords: phosphoprotein; skeletal muscle

Query Match 18.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
||
6 LP 7

Db

RESULT 62
E33932
I9 mu chain D region (E7) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-l
A;Reference number: A33932; MUID:89282823; PMID:2499887
A;Accession: E33932
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-7 <BAC>
A;Cross-references: GB:M27106
C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FY 6
||
3 FY 4

Db

RESULT 63
PX0008
glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)
N;Alternate names: UDP-glucuronyltransferase

```

C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 07-Feb-1997
C:Accession: PX0008
R:Yokota, H.; Yuasa, A.; Sato, R.
J. Biochem. 104, 531-536, 1988
A:Title: Purification and properties of a form of UDP-glucuronyltransferase from liver
A:Reference number: PX0008; MUID:89197852; PMID:3149280
A:Accession: PX0008
A:Molecule type: protein
A:Residues: 1-7 <YOK>
C:Keywords: Glycosyltransferase; hexosyltransferase; liver

Query Match      18.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 KL 8
        ||
DB      2 KL 3

RESULT 64
S66442
glutathione S-transferase P - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S66442
R:Nishikura, J.; Sakai, M.; Nishi, S.; Hatanaka, Y.
Eur. J. Biochem. 232, 106-110, 1995
A:Title: Identification of the electrophilic substrate-binding site of glutathione S-transferase
A:Reference number: S66442; MUID:96048035; PMID:7556138
A:Accession: S66442
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <NIS>

Query Match      18.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LP 9
        ||
DB      2 LP 3

RESULT 65
S45648
Na+-transporting ATP synthase (EC 3.6.1.-) alpha chain - Acetobacterium woodii (fragment)
N:Alternate names: ATPase alpha chain
C:Species: Acetobacterium woodii
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C:Accession: S45648
R:Reidlinger, J.; Mueller, V.
Eur. J. Biochem. 223, 275-283, 1994
A:Title: Purification of ATP synthase from Acetobacterium woodii and identification as a
A:Reference number: S45648; MUID:94307271; PMID:8033902
A:Accession: S45648
A:Molecule type: protein
A:Residues: 1-3; 4-7 <REI>
A:Experimental source: DSM 1030
C:Keywords: hydrolase

Query Match      18.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LP 9
        ||
DB      3 LP 4

RESULT 66
S15597
orf 4 rara 5'-region - human
C:Species: Homo sapiens (man)
C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
C:Accession: S15597
R:Brand, N.J.; Petkovich, M.; Chambon, P.
Nucleic Acids Res. 18, 6799-6806, 1990
A:Title: Characterization of a functional promoter for the human retinoic acid receptor-.
A:Reference number: S15594; MUID:91088249; PMID:2175878
A:Accession: S15597
A:Molecule type: DNA
A:Residues: 1-7 <BRA>
A:Cross-references: EMBL:X56058; NID:935876
A:Note: This ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0
C:Comment: This sequence is not thought to be translated.
C:Genetics:
A:Gene: GDB:RARA
A:Cross-references: GDB:120337; OMIM:180240
A:Map position: 17q12-17q12

Query Match      18.2%; Score 2; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MP 2
        ||
DB      1 MP 2

RESULT 67
A61348
red pigment-concentrating hormone - northern shrimp
N:Alternate names: blanching hormone
C:Species: Pandalus borealis (northern shrimp)
C:Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: A61348; S07139
R:Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A:Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A:Reference number: A61348; MUID:72228738; PMID:5041363
A:Accession: A61348
A:Molecule type: protein
A:Residues: 1-8 <FER1>
R:Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A:Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus borealis
A:Reference number: S07139; MUID:75054965; PMID:4433569
A:Accession: S07139
A:Molecule type: protein
A:Residues: 'B'; 2-8 <FER2>
A:Note: The amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C:Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pi-
red pigment-containing cells.
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutami
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match      18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 NF 5
        ||
DB      3 NF 4

RESULT 68
A28004
adipokinetic hormone G - two-spotted cricket
N:Alternate names: AKH-G
C:Species: Gryllus bimaculatus (two-spotted cricket)
C:Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997
C:Accession: A28004

```

R;Gaede, G.; Rinehart, K.L.
 Biochem. Biophys. Res. Commun. 149, 908-914, 1987
 A;Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide
 A;Reference number: A28004; MUID:98106553; PMID:3426616
 A;Accession: A28004
 A;Molecule type: protein
 A;Residues: 1-8 <GAE>
 A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5
 ||
 Db 3 NF 4

RESULT 69
 S08995
 Hypertrehalosemic hormone I - oriental cockroach
 N;Alternate names: Pea-CAH-I
 C;Species: Blatta orientalis (oriental cockroach)
 C;Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
 C;Accession: S08995
 R;Gaede, G.; Rinehart, K.L.
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
 A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora
 entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
 A;Reference number: S08995; MUID:90253659; PMID:2340112
 A;Accession: S08995
 A;Molecule type: protein
 A;Residues: 1-8 <GAE>
 A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5
 ||
 Db 3 NF 4

RESULT 70
 S10596
 Adipokinetic hormone - pond skimmer
 C;Species: Libellula auripennis
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997
 C;Accession: S10596
 R;Gaede, G.
 Biol. Chem. Hoppe-Seyler 371, 475-483, 1990
 A;Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating ho
 A;Reference number: S10596; MUID:90359055; PMID:2390213
 A;Accession: S10596
 A;Molecule type: protein
 A;Residues: 1-8 <BIO>
 C;Comment: This peptide has both adipokinetic and hypertrehalosemic activities.
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Qy 4 NF 5
 ||
 Db 3 NF 4

RESULT 71
 A49823
 Adipokinetic hormone I - American cockroach
 N;Alternate names: Periplaneta americana CO-1
 C;Species: Periplaneta americana (American cockroach)
 C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
 C;Accession: A49823
 R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.
 Proc. Natl. Acad. Sci. U.S.A. 91, 5575-5579, 1994
 A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp
 A;Reference number: A49823; MUID:84298179; PMID:6591205
 A;Accession: A49823
 A;Molecule type: protein
 A;Residues: 1-8 <SCA>
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5
 ||
 Db 3 NF 4

RESULT 72
 A44960
 Neuropeptide Led-CC-I - Colorado potato beetle
 C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: A44960
 R;Gaede, G.; Kellner, R.
 Peptides 10, 1287-1289, 1989
 A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and
 A;Reference number: A44960; MUID:90160053; PMID:2576128
 A;Accession: A44960
 A;Molecule type: protein
 A;Residues: 1-8 <GAE>
 C;Superfamily: adipokinetic hormone
 C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5
 ||
 Db 3 NF 4

RESULT 73
 A43976
 Hypertrehalosemic hormone - yellow mealworm
 C;Species: Tenebrio molitor (yellow mealworm)
 C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999
 C;Accession: A43976
 R;Gaede, G.; Rosinski, G.
 Peptides 11, 455-459, 1990
 A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid be
 A;Reference number: A43976; MUID:90341081; PMID:2381871
 A;Accession: A43976

A:Molecule type: protein
A:Residues: 1-8 <GAE>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
||
DB 3 NF 4

RESULT 74
B43976
hypertrehalosemic hormone - beetle (Zophobas rugipes)
C:Species: Zophobas rugipes
C:Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999
C:Accession: B43976
R:Gaede, G.; Rozinski, G.
Peptides 11; 485-459, 1990
A:Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle
A:Reference number: A43976; PMID:90341031; PMID:2381871
A:Accession: B43976
A:Molecule type: protein
A:Residues: 1-8 <GAE>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
||
DB 3 NF 4

RESULT 75
S55310
adipokinetic hormone - damselfly (Pseudagrion inconspicuum)
N:Alternate names: Psi-AKH
C:Species: Pseudagrion inconspicuum
C:Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C:Accession: S55310
R:Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A:Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum
A:Reference number: S55310; PMID:94379987; PMID:8093008
A:Accession: S55310
A:Molecule type: protein
A:Residues: 1-8 <JAN>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
||
DB 3 NF 4

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 5.32447 Seconds
(without alignments)
97.154 Million cell updates/sec

Title: US-09-641-801-6
Perfect score: 11
Sequence: 1 MPONFYKLPQM 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	27.3	9	1	BUK_CLOPA
2	3	27.3	11	1	CXLI_CONMR
3	3	27.3	13	1	CXLI_CONMR
4	3	27.3	15	1	GTS_ASADI
5	3	27.3	15	1	MCA2_RHOOP
6	3	27.3	15	1	SODM_ENTAE
7	3	27.3	18	1	A2M_OCTVU
8	3	27.3	18	1	LUXB_KRYAS
9	3	27.3	20	1	CATA_ACTRA
10	3	27.3	20	1	FIBB_SHEEP
11	3	27.3	20	1	MI17_BOVIN
12	2	18.2	4	1	FYRI_ATEL
13	2	18.2	5	1	PRCT_PERAM
14	2	18.2	6	1	FARP_MONEX
15	2	18.2	6	1	QVM_FEDDE
16	2	18.2	6	1	TRPI_PSEPU
17	2	18.2	7	1	CARP_MTED
18	2	18.2	7	1	FARI_MACRS
19	2	18.2	7	1	FARI_PROCL
20	2	18.2	7	1	FARI_PANRE
21	2	18.2	7	1	FARB_CALVO
22	2	18.2	7	1	HY7_PIG
23	2	18.2	7	1	IGAO_DACDE
24	2	18.2	7	1	UNO6_PINPS
25	2	18.2	7	1	WMA2_ACHFU
26	2	18.2	7	1	AKHG_GRYBI
27	2	18.2	8	1	AKH_LIBAU
28	2	18.2	8	1	ALL1_CYPDO
29	2	18.2	8	1	ALL1_CYPDO
30	2	18.2	8	1	ALL6_CYPDO
31	2	18.2	8	1	COM2_CONPU
32	2	18.2	8	1	COAG_RAT
33	2	18.2	8	1	FARI_PANRE

34	2	18.2	8	1	FARI_PENMO
35	2	18.2	8	1	FAR2_MACRS
36	2	18.2	8	1	FAR3_HOMAM
37	2	18.2	8	1	FAR4_HOMAM
38	2	18.2	8	1	HTF1_PERAM
39	2	18.2	8	1	HTF1_TENMO
40	2	18.2	8	1	LCK3_LEUMA
41	2	18.2	8	1	NPB_BOVIN
42	2	18.2	8	1	RPCH_PANBO
43	2	18.2	8	1	UPAA_HUMAN
44	2	18.2	9	1	AL10_CARMA
45	2	18.2	9	1	FARI_CALVO
46	2	18.2	9	1	FAR2_PANRE
47	2	18.2	9	1	FAR3_MACRS
48	2	18.2	9	1	FAR3_PENMO
49	2	18.2	9	1	FAR8_MACRS
50	2	18.2	9	1	OXYT_CYPCA
51	2	18.2	9	1	OXYT_RABIT
52	2	18.2	9	1	OXYT_RAJCL
53	2	18.2	9	1	OXYV_SQUAC
54	2	18.2	9	1	RS10_SERMA
55	2	18.2	9	1	TKCI_CALVO
56	2	18.2	9	1	TKLI_LOCOMI
57	2	18.2	10	1	ANG1_BOTVA
58	2	18.2	10	1	BPP2_BOTIN
59	2	18.2	10	1	BPP2_BOTIN
60	2	18.2	10	1	CATE_SHEEP
61	2	18.2	10	1	COXK_ONCMY
62	2	18.2	10	1	FAR6_PANRE
63	2	18.2	10	1	FAR7_MACRS
64	2	18.2	10	1	FAR7_MACRS
65	2	18.2	10	1	GON3_ONCKE
66	2	18.2	10	1	GONL_SQUAC
67	2	18.2	10	1	HTF1_ROMMI
68	2	18.2	10	1	HTF1_NAUCI
69	2	18.2	10	1	MOSQ_CLYJA
70	2	18.2	10	1	PNEU_HUMAN
71	2	18.2	10	1	PNEU_RAT
72	2	18.2	10	1	RL16_ACHLA
73	2	18.2	10	1	TEMK_PANTE
74	2	18.2	10	1	TKL2_LOCOMI
75	2	18.2	10	1	TKL3_LOCOMI
76	2	18.2	10	1	TKN1_SCYCA
77	2	18.2	10	1	TKNE_RANCA
78	2	18.2	10	1	TKNE_RANRI
79	2	18.2	10	1	TKN1_FHYBI
80	2	18.2	10	1	TKSI_ABDAA
81	2	18.2	10	1	TKS2_ABDAA
82	2	18.2	10	1	URA7_HUMAN
83	2	18.2	10	1	UXA6_CHLTR
84	2	18.2	10	1	VEG6_BACSU
85	2	18.2	11	1	BPP3_BOTIN
86	2	18.2	11	1	BPP4_BOTIN
87	2	18.2	11	1	BPPB_AKSHA
88	2	18.2	11	1	CEPI_ACHFU
89	2	18.2	11	1	EGG_CLOPA
90	2	18.2	11	1	LPW_THSTH
91	2	18.2	11	1	MHI_KLEPN
92	2	18.2	11	1	NXSN_PSETE
93	2	18.2	11	1	RANC_RANPI
94	2	18.2	11	1	TZPI_PROVU
95	2	18.2	11	1	TIN4_HOPTI
96	2	18.2	11	1	TKN1_UPEIN
97	2	18.2	11	1	TKN2_UPERU
98	2	18.2	11	1	TKN2_UPERU
99	2	18.2	11	1	TKNA_CHICK
100	2	18.2	11	1	TKNA_CHICK

ALIGNMENTS

RESULT 1

BUK_CLOPA
ID - BUK_CLOPA STANDARD; PRT; 9 AA.
AC P81337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).
GN BUK.
OS Clostridium pasteurianum
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RA MEDLINE=98291870; PubMed=9629918;
RA Flengrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl
phosphate to butyrate (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.
CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the acetate kinase family.
DR HAMAP, MF_00542; ; 1
DR InterPro, IPR000890; Acetate kin.
DR PROSITE; PS01075; ACETATE KINASE_1; PARTIAL.
DR PROSITE; PS01076; ACETATE KINASE_2; PARTIAL.
KW Transferase; Kinase.
FT NON TER 9
FT SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match 27.3%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
DB 2 YKL 4

RESULT 2
CXLI_CONNR STANDARD; PRT; 11 AA.
AC P58807;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda-conotoxin CMrVIA.
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=42752;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RA Seow K.T., Bay B.-H.;
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
pattern and protein folding. Isolation and characterization from the
venom of Conus marmoreus.";
RL J. Biol. Chem. 275:39516-39522(2000).
CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1237.93; MW ERR=0.21; METHOD=Electrospray.
CC -!- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.
KW Neurotoxin; Toxin; Hydroxylation.
FT DISULFID 2 11

FT DISULFID 3 8
FT MOD_RES 10 10 HYDROXYLATION.
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;
Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 6.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
DB 5 YKL 7

RESULT 3
CXLI4_CONNR STANDARD; PRT; 13 AA.
ID AC P58810;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda/chi-conotoxin MrIB (Chi-MrIB).
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=42752;
RN [1]
RP SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=21419681; PubMed=11528421;
RA Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
RA Atkins A., Falant E., Craik D.J., Adams D.J., Alewood P.F.,
RA Lewis R.J.;
RT "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
noradrenaline transporter.";
RL Nat. Neurosci. 4:902-907(2001).
CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- PTM: Exists in two forms, due to cis-trans isomerization at His-
11-Hyp-12.
CC -!- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.
CC -!- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.
DR PDB; 1IEO; 03-APR-02.
KW Neurotoxin; Toxin; Hydroxylation; 3D-structure.
FT DISULFID 4 13
FT DISULFID 5 10
FT MOD_RES 12 12 HYDROXYLATION
SQ SEQUENCE 13 AA; 1382 MW; 277AAC376EAD2B58 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 7.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
DB 7 YKL 9

RESULT 4
GTS_ASADI STANDARD; PRT; 15 AA.
ID AC P83246;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucathione S-transferase (EC 2.5.1.18) (GST class-sigma) (adGST)
(Fragment).
OS Asaphis dichotoma.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Tellinoidea; Psammobiidae; Asaphis.
OX NCBI_TaxID=184428;
RN [1]

RP SEQUENCE, FUNCTION, SUBUNIT, MASS SPECTROMETRY, AND CIRCULAR DICHROISM
RP ANALYSIS.

RC TISSUE=Intestine, and Liver;
RX MEDLINE=22135252; PubMed=12139969;
RA Yang H.-L., Nie L.-J., Zhu S.-G., Zhou X.-W.;
RT "Purification and characterization of a novel glutathione S-
arch. Biochem. Biophys. 403:202-208(2002).
RL Arch. Biochem. Biophys. 403:202-208(2002).
CC -!- FUNCTION: Has a strong specific activity toward 1-chloro-2,4-
dinitrobenzene and etharynic acid.
CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -!- SUBUNIT: Homodimer.
CC -!- MASS SPECTROMETRY: MW=23138; METHOD=MALDI.
CC -!- MISCELLANEOUS: In A. dichotoma there are at least two isozymes of
glutathione S-transferase.
CC -!- MISCELLANEOUS: Optimal pH is 8.5 with 1-chloro-2,4-dinitrobenzene
as the substrate.
CC -!- MISCELLANEOUS: The Km for 1-chloro-2,4-dinitrobenzene and
glutathione are 0.68 +/-0.05 and 0.106 +/-0.005 mM, and the Vmax
is 0.1446 +/-0.0072 and 0.033 +/-0.002 mmol/min x mg enzyme,
respectively.
CC -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. SIGMA FAMILY.
DR GO; GO:0004364; F:Glutathione transferase activity; NAS.
DR GO; GO:0006803; P:Glutathione conjugation reaction; NAS.
KW Transferase.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1767 MW; CB3E4BF92D3CB09 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.9e-02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
DB 3 YKL 5

RESULT 5

MC2 RHOP
ID MCA2 RHOP STANDARD; PRT; 15 AA.
AC P56870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Purative maleylacetate reductase II (EC 1.3.1.32) (Fragment).
OS Rhodococcus opacus (Nocardia opaca).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=37919;
RN [1]
RP SEQUENCE.
RC STRAIN=ICP;
RX MEDLINE=98324954; PubMed=9657989;
RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
RT "Characterization of a maleylacetate reductase encoding region from
Rhodococcus opacus ICP.";
RL J. Bacteriol. 180:3503-3508(1998).
CC -!- CATALYTIC ACTIVITY: 3-oxoadipate + NAD(P) (+) = 2-maleylacetate +
NAD(P)H.
CC -!- PATHWAY: 3-chlorocatechol degradation (beta-ketoadipate pathway).
CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
PRODUCTS AND AS INDUSTRIAL EFFLUENT.
CC -!- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE
FAMILY.
CC InterPro; IPR001670; Fe-ADH.
DR PROSITE; PS00913; ADH_IRON_1; PARTIAL.
DR PROSITE; PS00060; ADH_IRON_2; PARTIAL.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD038F025E CRC64;

Query Match 27.3%; Score 3; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.9e-02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
DB 8 LPQ 10

RESULT 6

SODM ENTAE
ID SODM ENTAE STANDARD; PRT; 15 AA.
AC P22739;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
GN SODA.
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RP SEQUENCE.
RX MEDLINE=91248479; PubMed=1368658;
RA Kim S.W., Lee S.O., Lee T.H.;
RT "Purification and characterization of superoxide dismutase from
RT Aerobacter aerogenes.";
RL Agric. Biol. Chem. 55:101-108(1991).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: IRON.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.
DR PIR; P0615; P0615.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Iron.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1756 MW; 352F3D94920B642 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.9e-02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
DB 4 LPQ 6

RESULT 7

A2M OCTVU
ID A2M OCTVU STANDARD; PRT; 18 AA.
AC P30800;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-2-macroglobulin homolog (Alpha-2-M) (Fragment).
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=6645;
RN [1]
RP SEQUENCE.
RX MEDLINE=92344633; PubMed=1379044;
RA Thøgersen I.B., Salvesen G., Brucato P.H., Pizzo S.V., Enghild J.J.;
RT "Purification and characterization of an alpha-macroglobulin
RT proteinase inhibitor from the mollusc Octopus vulgaris.";
RL Biochem. J. 285:521-527(1992).
CC -!- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A
UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH,

CC CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES
 CC FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT
 CC REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH
 CC TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST
 CC LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR
 CC WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE
 CC BAIT REGION A THIOLESTER BOND IS HYDROLYZED AND MEDIATES THE
 CC COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
 CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
 CC PIR: S23971; S23971.
 CC DR GO: G0:0016975; F1:alpha-2 macroglobulin; NAS.
 CC DR InterPro: IPR001599; MacroglblnA2.
 CC DR Pfam: PF00207; A2M; 1.
 CC DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
 CC KW Serine protease inhibitor; Glycoprotein; Plasma; Bait region;
 CC Thioester bond.
 CC KW NON TER 1 1 Isoglutamyl cysteine thioester (Cys-Gln).
 CC FT CROSSLNK 5 8
 CC FT NON TER 18 18
 CC SEQUENCE 18 AA; 2011 MW; D8D61C473D901C9D CRC64;
 CC
 CC Query Match 27.3%; Score 3; DB 1; Length 18;
 CC Best Local Similarity 100.0%; Pred. No. 1e+03; 0; Indels 0; Gaps 0;
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 4 NPY 6
 CC DB 12 NPY 14
 CC
 CC RESULT 8
 CC LUXB KYAS STANDARD; PRT; 18 AA.
 CC ID LUXB KYAS
 CC AC P18360;
 CC DT 01-NOV-1990 (Rel. 16; Created)
 CC DT 01-NOV-1990 (Rel. 16; Last sequence update)
 CC DT 15-DEC-1998 (Rel. 37; Last annotation update)
 CC DE Alkanal monooxygenase beta chain (EC 1.14.14.3) (Bacterial luciferase
 CC beta chain) (Fragment).
 CC GN LUXB
 CC OS Kryptophanon alfredi symbiont.
 CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 CC OC Vibrionaceae; light emitting symbionts of fish.
 CC OX NCBI_TaxID=28177;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=91076680; PubMed=2256783;
 CC RA Haygood M.G.;
 CC RT "Relationship of the luminous bacterial symbiont of the Caribbean
 CC flashlight fish, *Kryptophanon alfredi* (family Anomalopidae) to
 CC other luminous bacteria based on bacterial luciferase (luxA) genes.";
 CC RL Arch. Microbiol. 154:496-503(1990).
 CC CC -!- FUNCTION: LIGHT-EMITTING REACTION IN LUMINOUS BACTERIA. THE
 CC SPECIFIC ROLE OF THE BETA SUBUNIT IS UNKNOWN, BUT IT IS ABSOLUTELY
 CC REQUIRED FOR BIOLUMINESCENCE ACTIVITY.
 CC -!- CATALYTIC ACTIVITY: RCHO + FMNH(2) + O(2) = RCOOH + FMN + H(2)O +
 CC light
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
 CC
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 CC -----
 CC EMBL: M36597; AAA91214.1; ..
 CC DR InterPro: IPR002103; Bac luciferase.
 CC DR PROSITE: PS00494; BACTERIAL LUCIFERASE; PARTIAL.
 CC KW Photoprotein; Luminescence; Oxidoreductase; Monooxygenase;

KW Flavoprotein; FMN.
 FT NON TER 18 18
 SQ SEQUENCE 18 AA; 2153 MW; 8CB3B6955CCB2E7A CRC64;
 CC
 CC Query Match 27.3%; Score 3; DB 1; Length 18;
 CC Best Local Similarity 100.0%; Pred. No. 1e+03; 0; Indels 0; Gaps 0;
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 3 QNF 5
 CC DB 8 QNF 10
 CC
 CC RESULT 9
 CC CATA ACIRA STANDARD; PRT; 20 AA.
 CC ID CATA ACIRA
 CC AC P81422;
 CC DT 15-DEC-1998 (Rel. 37; Created)
 CC DT 15-DEC-1998 (Rel. 37; Last sequence update)
 CC DT 15-JUL-1999 (Rel. 38; Last annotation update)
 CC DE Catechol 1,2-dioxygenase (EC 1.13.11.1) (Fragment).
 CC OS Acinetobacter radioreisistens.
 CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC OC Moraxellaceae; Acinetobacter.
 CC OX NCBI_TaxID=40216;
 CC RN [1]
 CC RP SEQUENCE
 CC RX MEDLINE=98034166; PubMed=9369233;
 CC RA Briganti F., Pessione E., Giunta C., Scozzafava A.;
 CC RT "Purification, biochemical properties and substrate specificity of a
 CC catechol 1,2-dioxygenase from a phenol degrading Acinetobacter
 CC radioreisistens.";
 CC RL FEBS Lett. 416:61-64(1997).
 CC CC -!- CATALYTIC ACTIVITY: Catechol + O(2) = cis,cis-muconate.
 CC -!- COPACTOR: FERRIC ION.
 CC -!- PATHWAY: FIRST STEP IN THE DEGRADATION OF CATECHOL TO SUCCINATE
 CC AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.
 CC -!- SUBUNIT: HOMODIMER WHICH DISSOCIATES INTO ACTIVE MONOMERIC
 CC SUBUNITS AT HIGH IONIC STRENGTHS.
 CC -!- SIMILARITY: BELONGS TO THE INTRADIOL RING-CLEAVAGE DIOXYGENASE
 CC FAMILY.
 CC DR InterPro: IPR00627; Dioxygenase.
 CC DR PROSITE: PS00083; INTRADIOL DIOXYGENAS; PARTIAL.
 CC KW Aromatic hydrocarbons catabolism; Oxidoreductase; Dioxygenase; Iron.
 CC FT NON TER 20 20
 CC SEQUENCE 20 AA; 2279 MW; 70E8A5038F602327 CRC64;
 CC
 CC Query Match 27.3%; Score 3; DB 1; Length 20;
 CC Best Local Similarity 100.0%; Pred. No. 1.1e+03; 0; Indels 0; Gaps 0;
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 3 QNF 5
 CC DB 14 QNF 16
 CC
 CC RESULT 10
 CC FIBB SHEEP STANDARD; PRT; 20 AA.
 CC ID FIBB SHEEP
 CC AC P14470;
 CC DT 01-JAN-1990 (Rel. 13; Created)
 CC DT 01-JAN-1990 (Rel. 13; Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41; Last annotation update)
 CC DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
 CC GN FGB.
 CC OS Ovis aries (Sheep), and
 CC OS Capra hircus (Goat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Bovidae; Caprinae; Ovis.
 CC OX NCBI_TaxID=9940, 9925;
 CC RN [1]
 CC RP SEQUENCE.